
E v o l D i r

June 1, 2004

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

Forward

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

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

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Conferences

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Iceland EvolFishEthology Aug17-21

Ecological and Evolutionary Ethology of Fishes
Saudárkrókur NW-Iceland 17-21, August 2004

Second call

Information and registration at:
www.skagafjordur.com/eeef

Three main symposia are proposed:

1. Evolution and ecology of biological diversity in fishes

The main focus of this symposium is the growing recognition of ecological factors as primary forces in the generation and maintenance of biodiversity. Studies on fishes, often with focus on behaviour along with other attributes, have been particularly important in this area.

2. Ecological approaches to fisheries management and conservation

Ecosystem concerns, and awareness of human impacts on freshwater and marine resources has increased rapidly during the last decades. Today, responsible fisheries, aim at sustainable development of fish stocks both ecologically and socially. Contributions on all aspects relating to ecosystem conscious management are welcomed. Examples include the influence of behaviour and life history on population dynamics and harvesting potentials of fish stocks, how exploitation and global environmental changes may affect behaviour and life history, and sustainable aquaculture.

3. Evolutionary genetics and ecology of fishes

Evolutionary genetics and molecular ecology is becoming of major importance to fish ecology, evolution and

behaviour. This field is marked by recent important breakthroughs in studies of population structure, studies on the evolution of genetic isolation and speciation and in studies on genetic control and evolution of quantitative characters. Subjects covered in this session include ecological selection, identification of traits and mapping of genes that are under natural selection, rapid responses to environmental changes, and small-scale variation in ecological traits.

Contributions will consist of both oral and poster presentations. Proceedings from the meeting will be published by Kluwer, in the journal *Environmental Biology of Fishes*.

Program committee: Bjarni Jónsson Institute of Freshwater Fisheries Gudrún Marteinsdóttir Marine Research Institute / Univ. Iceland Skúli Skúlason Hólar University College Sigurdur S. Snorrason University of Iceland David L.G. Noakes University of Guelph

Registration and information

www.skagafjordur.com/eeef eeef@holar.is

bjarni@holar.is eik@holar.is

On the behalf of the organising committee

Bjarni Jónsson

Marseille EvolBiol Sep22-24

The next evolutionary biology meeting at Marseille will take place this year from September 22 to September 24. The early registration dead line is over. According to the first abstract submission, the program should 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), gene duplication and evolution, functional phylogenies, amphioxus genomics and biology, concept of evolution

You can submit and register on line on the meeting web site

<http://www.up.univ-mrs.fr/evol/congres/> The dead line is the 06/15/2004

pierre pontarotti <Pierre.Pontarotti@up.univ-mrs.fr>

PennState Genomes Jun17-20

Final Announcement

INTERNATIONAL MEETING Genomes and Evolution 2004 <http://www.outreach.psu.edu/C&I/-genomes/> Highlighting research at the interface of molecular biology and evolution

Location: The Pennsylvania State University University Park, Pennsylvania, USA

Dates: June 17-20, 2004

Plenary talks by: Leroy Hood, Walter Gehring, and John Avise

And international leaders in genomics and evolution speaking in nine diverse symposia: Early Evolution of Life Genome Evolution Molecular Phylogeny and Molecular Clocks Development and Evolution Genome Evolution in Primates Origins and Evolution of Genetic Systems Molecular Polymorphisms and Evolution Molecules and Biodiversity Adaptive Evolution

Annual Meeting of the Society for Molecular Biology and Evolution Annual Meeting of the American Genetic Association A special (low) rate for graduate students has been arranged. See the website (URL above) now for details

May 6th update: there are more than 500 registrants, but space is still available so register soon.

SandbjergDenmark EvolStress Aug22-26

First announcement:

Symposium:

“Progress in Environmental Stress, Adaptation and Evolution”

August 22-26, 2004 at Sandbjerg, Denmark

Sponsors:

European Society of Evolutionary Biology (ESEB)

Center for Environmental Stress Research, University of Aarhus (DK)

Aim:

Most organisms and populations have to cope with hostile environments, threatening their existence. Their ability to respond phenotypically and genetically to these challenges and to evolve adaptive mechanisms is, therefore, crucial. The aim of the symposium is to understand, from an evolutionary perspective, the impact of stress on biological systems. We have invited speakers that at different organizational levels, from genes to individuals and populations, explore how organisms adapt to (extreme) environments genetically and physiologically, how stress changes genetic structure and affects life histories and how environmental and genetic stress shape selection pressure and causes extinction of populations.

These issues have already been dealt with in a symposium on “stress and evolution” during the 5th International Congress of Evolutionary Biology and Systematics in Budapest (1966), and in the end resulted in a book edited by us “Environmental Stress, Adaptation and Evolution (1997)” published in the Birkhuser EXS series (EXS 83). It is now nearly ten years later and knowledge and (genomic) techniques in this research field have progressed rapidly. Therefore, we are thinking a follow-up to be timely and are organising this small, 3 day symposium on the same issues

Structure:

The number of participants will be limited to around 50, of which 15 are reserved for invited speakers (for list see below). There will be room for maximal 40 presentations of which 25 are open for contributed talks (25 min.). In conjunction with the symposium a special thematic issue of the Journal of Evolutionary Biology will be published on the topic that will contain high quality papers by the invited speakers. In addition, it will be possible for contributed papers to be included in this special issue of JEB. This will ensure that the papers get lots of exposure in this thematic setting. Papers for the special issue will be selected by the organisers of the symposium and the chief editor of JEB, Juha

Merila. Mind that all manuscripts, including those of the invited speakers, will not be treated favourably for this special issue. They are subject to normal, rigorous peer-review and scope limits of the journal: they have to address important evolutionary, and not purely functional, problems.

Participation:

Those that are interested in the symposium topic and want to participate and/or present a paper are kindly invited to contact the organisers from now on. Please do send your application to Corneel Vermeulen (c.j.vermeulen@biol.rug.nl) who will collect and structure applications (but for safety do send also a cc to both Volker Loeschcke (volker.loeschcke@biology.au.dk) and Kuke Bijlsma (r.bijlsma@biol.rug.nl)), preferably before the 1st of June. As we, in addition to the invited speakers, can only accommodate around 35 participants, the symposium might easily become over-booked. If this is the case the organisers will select participants and contributions that seem to fit that symposium and the special volume of JEB the best. Therefore it is important that tentative participants provide a few lines about their research interests, and if they want to present a contribution, please provide also a title and a substantial abstract (up to 200 words). Membership of ESEB is not prerequisite, but gives a discount of the conference fee and might give some priority.

Practical information:

Title: Progress in Environmental Stress, Adaptation and Evolution

Date: August 22-26, 2004

Organisers: Volker Loeschcke, Dept. of Ecology and Genetics, University of Aarhus (DK)

Kuke Bijlsma, Evolutionary Genetics, University of Groningen (NL)

Place: Sandbjerg Manor House, in the south of Jutland, Denmark. This is a conference centre of the University of Aarhus in a very nice and rural setting, easily reached by train and plane. For info see: www.sandbjerg.dk/en/.

Participants: maximal number approximately 50 (except for some invited speakers allotted to ESEB members).

Costs: The conference fee is Euro 450 for ESEB members Euro 550 for non-members. (Thus ESEB members get a discount of Euro 100, which is more than twice the yearly membership fee including the printed version of JEB and almost four times for online-only members. So it pays to become a member!). The conference fee

covers all costs including full board and lodging from Sunday evening August 22 to Thursday morning August 26.

Invited speakers that have accepted:

Jean R. David, CNRS, France

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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>

TiltonNH GordonTheoBiol Jun6-11

Gordon Research Conference on Theoretical Biology & Biomathematics June 6-11, 2004 Tilton School Tilton, NH <http://www.grc.uri.edu/programs/2004/-theobio.htm>

Apply and submit an abstract for a poster using the icon at the bottom of the webpage. Some support for students/postdocs may be available.

2004 GRC on Theoretical Biology & Biomathematics June 6-11, 2004 Tilton School Tilton, NH Chairs: Tim C Elston & Raymond Mejia Vice Chair: Paul C Bressloff

SUNDAY 2:00 pm - 9:00 pm Arrival and Check-in 6:00 pm Dinner 7:30 pm - 9:30 pm Motors and Biological Motion Discussion Leader: Ed Pate (Washington State University) Sean Sun (Johns Hopkins University) Roger Cooke (UC, San Francisco)

MONDAY 7:30 am - 8:30 am Breakfast 8:30 am Group Photo 9:00 am - 12:30 pm Spatial Components in the Modeling of Ecological Processes Discussion Leader: Graciela Canziani (Universidad del Centro, Tandil) Renato Casagrandi (Politecnico di Milano) Horst Malchow (Universität Osnabrück) Mike Neubert (Woods Hole Oceanographic Institute) 12:30 pm Lunch 6:00 pm Dinner 7:30 pm - 9:30 pm Innovations in Theoretical Immunology Discussion Leader: Ramit Mehr (Bar-Ilan University) Can Kesmir (Utrecht University) Nigel Burroughs (University of Warwick) 9:30 pm Poster Session

TUESDAY 7:30 am - 8:30 am Breakfast 9:00 am - 12:30 pm Neurobiology of Breathing, Whiskering and Electrolocation Discussion Leader: Paul Bressloff (University of Utah) Jeffrey Smith (NIH) Andre Longtin (University of Ottawa) Bard Ermentrout (University

of Pittsburgh) 12:30 pmLunch 6:00 pmDinner 7:30 pm - 9:30 pmEmergent Species/Diseases and Invasion Discussion Leader: Carlos Castillo-Chavez (Cornell University) Simon Levin (Princeton University) Sally Blower (UCLA) 9:30 pmPoster Session

WEDNESDAY 7:30 am - 8:30 amBreakfast 9:00 am - 12:30 pmSystems Biology Discussion Leader: James Liao(UCLA) Mark Goulian (University of Pennsylvania) Benno Schwikowski (Institute for Systems Biology) Isidore Rigoutsos (IBM Thomas J Watson Research Center) 12:30 pmLunch 6:00 pmDinner 7:30 pm - 9:30 pmModeling transcriptional control in gene regulatory networks Discussion Leader: Jeff Hasty (UCSD) John Reinitz (SUNY) Terry Hwa (UCSD) 9:30 pmPoster Session

THURSDAY 7:30 am - 8:30 amBreakfast 9:00 am - 12:30 pmBiofluids and Biological Gels Discussion Leader: Aaron Fogelson (University of Utah) Jim Keener (University of Utah) Robert Guy (University of Utah) Kasia Rejniak (Mathematical Biosciences Institute) 12:30 pmLunch 6:00 pmDinner 7:30 pm - 9:30 pmThe Future of Biomathematics and Theoretical Biology Discussion Leader: Alan Hastings(UC Davis) Lee Segel (Weizmann Institute of Science) Kim Cuddington (Ohio University) 9:30 pmPoster Session

FRIDAY 7:30 am - 8:30 amBreakfast 9:00 amDepart

<http://www.grc.uri.edu/programs/2004/theobio.htm>
Raymond Mejia <ray@helix.nih.gov>

ULublin Rodents Jul12-16

The 9th International Conference Rodens et Spatium on Rodent Biology will be held 12-16 July 2004 at the Catholic University of Lublin, Poland. Initiated in 1987 at Lyon, France, this biennial series focuses on the general biology of rodents relative to their environment, and includes: ethology, ecology, biogeography, taxonomy, evolutionary or conservation biology. Rodens & Spatium conferences typically attract 100-200 participants from 20-40 countries with a worldwide representation. The meeting is participant-friendly and open especially to young scientists from a broad variety of cultures and disciplines, united around a common organism: the rodent. The official language of the Conference is English. A friendly atmosphere, multi-cultural setting, modern topics and an affordable price are key features for the continuing success of the Rodens & Spatium Series during its almost 17 years of existence.

Deadlines: Final registration, abstract submission: 15 June 2004

For further information, and electronic registration forms: See the conference web site: www.ekolublin.pl/-rodens

Or contact:

Ewa Krywko

Catholic University of Lublin

Department of Zoology and Ecology

Al. Krasnicka 102

20-718 Lublin, Poland

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UToulouse OrchidSystematics

NEW PERSPECTIVES ON THE SYSTEMATICS & ECOLOGY OF ORCHIDS

18/20 November 2004

At the University of Toulouse <http://www.ladybio.ups-tlse.fr/Orchid-Symposium> Meeting Summary

Our knowledge of the Orchid family has recently undergone several significant advances.

Concerning systematics, the first morphological classification was produced by Swartz two centuries ago, and the latest by Dressler in 1993. Dressler's classification is one of the most comprehensive morphologically-based classifications to date. However, traditional morphologically based classifications rely heavily on characters, which are often few, if not unique, and can express considerable convergence due to ecological selection. The use of molecular markers and cladistics methods has produced a shift toward a more complex classification of Orchids. It provided strong cladistical support to 5 subfamilies Apostasioideae, Cypripedioideae, Vanilloideae, Orchidoideae and the Epidendroideae within the Orchidaceae, but leaves aside some unresolved relationships at lower levels.

To fulfil their life cycle, orchids use two kinds of symbionts, i.e. insects for pollination and fungi for hydro-mineral nutrition: in both cases, cheating strategies repeatedly arose during orchid evolution. Insect-orchid relationships have been well studied at the biochemical

and physiological level, and are believed to drive speciation in at least some cases. Non-rewarding orchids, either devoid of nectar or acting as mate mimicry, provide good models for the study evolution of mutualism. Underground association with fungi (mycorrhizae) are necessary for the development of orchids, especially at germination, when the fungus provides both mineral and carbon resources to the reserveless seedling. The latter strategy lasts up to adulthood in mycoheterotrophic, achlorophyllous species. Current research using molecular techniques has clarified fungal identity and specificity level in various associations, but the exact nature of the relationship with the fungi often remains unclear.

This meeting will highlight new developments on the phylogenetic classification, ecology and evolution of Orchids, as well as their implications in the field of biodiversity conservation.

Organised by Dr Laure Civeyrel, Dr. Marc-Andre

Selosse, Prof. Guy Durrieu and Dr Gerard Joseph.

Speakers include:

Mark Chase, Royal Botanical Gardens, Kew,

Mike Fay, Royal Botanical Gardens, Kew

Further information and registration details can be found on the website <http://www.ladybio.ups-tlse.fr/-Orchid-Symposium> Or contact Laure Civeyrel on npseo@cict.fr

Laure Civeyrel tel +33 (0)561 55 67 50 fax +33 (0)561 55 61 96 web <http://www.ladybio.ups-tlse.fr/Orchid-Symposium> Laboratoire Dynamique de la Biodiversité Université Paul Sabatier, IV R3 118 Route de Narbonne 31062 Toulouse cedex 4, France

Laure Civeyrel <civeyrel@cict.fr>

GradStudentPositions

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Cambridge Kew EvoDevo

Eco-Evo-Devo PhD studentship in Cambridge/Kew

PhD to be supervised by Dr Beverley Glover (University of Cambridge) in collaboration with Dr Paula Rudall and Dr Vincent Savolainen (Jodrell Laboratory, Royal Botanic Gardens, Kew). See details below.

IMPORTANT: To apply, please visit <http://www.plantsci.cam.ac.uk/plantsci/research/>

[phdstudentships/ highlighted.html](#) and follow strictly the application procedure. In addition, please also send your CV and a brief letter explaining the reasons for applying to the 'beetle-daisy' project via email to Dr Beverley Glover (bjg26@cam.ac.uk) by 10 June 2004.

Note that stipends are paid only to UK residents.

In search of the 'beetle identity gene' in the fly-pollinated beetle daisy *Gorteria diffusa* in southern Africa

Gorteria diffusa is a South African species of Asteraceae which is commonly named the 'beetle daisy' after

the beetle-like structures (raised dark spots) that are present at the bases of the large petals of some (1â3) of the ray florets (see attached figure). Pollination studies in South Africa have demonstrated that these 'beetle' structures are most likely mimics not of beetles but instead of small bee-flies, which are the actual pollinators of *Gorteria* (Johnson & Midley, 1997). Johnson & Midley's (1997) investigation also showed that the morphology of the dark spot is surprisingly complex, consisting of at least three different cell types. Such variation in cell types may well enhance the attractiveness of the corolla spot by dispersing light in different ways (Kay et al. 1981); the possibility that at least some of the cells are also scent-secreting (osmophores) cannot be excluded (Vogel 1990).

Our preliminary observations suggest that these cell types are differentiated late in floral development, shortly before anthesis, and are sometimes imperfectly formed or even aborted. Similar (but less complex) structures are also present in some related species, but usually on all florets. Dark spots in the centre of the flower are also a feature of several other families, including Papaveraceae (the poppy family) and Geraniaceae (the pelargonium family), presumably with a similar attractive function.

The evolution of adaptive petal cell morphology is potentially rewarding field for evo-devo studies. It is possible that a single gene might control the expression of these beetle-like structures in the ray florets of *Gorteria diffusa*. Timing of development of the ray florets, which are zygomorphic, relative to the central (distal) actinomorphic disk florets may be a factor in such expression (Gillies et al. 2002). In *Antirrhinum*, differentiation of specialised conical-papillate cells results from expression of the MIXTA gene late in petal development, although this is itself dependent on earlier expression of the B-function genes DEFICIENS and GLOBOSA (Glover and Martin 2002). Orthologs of MIXTA may therefore represent potential candidates for the 'beetle identity gene' in *Gorteria diffusa*.

The project will aim to:

1. Phylogeny and phylogeography - Study the evolution of the pollination 'beetle' clues in a phylogenetic framework by producing a broad molecular phylogenetic hypothesis for the tribe Arctotideae (especially *Berkheya*, *Cullumia*, *Heterorhachis*, *Didelta*, *Cuspidia*, *Gundelia*, *Gorteria*, *Hirpicium* and *Gazania*). A morphology-based phylogenetic trees of Arctotideae-Gorteriinae has been produced by Per Ola Karis from Stockholm University and a preliminary molecular-based phylogenetic is in press in *Taxon* (Funk et al.; ITS trnL-F; ndhF). As *Gorteria diffusa* also shows geographic variation

and potential differential pollination behaviour (current field study Jeremy Midgley and Steve Johnson), it is aimed to produce a phylogeographical study (e.g. AFLP DNA fingerprinting) to be compared with pollination data. Collaborators: Per Ola Karis (with Nigel Barker), Jeremy Midgley and Steve Johnson. 2. Carry out a detailed comparative investigation of the structure and ontogeny of both (a) the peculiar 'beetle' structures, building on previous work by Johnson and Midley (1997) and a pilot study done at Kew, and (b) 'normal' dark spots in ray florets of other Asteraceae. 3. Aim towards identifying the 'beetle identity gene' by identifying orthologous sequences of MIXTA (*Antirrhinum*) and PhMYB1 (*Petunia*) in *Gorteria* and perform micro RT PCR at critical developmental stages.

References Gillies ACM, Cubas P, Coen ES and Abbott RJ. 2002. Making rays in the Asteraceae: genetics and evolution of radiate versus discoid flower heads. Pages 233â246 in: *Developmental Genetics and Plant Evolution*. Eds. QCB Cronk, RM Bateman & JA Hawkins. Taylor & Francis, London. Glover BJ, and Martin C. 2002. Evolution of adaptive petal cell

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Cardiff Livestock Conservation Genetics

PhD Studentship Available in Livestock Conservation Genetics

A studentship is available from October 2004 to work on developing methods to detect admixture in populations using a combination of molecular markers and Bayesian genealogical simulation. The project is funded by Cardiff University, the Rare Breeds Survival Trust and the Dexter Cattle Society and will use the threatened Dexter cattle breed as a primary model for refining current methods for detecting admixture. The student would be based mostly in Cardiff, in the molecular ecology laboratory of Prof Bruford but would also be partly supervised by Dr Lounes Chikhi (Paul Sabatier University, Toulouse) and would spend periods in Toulouse extending and applying genealogical models. We are looking for applicants with a strong interest in conservation genetics, who are interested to combine molec-

ular work with theoretical development in this rapidly advancing field. Some recent publications in this area include: Chikhi et al (2004) *Heredity* 92: 396-401 (currently freely available from Heredity home page) ; Bruford et al (2003) *Nat Rev Genet* 4: 900-910 ; Chikhi et al (2001) 198: 1347-1362.

Please address informal enquiries to Prof M Bruford (BrufordMW@Cardiff.ac.uk). Application forms are available from <http://www.cf.ac.uk/biosi/research/postgrad/index.html>

MICHAEL

<michael.bruford@btopenworld.com>

BRUFORD

For further information, please contact Dr Jane Stout (stoutj@tcd.ie).

Please apply by sending a letter, outlining your suitability for the post, and your full curriculum vitae, containing the names and contact details (address, telephone, e-mail and fax) of three referees, to Dr Jane Stout (stoutj@tcd.ie).

Deadline for applications 30.06.04

————— Dr Jane C. Stout Broad Curriculum Lecturer Botany Department Trinity College University of Dublin Dublin 2 Ireland Tel: +353-1-6083761 (office) +353-87-7916422 (mobile) Fax: +353-1-6081147 Email: stoutj@tcd.ie

Dublin ExoticPlants

PhD Studentship: Impacts of exotic plants on native plant-pollinator mutualisms

Applications are invited for a 3 year PhD studentship, commencing October 2004, funded by Science Foundation Ireland (SFI). The project, under the supervision of Dr Jane Stout (Botany Department) and Dr Mark Brown (Zoology Department), will make a comprehensive study of the potential direct and indirect impacts of exotic *Rhododendron ponticum* on native ecosystems in Ireland. An inter-disciplinary integrated laboratory and field approach will be used to determine the positive and negative impacts that this alien species may have on native plants and pollinators.

The successful applicant will receive a studentship award of 15,000 per year, in addition to tuition fees (full fees are only available for students from EU countries).

Applicants must have (or expect to get) a first or upper second class Bachelors, or Masters, degree in a biological science (Biology, Ecology, Environmental Sciences or similar). Previous experience in carrying out biological field surveys of higher plants and insects, and of molecular techniques (DNA extraction, microsatellite analysis), would be advantageous but is not essential, and competence in statistical analysis is highly desirable. Candidates should be enthusiastic, highly motivated, competent in written and spoken English, and hold a full driving licence.

The position will be based in the Botany Department, at Trinity College, in the heart of Dublins city centre (www.tcd.ie).

Helsinki Dispersal theory

POST GRADUATE FELLOWSHIP IN MATHEMATICAL BIOLOGY IN HELSINKI, FINLAND

Statisticians / mathematicians / biologists with strong modeling background are invited to apply for a three-year post graduate fellowship, which is available from August 2004 onwards in the Metapopulation Research Group (www.helsinki.fi/science/metapop), Department of Biological and Environmental Sciences, University of Helsinki, Finland. Monthly salary is ca. 1800 EUR.

The PhD project is aimed at developing methods for analyzing mark-recapture data collected from heterogeneous landscapes. The project involves 1) development of dispersal models, 2) development of Bayesian methods for parameter estimation, and 3) applications to existing butterfly data sets.

The project stems from a dispersal model that we have developed earlier (Ovaskainen 2004; *Ecology* 85, 242-257). The model is based on a diffusion approximation of random walk including edge-mediated behavior, and it applies to heterogeneous landscapes. The PhD project is aimed at incorporating several biologically motivated extensions, including 1) co-variates such as environmental conditions, 2) variation between individuals, 3) linear landscape elements such as road-sides and brooks, 4) applications employing trapping data and radio-tracking data.

The project involves programming with C++, the knowledge of which is counted as an advantage.

Applications including a short CV and two letters of

reference should be submitted by 30 June 2004 to Dr. Otso Ovaskainen by email, otso.ovaskainen@helsinki.fi.

Further information: Otso Ovaskainen (otso.ovaskainen@helsinki.fi, phone +358 9 191 57924), Metapopulation Research Group, Department of Biological and Environmental Sciences, PO Box 65 (Viikinkaari 1), 00014 University of Helsinki, Finland.

ImperialKew EvolDiversity

PhD Position Available ? Oct 2004

Department of Biological Sciences Imperial College London

and the Royal Botanic Gardens, Kew

Speciation and the evolution of flowering plant or fungal diversity CASE studentship with the Royal Botanic Gardens, Kew

Why does life evolve into diverse species? What are the major causes of speciation? How do the environment and biological traits affect speciation rates? What are the adaptive causes and consequences of species diversity? This project will explore fundamental evolutionary questions on the evolution of diversity using a range of approaches applied to plant or fungal study groups. The exact project will be decided between the applicant and the supervisor ? more details on request. The project will provide broad training in evolutionary theory and analysis, molecular lab work and phylogenetics, experiments and fieldwork (UK and overseas), and will be based jointly at the Silwood Park campus of Imperial College London and at Kew.

For further details see <http://www.bio.ic.ac.uk/research/tgb/> or contact Tim Barraclough by email t.barraclough@imperial.ac.uk. **Please contact me straight away if interested**

— Dr. Timothy G. Barraclough, Imperial College London and Royal Botanic Gardens, Kew

— Department of Biological Sciences Imperial College London Silwood Park Campus Ascot, Berkshire SL5 7PY, UK Telephone: +44 (0)20 7594 2247 Fax: +44 (0)20 7594 2339 Web-page: www.bio.ic.ac.uk/research/tgb Tim Barraclough <t.barraclough@imperial.ac.uk>

— **New MSc course - Ecology, Evolution & Conser-

vation** www.imperial.ac.uk/bio/teaching/pg/msc/-eec Tim Barraclough <t.barraclough@imperial.ac.uk>

Stockholm PlantSyst

PhD Studentship in Plant Systematics at Stockholm University

Final date for application: June 30, 2004

Applications are invited for a PhD studentship (forskarutbildning) at the Department of Botany, Stockholm University, Sweden. The successful candidate will be working on molecular phylogenetics and floral evolution among first branching lineages of the Acanthaceae (Lamiales). The molecular part of the project is part of an international collaboration on the phylogeny of Acanthaceae. The studentship offers the possibility for training and research in molecular phylogenetics and morphological/anatomical methods. The project also entails field work in the tropics/subtropics. Requirements include a M.Sc. (Fil. Mag.) or an equivalent degree in plant biology, preferably in systematics; experience in either molecular (DNA sequencing) or morphological (microtome, SEM) techniques; potential/ability to write and publish in English; and a strong interest in phylogenetic methodology and evolutionary biology. Funding for the two first years will be covered by a faculty studentship (utbildningsbidrag, 13650 SEK/month) from Stockholm University. Upon satisfactory progress, the PhD-student can apply for a PhD-employment limited to three years, starting with a salary of 17900 SEK per month. The successful candidate is expected to work as a teaching assistant for up to 20% of the total PhD duration. Starting date is September 1, 2004, but is negotiable. Application will close on June 30, 2004. Candidates should send their Curriculum vitae, two letters of recommendation, attested copies of degrees and transcripts of academic records, a copy of their M.Sc. thesis or equivalent, and a short account (not more than two pages) on their research interest to the following address:

Ove Eriksson Tel.: +46 (0)8 16 12 04 Prof., Head of Department Fax: +46 (0)8 16 22 68 Department of Botany <<http://www.botan.su.se/>>www.botan.su.se Stockholm University <<mailto:ove.eriksson@botan.su.se>>ove.eriksson@botan.su.se Lilla Frescativägen 5 SE-106 91 Stockholm Sweden

For further information on the announced position and the research project contact:

Jürg Schönenberger Tel.: +46 (0)8 16 12 15
 Assist. Lecturer <<http://www.botan.su.se/>-
 >Fax: +46 (0)8 16 55 25 Department of Botany
 <<mailto:schonenberger@botan.su.se>>
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 Stockholm Sweden

TexasStateU Mollies

BEHAVIORAL ECOLOGY OF SAILFIN AND AMAZON MOLLIES

Research Assistantship for M. S.

Applications are being sought for one student interested in pursuing an academic career studying various aspects of the behavior (mate choice and sperm use) of sailfin and Amazon mollies starting summer/fall 2004. Amazon mollies, *Poecilia formosa*, are a unisexual (all female) fish species that are parasitic on the closely related bisexual sailfin molly, *P. latipinna*. Conflict exists between male sailfin mollies trying to mate with the right species, and the unisexual females trying to appropriate a mating from these males. Dr. Andrea Aspbury and I have funding for a masters research assistant to study aspects of this system. See <http://www.bio.txstate.edu/~gabor/gabor.htm> for details about my lab and my research interests and <http://www.bio.txstate.edu/~gabor/aspbury/aspbury.htm> to read about Dr. Aspbury's research interests.

The Department of Biology offers a strong environment in evolutionary ecology as the basis for training in behavioral ecology. Students will benefit from interactions with other faculty interested in evolutionary questions: Dr. Jim Ott (Insect-plant interactions and ecological genetics), Dr. Mike Forstner (Vertebrate systematics and population genetics), and Dr. Chris Nice (Specialization in insects and phylogeography).

Texas State University is committed to excellence in graduate training. The successful student will be responsible for performing research on specific aspects of the proposed study system. The stipend is \$12,000 / 12 months and includes health insurance and a waiver of out-of-state tuition fees (in-state tuition fees apply to all students and cannot be waived). The Research Assistantship is renewable for a second year at the same rate.

For information on applications see <http://www.gradcollege.txstate.edu/applicationproc.html>.

Please also see the Department of Biology for admission information (<http://www.bio.txstate.edu/>) and Texas State University (<http://www.bio.txstate.edu/amsu.txstate.edu/>) web sites for more information.

To apply for this position please send a letter of interest to Dr. Gabor (gabor@txstate.edu) & Dr. Aspbury (aspbury@txstate.edu) stating why you are interested in doing this work. Also send a CV/resume of related research, coursework, grades, GRE scores and any other relevant experience via email (preferably) or snail mail. We will respond as soon as we get this information and will consider candidates until a suitable one is found.

- ***** Caitlin R. Gabor, Ph. D. Assistant Professor Texas State University (Formerly SWT) Department of Biology, Science Building Room 384 San Marcos, TX 78666-4615 Work: (512) 245-3387; Fax: (512) 245-8713 E-mail: gabor@txstate.edu

<http://www.bio.txstate.edu/~gabor/gabor.htm> *****
 Caitlin Gabor <gabor@txstate.edu>

UGroningen SeychellesWarbler

PhD on parasites in the Seychelles warbler

Gastrointestinal parasites, MHC genes and fitness in a wild avian population

Within vertebrates, the major histocompatibility complex (MHC) genes within an individual determine how well it copes with the array of parasites it encounters in its environment. An individual's fitness (survival and reproductive success) will therefore, at least in part, depend upon the MHC genes it contains. Gastrointestinal parasites (GI) occur worldwide and can be extremely detrimental to the fitness of individuals. Few studies have assessed the impact of GI parasites from an evolutionary perspective, and even fewer have taken into account the affect of the MHC. None have done so using birds. This project will investigate the affect of GI parasites and their interaction with the MHC in the simple and isolated system provided by the Cousin Island population of Seychelles warbler (*Acrocephalus sechellensis*). PCR-based molecular protocols will be used to screen MHC, while microscopic investigation of eggs within faecal samples will provide a non-invasive method for determining the intensity of GI parasites within individuals. Fieldwork to continue the population monitoring and the collection of samples and fitness data will be done in conjunction with the

Seychelles warbler research project team. The results will contribute towards determining the importance of MHC variation and parasite-mediated selection in wild animal populations.

Dr David S. Richardson and Prof. Jan Komdeur: Jointly funded by UEA and JK (University of Groningen, Holland) for three years starting January 2005.

Further details

We are looking for an enthusiastic, dedicated and resilient student with an interest in evolutionary and molecular ecology. The student will spend a large part of their time in the laboratory, isolating parasite eggs from faeces, extracting DNA and using basic molecular techniques such as PCR and DGGE. Therefore, although not essential, molecular lab experience will be an advantage, as will good organisational skills. Fieldwork will be for 2-3 months per year and, as the field site is small and isolated, the student must be able to work well independently, or within a small group. The studentship will be based at UEA with D. S. Richardson, but will visit Groningen each year.

This PhD is being re-advertised as the start date has now been delayed until January 2005. Previous applicants do not need to reapply. Although there is no official deadline please apply ASAP. We expect to interview candidates in early September

Please send the completed UEA application form, two references (completed reference forms) ASAP. Both forms and application details are available at <http://www.uea.ac.uk/bio/studentships/welcome.html> When complete, please sign, date and return the form with all the necessary documentation to:

Graduate Studies Office

Science Group

University of East Anglia

phone +44 (0)1603 593002

Fax (0)1603 593045

Email scipg@uea.ac.uk

Norwich NR4 7TJ UK

Web site <http://www.uea.ac.uk> For informal enquiries contact

Dr. David S. Richardson

Telephone 01603 591496

email david.richardson@uea.ac.uk

FAX 01603 592250

Dr. David S. Richardson School of Biological Sciences,

University of East Anglia, Norwich NR4 7TJ England

Telephone 01603 591496 email

david.richardson@uea.ac.uk FAX 01603 592250

ULondon KinSelection

PhD Studentship: WHY SUBJECT YOUR KIN TO COMPETITION? – A COMPARATIVE STUDY OF KIN SELECTION IN TWO IMPORTANT PEST SPECIES

Supervisors: Drs Peter Credland and Robert J.H. Payne School of Biological Sciences, Royal Holloway college, University of London Application deadline 11th June 2004.

Applicants must have 1st or upper 2nd class degree or equivalent, which should be in either biology or in any numerate discipline (mathematics, physics etc). Only open to UK citizens or those resident in UK for past three years. The project will combine laboratory investigation and modelling of the costs and benefits of aspects of beetle egg-laying behaviour. The project will train the student in experimental design, insect culture and handling techniques, data collection and statistical analysis. Students with the relevant background may also learn how to develop and analysis relevant mathematical models.

BACKGROUND AND RATIONALE. Seed beetles (Bruchidae) are economically important pests of stored seeds in most tropical and temperate areas of the world. The egg-laying behaviour of the Bruchidae depends not only on the species type, but also on the size and type of host seed, and on local population density. Females of *Zabrotes subfasciatus* lay eggs in a notably more clumped and non-uniform manner than those of *Callosobruchus maculatus*. The degree to which females avoid already occupied seeds also varies, and appears to be mediated by pheromones on the eggs. Understanding such behavioural differences between species will be an important aid in predicting the ecological responses of the beetles to possible future changes in environment, seed storage methods, or biocontrol practices. On a practical level, knowledge of individual-level behaviour is useful because it can be used to construct population-level models of population ecology. This can be key in designing biocontrol measures, which often lead to unforeseen consequences, particularly when target organisms display contingent behaviours. On a more purely scientific level, comparison of these two species will al-

low an investigation of fundamental ideas concerning cooperation and conflict between related individuals, and of parent-offspring conflict.

OBJECTIVES AND METHODS. This project will develop understanding of the interaction between kin selection and kin competition in two economically important species that infest stored seed. The starting point will be to seek to explain why females of the Mexican bean weevil *Zabrotes subfasciatus* lay their eggs in clumped groups on only a small proportion of available seeds, whereas females of *Callosobruchus maculatus* generally avoid laying eggs on seeds that already bear other eggs. A number of different costs and benefits will need to be examined. On one hand it is costly to females to spend time checking the status of potential host seeds, but on the other hand it is costly to larvae to have to compete with other larvae for occupation of a seed. How then do we reconcile the interests and relative costs to the parent and its offspring? The project will examine how these costs differ between species, and how they vary depending on the type and size of host seed. It is expected that larval competitiveness should be greater where host seeds are smaller, where population density is higher, where the amount of limiting resource is lower, and where relatedness between co-residents is lower. Can we use this to explain why *Z. subfasciatus* lays its eggs in clumps? Could it be because larvae of *Z. subfasciatus* are more related than those of *C. maculatus*? Could it perhaps be a form of anti-parasite behaviour, analogous to anti-predator flocking in birds? Do egg-laying patterns determine levels of larval competitiveness, or vice versa?

The deadline for applications is 11th June 2004. Please use the appropriate form downloadable from: <http://www.rhul.ac.uk/studying/Graduate-School/>. Please send completed forms, plus statements from two referees by post to Dr Peter Credland, School of Biological Sciences, Royal Holloway, University of London, Egham, Surrey, TW20 OEX, UK. Initial enquiries to Peter Credland by email <P.Credland@rhul.ac.uk>

UStAndrews FlySong

The evolutionary genetics of song in flies; from QTL to candidate gene.

A NERC PhD studentship is available at the University of St Andrews for a joint project between the laboratories of Prof. M. G. Ritchie (St Andrews) and Dr

Stephen Goodwin (University of Glasgow). The aims of the project are to combine an evolutionary approach to the evolution of song differences amongst species of *Drosophila* with molecular and neurogenetic approaches to behaviour genetics. Quantitative Trait Loci approaches have identified chromosomal regions implicated in the evolution of species-specific song traits important to speciation. Candidate genes previously known to influence song are implicated in some of these regions. The student will assess the role of candidate genes directly using modern behaviour genetic techniques such as gene knockout or transfer between species and the molecular evolution of the genes will be analysed by sequence analysis. This project has the potential to provide breakthroughs in the understanding of the genetics of species differences in behaviour. Further details available by e-mailing mgr@st-and.ac.uk or s.goodwin@bio.gla.ac.uk

Formal application materials are available from: The Postgraduate Secretary, Jane Williamson, Gatty Marine Laboratory, University of St. Andrews, St. Andrews Fife KY16 8LB Scotland e-mail: pgbiology@st-and.ac.uk

Stephen F. Goodwin IBLs-Division of Molecular Genetics, 56 Dumbarton Road Anderson College, University of Glasgow, Glasgow G11 6NU, UK phone (+44) 141 330 2948 FAX (+44) 141 330 4878

e-mail: s.goodwin@bio.gla.ac.uk

Homepage & Research Group: <http://www.gla.ac.uk:443/ibls/staff/staff.php?who8435>

UStAndrews FlySongs

Sorry; this is only available to UK citizens.

The evolutionary genetics of song in flies; from QTL to candidate gene.

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important to speciation. Candidate genes previously known to influence song are implicated in some of these regions. The student will assess the role of candidate genes directly using modern behaviour genetic techniques such as gene knockout or transfer between species and the molecular evolution of the genes will be analysed by sequence analysis. This project has the potential to provide breakthroughs in the understanding of the genetics of species differences in behaviour. Further details available by e-mailing mgr@st-and.ac.uk or s.goodwin@bio.gla.ac.uk

Formal application materials are available from: The Postgraduate Secretary, Jane Williamson, Gatty Marine Laboratory, University of St. Andrews, St. Andrews Fife KY16 8LB Scotland e-mail: pgbiology@st-and.ac.uk

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

Research group website: <http://www.st-and.ac.uk/~bugs> Treasurer of the Association for the Study of Animal Behaviour ASAB information: <http://www.societies.ncl.ac.uk/asab/> ~~~~~

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## UVictoria Genomics

Graduate student positions. The Comparative Genomics Lab at the University of Victoria in British Columbia, Canada (<http://www.uvic.ca/>) invites applications for two graduate student positions (MSc or PhD). Preferred starting date is September 2004. Project one involves the study of chemoreceptor gene family evolution using transgenic worms (*C. elegans*). Project two is a largely bioinformatics-based study of gene and genome duplication in fish. Molecular biology, fluorescence microscopy, and *C. elegans* experience will benefit applicants for the first position. Candidates for the second position should have some programming skills and have a demonstrated interest (experience and/or course work) in evolutionary or molecular biology. Resources include a fully equipped molecular biology wet lab, a microscopy dark room with new microscopes, a small Linux network/cluster, and a quiet programming/reading/paper-writing room. In Victoria, we enjoy the benefits of island isolation (clean air, no traffic, ocean and mountain views), while maintain-

ing close ties with national and international collaborators. A salary of \$17,000 and \$18,000 per year (minimum) is guaranteed to MSc and PhD students respectively. Generous top-ups are available to students with fellowships. The University of Victoria consistently ranks among the top four comprehensive universities in Canada.

Selected publications: Vandepoele et al. 2004. PNAS 101:1638-1643 Taylor et al. 2003 Genome Res 13:382-390 Van de Peer et al. 2001 J Mol Eol 53:434-444 Taylor et al. 2001 Philos Trans R Soc Lond B 356:1661-1679 Taylor et al. 1999 Mol Biol Evol 16:567-572

Please correspond by e-mail or send cover letter and CV to:

Dr. John S. Taylor Department of Biology University of Victoria PO Box 3020 Station CSC Victoria, BC, V8W 3N5 Canada

(<http://web.uvic.ca/biology/People/taylor/-taylor.htm>)

John Taylor <taylorjs@uvic.ca>

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## UWellington tuatara skins

Two PhD Scholarships School of Biological Sciences, Victoria University of Wellington, New Zealand

1: Field studies of behaviour and reproduction of tuatara (Reptilia: *Sphenodon punctatus*)

As part of multidisciplinary efforts to conserve tuatara populations in New Zealand, and to gather information on population biology, behavioural ecology and genetics, a PhD scholarship is available for work on the mating system, mate choice, ranging behaviour, and reproductive strategies of this unique reptile. Fieldwork will involve repeated stays (1-2 months in duration) on Stephens Island, Cook Strait. A dense tuatara population exists on the island, and there is a field research station, housing, and an excellent infrastructure to support the project, both in the field and at the University. Applications should be sent to Dr Nicola Nelson, School of Biological Sciences, Victoria University of Wellington, PO Box 600, Wellington, New Zealand (E-mail: Nicola.Nelson@vuw.ac.nz, Phone +64 4 463 7443, Fax: +64 4 463 5331) before 1 August 2004.

2: The evolution of New Zealand skinks

The aim of this project is to construct a complete phy-

logeny of the New Zealand skinks. The New Zealand skinks are an endemic group comprising two genera, *Oligosoma* and *Cyclodina*, and as many as 40 species. This group is thought to have radiated rapidly as a response to changes in the New Zealand landscape since the Oligocene. Mitochondrial and nuclear DNA sequences will be used to place the New Zealand skinks into the international 'Tree of Life' project. When a robust phylogenetic tree has been established, it will be used to test a series of hypotheses about the mode of skink evolution in New Zealand. For example, some cryptic species may have evolved as recently as the Holocene through isolation on offshore islands after the last glacial maximum. The methodology for this research project would involve identifying appropriate mitochondrial and nuclear DNA markers, DNA sequencing and phylogenetic analyses. The successful applicant would conduct their research in the School of Biological Sciences at Victoria University. The ideal student would have an interest in vertebrate evolution and molecular phylogenetics, and be able to develop the project with their own ideas and initiative. Applications should be sent to Dr Peter Ritchie, School of Biological Sciences, Victoria University of Wellington, PO Box 600, Wellington, New Zealand (E-mail: Peter.Ritchie@vuw.ac.nz, Phone +64 4 463 5233 extn 8105, Fax: +64 4 463 5331) before 1 August 2004.

The Candidates: PhD applicants must have been awarded the degree of B.Sc. (Hons) or M.Sc. (or equivalent) before taking up the scholarship. The stipend is NZ\$20,000 per annum for 3 years. There is an additional NZ\$4,000 per year to cover tuition fees. Australian, French and German students are exempt from international student fees. Applicants should send a cover letter stating briefly why they are interested in this project, a curriculum vitae, and the names, addresses and e-mail of 2 referees.

School of Biological Sciences at Victoria University: The successful applicants will join an active research team, as part of the Allan Wilson Centre for Molecular Ecology and Evolution (<http://awcmee.massey.ac.nz>), at the School of Biological Sciences, Victoria University of Wellington. The School of Biological Sciences conducts research and teaching across most biological disciplines. Our emphasis ranges in scale from the biochemical reactions that take place within cells to the ecological interactions of animals and plants with their environments. Further information about the staff and research in the School can be found at <http://www.sbs.vuw.ac.nz>. Victoria University is located on a hillside overlooking the picturesque harbour and the

commercial and government sectors. There is a wide range of shops and businesses, cafes, theatre, film, music and art activities, with an International Arts Festival every two years. Wellington is close to unspoiled outdoor areas for recreation such as walking, cycling, skiing, climbing and boating and has a temperate climate. More information about Wellington is available at: [www.wcc.govt.nz/wellington/](http://www.wcc.govt.nz/wellington/). Peter Ritchie <Peter.Ritchie@vuw.ac.nz>

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## UZurich SpermBiology

PhD position, Sperm biology

A PhD position is available in the Zoological Museum of the University of Zürich, Switzerland. The successful applicant will join a group working on the biology of sperm in the yellow dung fly. The research will be on the integration of evolutionary and physiological perspectives but the exact details will depend on the interests and background of the successful applicant. Applications will be particularly welcome from two research directions: a) candidates able to integrate biological data into mathematical models of sperm movement and transport, and b) candidates interested in the physiological or microanatomical processes of sperm transport and function in insects.

Applicants must have a Diploma or Master's degree. Good computing or quantitative biological skills are essential. A working knowledge of English is a necessary. Knowledge of German would also be advantageous. The position is available for three years and is available from July 1, 2004. For inquiries contact [pward@zoolmus.unizh.ch](mailto:pward@zoolmus.unizh.ch).

Please send a curriculum vitae, list of publications and summary of research interests, in a single file by e-mail to [zmdirektion@zoolmus.unizh.ch](mailto:zmdirektion@zoolmus.unizh.ch), by 21th June or Prof Ward, Universität Zürich, Zoologisches Museum, Winterthurerstr. 190, 8057 Zürich

– Prof Paul I Ward Direktor Zoologisches Museum der Universität Zürich Winterthurerstrasse 190 CH 8057 Zürich Switzerland Phone +41 1 635 4760 Fax +41 1 635 4780

Direktionssekretariat: Rosemarie Keller Mail: [kellerro@zoolmus.unizh.ch](mailto:kellerro@zoolmus.unizh.ch) Phone +41 1 635 4761

Paul Ward <[pward@zoolmus.unizh.ch](mailto:pward@zoolmus.unizh.ch)>



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## Jobs

|                                            |    |                                       |    |
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### BrownU DrosophilaPopGenet ResAssist

Research Assistant: Drosophila population genetics

A research assistant position is available to work on several projects in Drosophila population genetics in the laboratory of David Rand and Brown University. Two primary projects are 1) Analyses of Drosophila thermal tolerance and clinal variation of a thermal QTL, and 2) Fitness effects of nuclear-mtDNA interactions. Both projects involve molecular and quantitative genetic assays of Drosophila strains, genetic mapping experiments and some biochemical assays of specific genotypes. The goals of both projects are to identify specific genes and gene interactions that are associated with fitness in different 1) thermal or 2) cytoplasmic environments.

Applicants should have some combination of experience with modern molecular techniques, Drosophila culture, computer skills and an interest in ecology, evolution or genetics. To apply, please send a CV, a short statement of research interests and experience, and contact information for three references to:

David Rand Department of Ecology and Evolutionary Biology Box G-W, 69 Brown Street Brown University Providence, RI 02912 Voice: (401) 863-2890

(Office) (401) 863-1063 (Lab) Fax: (401) 863-2166  
email: David\_Rand@brown.edu web page: <http://www.brown.edu/Departments/EEB/rand/index.htm>  
The start date is flexible, but preferably before 15 July 2004.

The Department of Ecology and Evolution at Brown is an interactive group with strengths that span genomics, evolutionary genetics, ecology, behavior and functional morphology.

<http://www.brown.edu/Departments/EEB/> Providence is recognized as the Venice of New England and is wonderful place to live:

<http://www.providenceri.com/>

David Rand Department of Ecology and Evolutionary Biology Box G-W, 69 Brown Street Brown University Providence, RI 02912 Voice: (401) 863-2890 (Office) (401) 863-1063 (Lab) Fax: (401) 863-2166 email: David\_Rand@brown.edu web page: <http://www.brown.edu/Departments/EEB/rand/index.htm>

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### IowaStateU SummerVol

Hi, I am looking for volunteers for summer fieldwork.

Investigations of population genetics and hybridization impacts of turtles in a desert-spring ecosystem will be conducted. Meals, housing, and transportation (within US or Mexico) are provided. Dates are flexible May 15-July 30 (part or all). Please contact smcgaugh@iastate.edu. Thank you, Suzanne

Interdepartmental Genetics Iowa State University 339 Science II Ames, IA 50011 office: (515)-294-1703

Suzanne McGaugh <smcgaugh@iastate.edu>

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## Munich BehaviourEcol

Assistant professor position (C1) in behavioral ecology  
The position is available beginning from July 1st 2004 for 3 years (renewable for another 3 years) at the LM University in Munich, Department Biology II

Scientific field of interest should lay in behavioral ecology of either social insects or evolutionary processes such as coevolution or sexual selection. The successful candidate should have already established an excellent publication record in behavioral ecology and should be able to conduct independent research. The appointee will be able to set up its own research group. Excellent up-to-date facilities are found at the new High tech Campus in Munich / Großhadern, where the laboratory will be based. Teaching of basic and advanced classes in evolutionary ecology are required. Successful candidates must hold a Ph D and be no older than 35 years. Persons with disabilities are encouraged to apply.

Applications including CV, publication record, recommendations and scientific plans should be sent until

June 1st 2004

to

Prof. Dr. Susanne Foitzik currently from 1st of July 2004 Lehrstuhl für Biology 1 Abteilung Verhaltensökologie University of Regensburg Lehrstuhl für Ökologie 93040 Regensburg Department Biology II Germany University of Munich Großhadener Str. 2 81377 München Germany

or per e-mail to: Susanne.Foitzik@biologie.uni-regensburg.de

Ph D position on "Coevolution in slavemaking ants and their hosts"

The position is available beginning from July 1st 2004

for 1  $\frac{1}{2}$  years (renewable) at the LM University in Munich, Department Biology II, Behavioral Ecology group

Social parasites exploit similar to avian brood parasites the brood care behaviour of their host species and especially slavemaking ants such as *Protomognathus americanus* obligatory depend on their hosts throughout their life. This can lead to tight evolutionary interactions between slavemaking and host populations, the intensity of which depends on parasite pressure and the community structure. The coevolutionary dynamics between social parasites and their hosts are studied in this project on a North American model system in respect to behavioral adaptations, ecological impact and the population genetic background. The successful candidate should have a solid background in behavioral ecology and be interested to use a variety of approaches such as genetic, chemical, ecological and behavioural methods. Longer field stays in the US and Canada are required for this project. The laboratory is based at the new High tech Campus in Munich / Großhadern.

Applications including CV, Diplom or Master thesis and resulting publications and recommendations should be sent until

June 1st 2004

to Prof. Dr. Susanne Foitzik currently from 1st of July 2004 Lehrstuhl für Biology 1 Abteilung Verhaltensökologie University of Regensburg Lehrstuhl für Ökologie 93040 Regensburg Department Biology II Germany University of Munich Großhadener Str. 2 81377 München Germany

or per e-mail to: Susanne.Foitzik@biologie.uni-regensburg.de

Lab technician position (BAT VIb) in behavioral ecology

This permanent position is available beginning from July 1st 2004 at the LM University in Munich, Department Biology II, Behavioral Ecology group, which is based at the new High tech Campus in Munich / Großhadern

The scientific focus of this newly founded research group is on the evolution and behavioral ecology of social insects, in particular on the coevolutionary dynamics of slavemaking ants and their hosts, sexual selection and sex ratios. We utilize a variety of different methods from molecular biology (PCR and sequencing) to chemical ecology (gaschromatography) and behavioral observations. Experience in these methods are an advantage. Ecological field work, especially in the US is possible. An interest in scientific work is expected. The responsibilities also includes the laboratory organ-

isation and maintenance of ant colonies. Experience with computers and some knowledge of the English is expected.

Applications sent until June 1st 2004 to

Prof. Dr. Susanne Foitzik currently from 1st of July 2004 Lehrstuhl für Biology 1 Abteilung Verhaltensökologie University of Regensburg Lehrstuhl für Ökologie 93040 Regensburg Department Biology II Germany University of Munich Großhadener Str. 2 81377 München Germany

or per e-mail to: Susanne.Foitzik@biologie.uni-regensburg.de

Susanne Foitzik <susanne.foitzik@biologie.uni-regensburg.de>

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## TexasStateUniv Salamanders

### POPULATION GENETICS OF SAN MARCOS SALAMANDERS

Instructional Assistantship + Research Assistantship for M. S.

Applications are being sought for a student interested in pursuing an academic career studying the population genetics of San Marcos salamanders, *Eurycea nana*, starting summer/fall 2004. San Marcos salamanders are a threatened species that reside only in the headwaters of the San Marcos River, San Marcos, Texas. A population of these salamanders are being maintained at the San Marcos National Fish Hatchery and Technology Center for refugium purposes. Dr. Chris Nice, Dr. Caitlin Gabor and Joe Fries have funding for up to three summers (\$10000) as a Research Assistant plus some money for supplies (\$6000) to examine aspects of the population genetics of these salamanders. We can also provide an Instructional Assistantship for at least four semesters. See <http://www.bio.txstate.edu/~gabor/gabor.htm> for details about Dr. Gabor's lab and her research interests. See <http://www.bio.txstate.edu/~cnice/nice.html> for details about Dr. Nice's lab and his research interests.

The Department of Biology offers a strong environment in evolutionary ecology as the basis for training in population genetics. Students will benefit from interactions with other faculty interested in evolutionary questions: Dr. Jim Ott (Insect-plant interactions and ecological genetics) and Dr. Mike Forstner (Vertebrate systemat-

ics and population genetics). Soon we will also have a Masters program in Population Biology.

Texas State University is committed to excellence in graduate training. The successful student will be responsible for performing research on specific aspects of the proposed study system. The stipend for research assistants is \$9,000 / 9 months and includes health insurance (in-state tuition fees apply to all students and cannot be waived). The Instructional Assistantship and is renewable for a second year at the same rate.

GRE (verbal and quantitative) scores of 1000 for MS, and a GPA of 2.75 are minimum requirements in the Biology Masters degree program. For information on applications see <http://www.gradcollege.txstate.edu/applicationproc.html>. Please also see the Department of Biology for admission information (<http://www.bio.txstate.edu/>) and Texas State University (<http://www.bio.txstate.edu/> [www.txstate.edu/](http://www.txstate.edu/)) web sites for more information.

To apply for this position please send a letter of interest to Dr. Gabor ([gabor@txstate.edu](mailto:gabor@txstate.edu)) stating why you are interested in doing this work. Also send a CV/resume of related research, coursework, grades, and any other relevant experience to me via email (preferably) or regular mail. I will respond as soon as I get this information and will consider candidates until a suitable one is found.

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Caitlin R. Gabor, Ph. D. Assistant Professor Texas State University (Formerly SWT) Department of Biology, Science Building Room 384 San Marcos, TX 78666-4615 Work: (512) 245-3387; Fax: (512) 245-8713 E-mail: [gabor@txstate.edu](mailto:gabor@txstate.edu)

<http://www.bio.txstate.edu/~gabor/gabor.htm>

Caitlin Gabor <[gabor@txstate.edu](mailto:gabor@txstate.edu)>

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## Tucson DrosophilaStockCenter Curator

The Tucson Drosophila Stock Center will be seeking a manager-curator to begin in the winter of 2004-2005. The ideal candidate will have a Ph.D. in a biological science and knowledge of different Drosophila species, strong communication skills, supervisory experience that will enable oversight of the stock keeping staff and students.

The Tucson *Drosophila* Species Stock Center at the University of Arizona campus maintains over 1400 strains of 230 different *Drosophila* species, providing samples to investigators worldwide. These flies represent the largest collection of eukaryotic organisms ever assembled whose evolutionary relationships have been extensively studied. This important resource is administered through the Center of Insect Science, a multidisciplinary program fostering collaborative research on a broad array of topics dealing with insect science.

Inquiries should be directed to Dr. Therese Markow, Director [tmarkow@arl.arizona.edu](mailto:tmarkow@arl.arizona.edu) <http://stockcenter.arl.arizona.edu/>

Therese Ann Markow Regents' Professor Dept. of Ecology and Evolutionary Biology Director, Center for Insect Science BSW 310 University of Arizona Tucson, AZ 85721

Office: (520) 621 3323 Laboratory (520) 626 2772 Fax: (520) 621 2590 Email: [tmarkow@arl.arizona.edu](mailto:tmarkow@arl.arizona.edu)

[http://cis.arl.arizona.edu/markow\\_lab/](http://cis.arl.arizona.edu/markow_lab/)

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## TuftsU MolEvolInfDisease

Research Assistant Position announcement: TuftsU\_MolEvolInfDisease A position is available to work on the molecular evolution of agents of infectious disease and their hosts in the laboratory of Stephen Rich at Tufts University School of Veterinary Medicine. The research assistant is needed to work as part of a research team, doing PCR, automated sequencing, data analysis and other duties. The primary project at the moment is to elucidate the population structure of *Plasmodium falciparum* in malaria endemic regions in the world's tropics.

**QUALIFICATIONS:** The successful applicant will have strong skills and documented experience in molecular biology (for example, DNA extraction, PCR, cloning, gel electrophoresis, DNA sequencing, etc) and the computer analysis of biological data. The applicant will also be highly organized, have an attention to detail, and be able to work as an independent part of a team. Background and interest in evolutionary theory and/or infectious diseases is also highly favorable.

The incumbent would join a unique research group within the Division of Infectious Diseases at the TUSVM. The campus is located in a rural setting approximately 30 miles west of Boston and 6 miles east

of Worcester, Mass..

The start date is flexible, but preferably before 1 August 2004.

To apply, please send a CV, a short statement of research interests and experience, and contact information for three references to:

Stephen M. Rich Associate Professor Division of Infectious Diseases Tufts University School of Veterinary Medicine North Grafton, MA 01536 Phone: 508-887-4749 E-mail (preferred means of communication): [stephen.rich@tufts.edu](mailto:stephen.rich@tufts.edu)

"Stephen M. Rich" <[stephen.rich@tufts.edu](mailto:stephen.rich@tufts.edu)>

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## UAuckland MathBioinformatics

Dear colleagues

The University of Auckland invites applications for a tenurable Lectureship/Senior Lectureship (equivalent to Assistant Professor/Associate Professor) in Mathematical Biology/Bioinformatics in the Department of Mathematics.

The Department of Mathematics, the largest and strongest in New Zealand, offers a full range of courses at the undergraduate and postgraduate levels, and has a growing PhD programme and a vibrant research culture spanning pure and applied mathematics and mathematics education. It is currently strengthening the University's programme in Mathematical Biology.

The successful applicant will be expected to teach courses in Bioinformatics, Mathematical Biology, and Applied Mathematics, as well as develop close research connections with the Bioinformatics Institute and the School of Biological Sciences. The ideal candidate will have expertise in the general area of Mathematical Bioinformatics, including Hidden Markov Models, Markov chain Monte Carlo methods, combinatorial bioinformatics methods, phylogenetics, and genetic/metabolic/biochemical network modelling.

More details may be found at the web-site <http://www.math.auckland.ac.nz/> and <http://www.math.auckland.ac.nz/Enquiries> of an academic nature should be addressed to the Head of the Department of Mathematics, Professor D.B. Gauld, telephone 64-9-373599, ext 88697, fax 64-9-3737457, email: [d.gauld@auckland.ac.nz](mailto:d.gauld@auckland.ac.nz), or the Professor of Applied Mathematics, Professor James Sneyd,

telephone 64-9-3737599 ext 87474, fax 64-9-3737457, email: [sneyd@math.auckland.ac.nz](mailto:sneyd@math.auckland.ac.nz). Closing Date: 31/05/2004

Allen Rodrigo Director, Bioinformatics Institute University of Auckland

Allen Rodrigo <[a.rodrigo@auckland.ac.nz](mailto:a.rodrigo@auckland.ac.nz)>

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### UFlorida VisitorProf

The Department of Zoology at the University of Florida invites applications for two, two-year Visiting Assistant Professorships, starting on August 16th, 2004. Successful applicants must have a Ph.D. and will be expected to teach two courses per semester, including Ecology or Functional Vertebrate Anatomy in the spring, Vertebrate Zoology or Ecology in the fall, and sections of a non-major, introductory course each semester. Research in collaboration with departmental faculty is encouraged but not required, and some limited research funds may be available. Salary will be \$35,000 for the nine-month academic year, plus the usual university payments toward health insurance and retirement. For more information on the department and links to relevant courses go to <http://www.zoo.ufl.edu>. Applicants should submit a cover letter, curriculum vitae, statement of teaching experience and philosophy, and names and emails of three references to Dr. David H. Evans at [devans@zoo.ufl.edu](mailto:devans@zoo.ufl.edu) before 1 June, 2004. Applications will be reviewed as received and the positions will be filled before 1 July, 2004. The University of Florida is an Equal Opportunity Employer.

Marta L. Wayne P.O. Box 118525 Department of Zoology University of Florida Gainesville, FL 32611-8525 (courier: B32 Bartram Hall) vox: 352-392-9925 fax: 352-392-3704 <http://www.zoo.ufl.edu/mlwayne> "Marta L. Wayne" <[mlwayne@zoo.ufl.edu](mailto:mlwayne@zoo.ufl.edu)>

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### UGeorgia MolEvol

Job: Research Coordinator, molecular evolutionary or ecological genetics

A full-time head research technician position is available beginning July 1, 2004 (or earlier if possible) in

the Avise lab at the University of Georgia. The position is for a minimum of one year, but prospects for a multi-year extension are high.

The position entails supervising and coordinating the lab's day-to-day research operations, which involve the use of molecular markers to study ecological and evolutionary topics. Proficiency in molecular-genetic techniques, especially all aspects of microsatellite analyses (e.g., DNA isolation, genomic library construction, PCR assays) and DNA sequencing methods and analysis are essential. Computer skills are also highly desirable, as is a willingness to participate occasionally in field collections. Current projects in the lab include microsatellite analyses of genetic mating systems in fishes and marine invertebrates. The lab is also interested in phylogeography and phylogenetics.

Athens, the home of the University of Georgia, is a lovely and relatively inexpensive college town with many social and cultural amenities. The working conditions, facilities, and intellectual atmosphere are excellent. See the Department of Genetics website at <http://www/genetics.uga.edu>. Review of applications will begin immediately and will continue until the position is filled. Interested persons should send (by e-mail) a resume/CV including laboratory skills, a statement of current interests and future plans, and the names and contact information of 2 references to: John Avise ([avise@uga.edu](mailto:avise@uga.edu)).

John C. Avise, Ph.D. Department of Genetics Life Sciences Building University of Georgia Athens, GA 30602 [avise@uga.edu](mailto:avise@uga.edu) 706-542-1456 fax: 706-542-3910

John Avise <[avise@uga.edu](mailto:avise@uga.edu)>

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### UHawaii Biodiversity

PCSU RESEARCH PROJECT TECHNICIAN - ID# 24250. Pacific Cooperative Studies Unit (PCSU), Biocomplexity of Introduced Diseases in Hawaii, and Pacific Islands Ecosystem Research Center (PIERC), and University of Hawaii at Hilo. Regular, Full-Time, RCUH Non-Civil Service position, located in Hawaii Volcanoes National Park on the island of Hawaii and University of Hawaii at Hilo. Continuation of employment is dependent upon program/operational needs, satisfactory work performance, and availability of funds. Minimum Monthly Salary: Commensurate with qualifications. Duties: Assists the Co-Principal Investigators with molecular genetic studies of native,



indigenous, and invasive species in Hawaii and the Pacific, including parasites and pathogens, and the application of molecular methods to disease diagnostics. Duties include, but are not limited to: application of basic laboratory skills, assist in ordering, purchasing and inventory of supplies, maintaining and replenishing chemical solutions for routine use, DNA extraction and qualification, genetic analyses using Polymerase Chain Reaction (PCR), gel electrophoresis, computer-based data analyses, summarizing laboratory data for reports. Minimum Qualifications: Bachelor's Degree from an accredited four (4) year college or university in Biology, Zoology, Wildlife Science, or other Biological discipline. Six to twelve (6-12) months of research experience using molecular genetics techniques including but not limited to extraction and quantification of DNA, and PCR set up and troubleshooting in a laboratory setting. Basic knowledge in the principles of molecular genetics, including but not limited to, a working knowledge of computer programs used for DNA sequence analysis. Able to organize and complete multiple laboratory procedures on a daily basis. Able to safely handle chemicals and work with high attention to detail for completion and verification of laboratory procedures. Willingness to assist in routine laboratory functions, including ordering and inventory of supplies, and maintenance of laboratory equipment. Able to complete genetic analyses using PCR. Ability to maintain and update databases for records and data storage. Able to successfully perform multi-task duties as described. Desirable Qualifications: One to three (1-3) years of research experience (paid or volunteer) involving the application of molecular methods to biologically related issues, including experience with real-time PCR, micro/spotted array methodology and familiarity with use of robotics workstation. Inquiries: Susan Jarvi, 974-7358 (Hawaii). Application Requirements: The preferred method of applying for this job is through our on-line application process. Please go to [www.rcuh.com](http://www.rcuh.com), click on "Employment" and navigate to "Job Announcements/Apply for a Job." However, if you do not have access to the Internet, you may apply by submitting resume; cover letter including ID#, referral source, narrative of your qualifications for position and salary history; names, phone numbers and addresses of three supervisory references and copy of degree(s)/transcripts/certificate(s) to confirm your credentials by fax (808) 956-5022 or mail to Director of Human Resources, Research Corporation of the University of Hawaii, 2530 Dole Street, Sakamaki Hall D-100, Honolulu, HI 96822 before the closing date. Closing Date: June 7, 2004. EEO/AA Employer.

Sue Jarvi Biology University of Hawaii 200 West Kawili Street Hilo, HI 96720 808 974-7358 FAX 808 974-7693

jarvi@hawaii.edu

Sue Jarvi <jarvi@hawaii.edu>

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## UHull EvolEcol

Candidates with research interests in evolutionary biology are strongly encouraged to apply.

Lecturer in Ecology Department of Biological Sciences University of Hull, UK

Lecturer B, full time

We are looking for an enthusiastic scientist who works at the interface of behavioural and evolutionary ecology to join our internationally recognized team of aquatic molecular, evolutionary and chemical ecologists. You will bring a good scientific profile with evidence of high quality research (publications, grants, fellowships etc.) and the desire to develop a successful research team at the University. Enthusiasm for research, and to stimulate students with modern, dedicated teaching of evolutionary ecology in undergraduate and post-graduate degree schemes are essential. We particularly encourage applications from interdisciplinary scientists who investigate the mechanisms of animal evolution either with molecular, behavioural, chemical or traditional methods. We offer a supportive environment with strategic investment into molecular and chemical ecology, a broad range of existing expertise that you should have an interest to collaborate with, new facilities and an atmosphere of achievement where working in a team is essential.

Salary: Lecturer B, depending on experience E.g. 26,270-33,679 UK pounds per annum

Reference: EM275 \_\_\_\_\_ Closing date: 17/05/2004 \_\_\_\_\_ For an informal enquiry please contact Dr J Hardege on 01482 465496 or 465187 email: [J.D.Hardege@hull.ac.uk](mailto:J.D.Hardege@hull.ac.uk)

Biology Dept Website <http://www.hull.ac.uk/-biosci/> Molecular Ecology Lab Website <http://www.hull.ac.uk/molecol/> Lectureship page <http://www.hull.ac.uk/biosci/Lectureship.html> For further information and details of how to apply, please contact the Human Resources Office quoting the vacancy reference.

Human Resources Office University of Hull HULL HU6 7RX UK Tel +44 (0)1482 465557 FAX +44 (0)1482 466660 [Science-Recruitment@hull.ac.uk](mailto:Science-Recruitment@hull.ac.uk)



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Dr David Lunt, Department of Biological Sciences,  
University of Hull, Hull HU6 7RX UK

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Phone: +44 (0)1482 465514 Fax: +44 (0)1482  
465458 Email: [d.h.lunt@hull.ac.uk](mailto:d.h.lunt@hull.ac.uk) WWW: <http://www.hull.ac.uk/biosci>

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Human Resources Office University of Hull HULL HU6  
7RX UK Tel +44 (0)1482 465557 FAX +44 (0)1482  
466660 [Science-Recruitment@hull.ac.uk](mailto:Science-Recruitment@hull.ac.uk)

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Dr David Lunt, Department of Biological Sciences,  
University of Hull, Hull HU6 7RX UK

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Phone: +44 (0)1482 465514 Fax: +44 (0)1482  
465458 Email: [d.h.lunt@hull.ac.uk](mailto:d.h.lunt@hull.ac.uk) WWW: <http://www.hull.ac.uk/biosci>

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## UHull EvolMolEcol

Research Fellow in Molecular Ecology

Department of Biological Sciences University of Hull,  
UK

Research Fellow, full time, 2 years in the first instance.

We are looking for a young, dynamic scientist who has a keen interest in evolutionary ecology to join our internationally recognized team of aquatic molecular ecologists. You will bring a good scientific profile with evidence of high quality research (publications, grants) and the desire to develop a successful research team to the University. Enthusiasm for research, and to stimulate postgraduate students with modern, dedicated research activities in ecology/biodiversity are essential. We are looking for an energetic, young scientist who investigates the mechanisms of (aquatic) ecology either with molecular, behavioural, or chemical methods. We offer a supportive environment with recent strategic investment into molecular ecology, a range of existing expertise that you should have an interest to collaborate with, new facilities and an atmosphere of achievement where working in a team is essential.

Salary: up to point 13 (currently approx. £27,300) according to experience

Reference: EM276 \_\_\_\_\_ Closing date:  
10/05/2004 \_\_\_\_\_

For an informal enquiry please contact Dr J Hardege on  
01482 465496 or 465187 email: [J.D.Hardege@hull.ac.uk](mailto:J.D.Hardege@hull.ac.uk)

Biology Dept Website <http://www.hull.ac.uk/biosci/> Molecular Ecology Lab Website <http://www.hull.ac.uk/molecol/> Fellowship page <http://www.hull.ac.uk/biosci/Fellowship.html> For further information and details of how to apply, please contact the Human Resources Office quoting the vacancy reference.

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## ULeeds EvolBiol

University of Leeds

Faculty of Biological Sciences, School of Biology

Teaching Fellow / Lecturer in Evolutionary Biology  
fixed term to 30th September 2006

Closing date 18th June 2004

The School of Biology seeks to strengthen its undergraduate and postgraduate programmes by appointing an outstanding scientist to make a major contribution to the teaching of organismal and evolutionary biology, and particularly aspects of evolutionary and population genetics, to biology, zoology, ecology and genetics students at all undergraduate and postgraduate (masters) levels.

Applicants should have a PhD (or equivalent experience) in evolutionary biology or evolutionary genetics, preferably with experience in some or all of the following areas: population biology, population genetics, ecological genetics and conservation genetics, as well as knowledge of and ability to teach biological statistics. The post is available for a fixed term either as a teaching fellow or as lecture 1A/B; appointees as temporary lecturer will be expected to undertake high quality research in evolutionary or organismal biology as a member of the Faculty's Ecology & Evolution research group. See [www.fbs.leeds.ac.uk](http://www.fbs.leeds.ac.uk) for further information.

Salary: Lecturer (£22,191 - £33,679 p.a. pay award pending) or Other Related 2 (£21,125 - £27,339 p.a. pay award pending). The post is available from June 2004.

Enquiries are also welcomed from independent researchers with their own fellowships in the areas de-

scribed above, or from those considering applying for fellowships, who can be offered suitable laboratory space and access to extensive equipment within a stimulating research environment.

Informal enquiries to Professor Jeremy Rayner (Alexander Professor of Zoology and Pro-Dean for Learning and Teaching) tel 0113 343 2873 email [j.m.v.rayner@leeds.ac.uk](mailto:j.m.v.rayner@leeds.ac.uk) or Dr Keith Hamer, Ecology & Evolution Research Group Leader tel 0113 343 2983 email [k.c.hamer@leeds.ac.uk](mailto:k.c.hamer@leeds.ac.uk)

Application forms and further particulars may be obtained from Mrs Gill Partridge, School of Biology, Miall Building, University of Leeds, Leeds LS2 9JT; email [g.m.partridge@leeds.ac.uk](mailto:g.m.partridge@leeds.ac.uk), tel. 0113 343 2880, fax 0113 343 2882.

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Professor Jeremy M. V. Rayner Pro-Dean for Learning and Teaching, Faculty of Biological Sciences and Alexander Professor of Zoology School of Biology L. C. Miall Building, University of Leeds, Leeds LS2 9JT, U.K. tel. (+44) (0)113 343 2873 (messages ...2828, fax ...2835) email: [j.m.v.rayner@leeds.ac.uk](mailto:j.m.v.rayner@leeds.ac.uk) web: <http://www.biology.leeds.ac.uk/staff/jmvr/flight/flight.htm> "J. M. V. Rayner" <[j.m.v.rayner@leeds.ac.uk](mailto:j.m.v.rayner@leeds.ac.uk)>

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## UMaryland ConservationGenet

Conservation Genetics of Oyster Restoration using Disease-Resistant Strains

A research associate position is opening in the conservation genetics laboratory of Dr. Matthew Hare in the Department of Biology of the University of Maryland, College Park. Research in the Hare laboratory focuses on conservation and evolutionary genetics and uses genetic markers as indicators of dispersal, gene flow, selection, hybridization and speciation in marine organisms. The open position is funded by SeaGrant/NOAA to measure the recruitment patterns of disease-resistant oyster strains used for restoration in Chesapeake Bay. More information on the Hare lab can be found at <http://www.life.umd.edu/biology/faculty/hare/index.html> The successful candidate will conduct microsatellite genotyping and DNA sequencing in support of laboratory goals. In addition to having research responsibilities, the candidate will interact closely with graduate students and postdocs and help in the training and supervision of undergraduate students

in the laboratory. The successful candidate will also be asked to help manage the day to day operation of the laboratory. Minimum of 1 year laboratory research experience is required. Successful candidates must have experience using standard techniques in population genetics research, with priority given to experience with microsatellite genotyping. Pay scale is commensurate with experience, starting at 24K.

Applicants should send (electronic preferred) a brief letter describing their prior research experience and current interests, a curriculum vitae, and the names and contact information of three references to Matthew Hare, Biology Department, Bio/Psych Bldg. #144, University of Maryland, College Park, MD 20742 (FAX: 301-314-9358; e-mail: [matt.hare@umail.umd.edu](mailto:matt.hare@umail.umd.edu)). Starting dates in July or August of 2004 are desired.

The University of Maryland is located in a suburb of Washington D.C. with easy access to a number of research institutions in the Baltimore/D.C. area including the Smithsonian, Johns Hopkins University, and the Center of Marine Biotechnology. More information about the Biology Department and the Behavior, Ecology, Evolution, and Systematics (BEES) program at UMCP is available at <http://www.life.umd.edu/biology/> and <http://www.life.umd.edu/grad/BEES/>

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

----- Dr. Matthew P. Hare Biology Department, bldg. 144 University of Maryland College Park, MD 20742 phone: 301-405-7264

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## UMuenster PlantEvol

The University of Muenster (Germany) seeks to appoint a

Full Professor of Botany (C4/W3 salary scale) in succession of Prof. von Willert.

Candidates should have an excellent track record of research in EVOLUTIONARY ECOLOGY and should have worked on genotypic and phenotypic adaptation in natural populations using experimental techniques.

The candidate is expected to contribute in part to compulsory teaching units, including basic botany (plant evolution; plant functional morphology and adaptation; field trips). Applicants must hold a doctorate and have a postdoctoral track record of independent academic

research and teaching (German Habilitation or equivalent experience). Foreign candidates are expected to acquire sufficient language skills for teaching in German within 2 years after taking up the position.

The position is substantially equipped, comprising an annual budget and core funding for scientific and technical posts.

The professorship will play a central role in a new institute in evolutionary biology and biodiversity studies which will be formed by the merger of the existing institutes of "Plant Ecology and "Animal Evolution and Ecology. In 2005 another professorship in the area of Botany will be advertised in this unit.

The WWU seeks to increase the proportion of female staff members in the faculty and therefore urges interested female candidates to apply. In case of equal qualifications, preference will be given to disabled applicants.

Applicants should send their CV, copies of transcripts and degree certificates, a list of publications and grant income to date, and a research plan not later than 15.07.2003 to the Dean of the School of Biological Sciences, University Münster, Hindenburgplatz 55, 48143 Münster, Germany. Electronic submissions in pdf-format and informal inquiries should be sent to: dekanat.bio@uni-muenster.de.

——— Prof. Dr. Nico K. Michiels Institute of Animal Evolution and Ecology Westphalian Wilhelms-University Muenster Huefferstrasse 1, D-48149 Muenster, Germany

Tel. +49 (0)251 83 24661 Mobile +49 (0)170 4758003 Fax. +49 (0)251 83 24668

michiels@uni-muenster.de <http://www.uni-muenster.de/Biologie.EvoEco/Evolbio/> Nico Michiels <michiels@uni-muenster.de>

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## UWaterloo MolEcol

The Department of Biology at University of Waterloo is searching for an Assistant Professor in the area of Molecular Ecology. The successful candidate will possess skills that complement the strong existing group of Aquatic Ecologists, and will bring molecular skills and approaches to that group. Areas that would complement the Department's current expertise include aspects of environmental microbiology and conservation biology; however, excellent candidates with other re-

search interests under the broad umbrella of Molecular Ecology will be seriously considered. While this tenure track position is at the Assistant Professor level, outstanding candidates at the Associate Professor level will also be considered. Candidates should possess a Ph.D. and post-doctoral experience. Duties include research, teaching at the undergraduate and graduate levels, and graduate student supervision. Candidates should be able to teach courses in molecular ecology and environmental biology. Applicants should send their curriculum vitae, the names of three referees and an outline (1-2 pages) of their proposed research program to: Chair, Department of Biology, University of Waterloo, Waterloo, Ontario, N2L 3G1, Canada. The closing date for applications is August 31, 2004 with a start date after January 1, 2005. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The University of Waterloo encourages applications from all qualified individuals, including women, members of visible minorities, native peoples, and persons with disabilities. These appointments are subject to the availability of funds. Additional information on the Department is available at: <http://www.science.uwaterloo.ca/biology>

Linda Zepf Chair's Secretary Department of Biology University of Waterloo Waterloo, ON N2L 3G1 Canada  
Phone: 519-888-4567 ext. 3943 Fax: 519-746-0614  
Email: lzepf@scimail.uwaterloo.ca

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## UppsalaU EvoFunctionalGenomics

Assistant Professor/Research Associate in Evolutionary Functional Genomics

at the Department of Evolution, Genomics and Systematics, Evolutionary Biology Centre (EBC), Uppsala University. Period of appointment: The position can be held for a maximum of four years.

Tasks: The position includes independent research, teaching within the undergraduate programme in Biology at Uppsala University, and supervision of PhD students. The research area comprises molecular studies to understand the functional significance of genetic variation at the level of individuals, populations or species. Eligibility: The successful candidate must have a Ph.D. Priority is given to applicants who completed their PhD within the last five years. For further information contact Professor Ulf Lagercrantz, e-mail: Ulf.Lagercrantz@ebc.uu.se, phone +46 (0)18 471 64 18.

Further details can be found at <http://www.personalavd.uu.se/ledigaplatser/engindex.html>

How to apply: The application must be written in English. The applicant is required to submit two copies of documents and one copy of publications according to instructions found on the web site <http://www.teknat.uu.se/english/instructions.php> or ordered from [Margareta.Sollenberg@uadm.uu.se](mailto:Margareta.Sollenberg@uadm.uu.se), phone +46 (0)18 471 1869.

Applications should be directed to the Vice-Chancellor and mailed so as to arrive at Uppsala University, Registrars Office UFV-PA 2004/1243. Box 256, S-751 05 Uppsala, Sweden, or fax +46 18 471 2000, no later than 7 may 2004. A fax should be followed by a signed original of the application sent within a week of the deadline.

[ulf.lagercrantz@ebc.uu.se](mailto:ulf.lagercrantz@ebc.uu.se)

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## Other

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### Allozyme applicators

Dear EVOLDIR members,

Although molecular tools are now the reference for population genetics, allozyme electrophoresis still constitutes an easy and useful tool for comparative purposes. We have been using Cellulose Acetate gels since years with good results, only experiencing problems with the quality of the supernatant applicator we are buying. It seems that the quality is not very good (breaking comb,

bad finishing, etc), so I was wondering what kind of allozyme applicators are used nowadays for CAGE and what their users find of the quality. For the moderate sum of around 500 , one can expect that it would at least last for several months/years ! We are currently purchasing an applicator from Helena Laboratories (model HL 4090) for 7 cm X 7 cm gels with 12 platina combs.

In summary: What companies deliver such applicators, what is their quality and for what price ?

I thank you in advance for you replies

sincerely,

Gregory Maes

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Gregory Maes Katholieke Universiteit Leuven Laboratory of Aquatic Ecology Fish Genetics Group Ch. de Beriotstraat, 32 B-3000 Leuven Belgium Phone: +32 16 32 39 66 (secretariat) or +32 16 32 45 72 (New office number !) Fax: +32 16 32 45 75 E-mail: gregory.maes@bio.kuleuven.ac.be website: <http://www.kuleuven.ac.be/bio/eco>

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### Astacus identification

Dear All,

Does anybody have expertise in identifying freshwater crayfish (Deutsch: Flusskrebse) of the genus *Astacus*? If so, I have some digital photos of specimens from Iran that I would need help in identifying to species level (if possible). Please send me your email address if you would like to help.

Best Regards,

Mark Schultz mbsc@deakin.edu.au

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### Bat samples

We are desperately looking for DNA or a tissue sample to extract DNA from from hairy-winged vampire bat (*Diphylla ecaudata*). If you can help us, this will be greatly appreciated and we will acknowledge you as

you see fit in any resulting publication. Thanks. David Liberles liberles@cbu.uib.no

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### Bayesian burn-in

Dear Member, We use MrBayes 3.0 for phylogenetic analysis and have a question about determining the generation of burn in. The Screen output of MrBayes 3.0 does not show a column of summarized likelihood score over the different chains as does in MrBayes 1.0 and 2.0. Does anyone know how to determine the Burn in this case? We need to look at the scores for all four chains to determine the generation when the score starts to be come stabilized (if four chains are run) or if there is a way to see the scores summarized over four chains? Thanks for any help! Sincerely, Jenny Xiang at NCSU, jenny\_xiang@ncsu.edu

Jenny Xiang <jenny\_xiang@ncsu.edu>

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### Bird Blood DNA

Dear all,

We are considering the purchase of a liquid handling robot. One of the tasks that we have in mind is extraction of genomic DNA from bird blood and tissue in 96-well plates. Magnetic beads and vacuum based protocols seem to be the two main techniques available. Does anyone have experience with bird blood and either of these approaches on a liquid handling robot? What are the respective dis-/advantages? One particular concern we have is the viscosity typical for bird blood in lysis buffer. Is the vacuum strong enough to draw the samples through?

We would appreciate any insights and advice you might have.

Many thanks,

Lukas Keller -----

Lukas Keller Zoologisches Museum Universität Zürich Winterthurerstr. 190 CH-8057 Zürich Switzerland

Tel: ++41 1 635 47 50 Fax: ++41 1 635 68 18 Email: lfkeller@zoolmus.unizh.ch -----



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## BloodSmear extraction

Hello, everyone, I am planning to extract DNA from air dried blood smears (from toads) on microscopic slides (10-12 years old). Although I have several ideas, I am wondering whether people have some experiences. Also, some (of course, the most important ones) were mounted with xylene based medium and may be not suitable for extraction at all? Thanks for your ideas, Matthias

Matthias Stöck Museum of Vertebrate Zoology, University of California, Berkeley, Department of Integrative Biology 3101 Valley Life Sciences Building #3160 Berkeley, CA 94720-3160 Email: matthias@berkeley.edu

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## BloodSmear extraction answers

Thanks for the reply.

### QUERY

>>I am planning to extract DNA from air dried blood smears (from toads) on microscopic slides (10-12 years old). Although I have several ideas, I am wondering whether people have some experiences. Also, some (of course, the most important ones) were mounted with xylene based medium and may be not suitable for extraction at all? Thanks for your ideas, Matthias Matthias Stöck Museum of Vertebrate Zoology, University of California, Berkeley, Department of Integrative Biology, 3101 Valley Life Sciences Building #3160 Berkeley, CA 94720-3160 >>

### ANSWERS:

Hi I have done a lot of work on archival slides that date back over 70 years. Mostly I have been recovering human mtDNA and nuDNA, but I also have had some success with some plasmodium DNA out of slides going back to the 1930's Actually, odd as it may sound, I find the best way to get DNA out of them (I have compared about 10 methods), is simply to use some very dilute SDS. Typically I pipette about 35-50ul of 0.002% SDS onto the slide, and scrape around/suck it up and down with the pipette. You can then per straight on

this, although I find it also helps to freeze and thaw it first. Of course, once you have done this, store the samples in the freezer. As far as I can tell, the SDS simply helps getting up the old material by acting as a detergent. I should probably mention that all my samples are Giemsa stained, and a mixture of methanol and non-methanol fixed. But I doubt it will make any difference if they are not stained. As for the ones with cover slips, you need to remove them first by bathing them in xylene. But they are a real pain in the arse, as you have to watch for cross contamination between samples, so each needs an individual bath, so I would stick with the non-slipped ones if possible. One further bit of advice - I find that getting mtDNA is easy from these extracts, but the fragments are limited to short length - typically less than 500bp (although my samples are a lot older than yours). As for nuclear, I again have most success with short frags (ie below 250bp). However the degradation is linked to a load of factors, so it is hard to generalise. So to summarize, I would recommend simply trying my simple method (modified from another paper I can ref for you if you want), and try some nice small amps to start with. Let me know if you need more advice Tom Gilbert

Also I forgot to mention that I always use the (exorbitantly priced) platinum taq hifidelity from Invitrogen, which is way more sensitive than any other enzyme I have tried. So my hints may be less successful if you are using other enzymes - although I expect that Invitrogen's cheaper option, platinum taq, may be just as good. As before though, it will all depend on the preservation of your DNA.

If you are interested, I do 25ul reactions with

2.5 ul 10X 1ul 50mM MgSO4 1-2 ul 10uM each primer up to 3ul of the SDS extract (depends if you are after mtDNA or nuDNA) 0.2ul 25mM DNTPS 0.2ul Enzyme DDH2O up to 25ul

And then give the reaction 40 cycles. You may note that I use a lot of primer. When I worked with ancient DNA, we always found that using large amounts of primer helped - basically as far as I can see, the more primer, the more chance of it binding to the limited number of template molecules there are in an ancient extract.

One last thing, you may or may not know this (and forgive me if I am lecturing unnecessarily), but be really careful of contamination. You will have pretty low levels of DNA in your slides compared to any modern samples, or any DNA in the environment from previous PCRs on the target regions. It is exceedingly easy to get results from the samples if this is the case....although they may well be results of contamination. If possible



I would recommend doing the 'extractions' and PCR set up somewhere well away from anywhere where you play with modern DNA, and analyse PCR products. Well away being in a different room at least, building better. Contamination is a real persistent bugger. Also the problem is worsened if you use the enzymes I mention, because they are so sensitive to copy number, they often pick up traces of contaminatio that other enzymes don't amplify. But again, all this is dependent on copy number of the original extract vs other sources of DNA. Hope this is helpful Tom Tom Gilbert Ecology and Evolutionary Biology University of Arizona Tucson AZ 85721-0088 Tel: 520-621-4881 Fax: 520-621-9190 mtpg@email.arizona.edu

Hi Matthias, I've attempted extractions from stained blood smears from lizards many times with very limited success. I think the only time I was successful (though mind you I was amplifying parasite DNA so something even rarer than host DNA) was on a very young (<2 yr old) smear. If slides are unstained and un-cover-slipped, they do work a little better. My two recommendations are to use Qiagen kits and elute in a very small volume (or

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

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## Cloning problems

Hi Everyone,

I have another kind of problem! From the RNA, cDNA is prepared and then cloning into T-vector as well as direct expression vector ( vaccinia virus vector with dual prpmoter) tried. In the expression vector, the positive clones are observed by colony pcr which is then follwed with miniprep and digestion. Digested plasmid shows the correct insert size but a smaller fragment of the vector backbone. Using a recombinant-deficient competent cells the results are still the same. Well, my insert is cloned using a single enzyme ie., the same enzyme on both ends. If anybody could help, please kindly send me a message.

Sangeeta Choudhury Centers for Disease Control and Prevention Atlanta, GA Tel # 404-639-1059 email : bke7@cdc.gov

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## Drosophila stocks 2

New Drosophila stocks:

The Tucson Drosophila Species Stock Center has incorporated the new stocks listed below (check website for collection info):

D. virilis 15010-1051.85 (inbred line, 15 generations) D. virilis 15010-1051.86 (inbred line, 15 generations)

D. melanogaster 14021-0231.25 (San Pablo Etla, Oaxaca, Mexico) D. melanogaster 14021-0231.26 (San Blas, Nayarit, Mexico) D. melanogaster 14021-1551.192 (Sinaloa, Mexico)

D. mercatorum 15082-1521.34 (Hawaii) D. mercatorum 15082-1521.35 (Hawaii, white-eyed mutant) D. mercatorum 15082-1525.07 (Hawaii, parthenogenetic strain)

D. santomea 14021-1571.0 (San Tome, Africa)

D. simulans 14021-1551.187 (Jalisco, Mexico) D. simulans 14021-1551.188 (Santa Cruz Island, California) D. simulans 14021-1551.189 (Oaxaca, Mexico) D. simulans 14021-1551.190 (Nayarit, Mexico) D. simulans 14021-1551.191 (Nayarit, Mexico) D. simulans 14021-1551.192 (Sinaloa, Mexico) D. simulans 14021-1551.193 (Edo de Mexico, Mexico)

Therese Ann Markow Regents' Professor Dept. of Ecology and Evolutionary Biology Director, Center for Insect Science BSW 310 University of Arizona Tucson, AZ 85721

Office: (520) 621 3323 Laboratory (520) 626 2772 Fax: (520) 621 2590 Email: tmarkow@arl.arizona.edu

[http://cis.arl.arizona.edu/markow\\_lab/](http://cis.arl.arizona.edu/markow_lab/)

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## Effective Pop Size

Hello everyone,

I need to calculate effective population sizes ( $N_e$ ) based on temporal variation in allele frequencies at microsatellite loci. Since these calculations involve multiple loci and several alleles per locus, it may be difficult doing it by hand. Do you know of a software that I can

use for this purpose?

I welcome any suggestions on how to calculate Ne from microsatellite data.

Thanks,

Johnson

Johnson O Ouma <jouma@iastate.edu>

## Effective Pop size answers

Hi everyone,

Here are the responses I received for my question on how to calculate Ne. I have compiled all the answers for the sake of those who may find them useful. Thanks to everyone who responded. Johnson

Here is the original question:

Hello everyone, >> I need to calculate effective population sizes (Ne) based on temporal > variation in allele frequencies at microsatellite loci. Since these > calculations involve multiple loci and several alleles per locus, it may be > difficult doing it by hand. Do you know of a software that I can use for > this purpose? >> I welcome any suggestions on how to calculate Ne from microsatellite data. >> Thanks, >> Johnson

try this - have not tried it

New software (NeEstimator) is available for free download from <http://www.dpi.qld.gov.au/fishweb/11629.html> NeEstimator software estimates effective population sizes (Ne) from allele frequency data. The user can estimate Ne using any of the three internal methods or three third party programs. Genotypes from a sample of the population are used as input. The user provides this data in GENEPOP, ARLEQUIN or simple column (eg. saved as a tab delimited text file from Microsoft Excel) format.

The three internal methods are as follows.

\* A point estimation method using linkage/gametic disequilibrium, (Hill, 1981). \* A point estimation method using heterozygote excess (Pudovkin, Zaykin and Hedgecock, 1996). \* A temporal method using moments based F-statistics (Krimbas and Tsakas, 1971; Nei and Tajima, 1981; Pollock, 1983 or Waples, 1989). The elapsed number of generations between temporal samples is required.

The three third party programs that NeEstimator is

able to utilise are as follows.

\* A temporal method using a Bayesian based approach called TM3 (<http://www.rubic.rdg.ac.uk/~mab/software.html>). \* A temporal method using a maximum likelihood based approach called MCLEEPS (<http://www.stat.washington.edu/thompson/Genepi/Mcleeps.shtml>). \* A temporal method using a pseudo likelihood approach called MLNE (<http://www.zoo.cam.ac.uk/ioz/people/wang.htm>).

I guess you can use Fluctuate. It is free software and you can get it from <http://evolution.genetics.washington.edu/lamarc/fluctuate.html> I haven't use it on Microsatellites but I guess you can do it. However I am not sure if it is available for Windows, but if you have a Mac it works fine. Vera I don't know of any specific software, but I've been working on a related problem (estimating the amount of variation in selection from genotype frequency time series). It would be almost trivial to adapt the code for your problem.

If you are familiar with the WinBugs software (or if you can find someone who is, and is willing to help), I can re-write my code and send it to you. Alternatively, you could send me the data and I run it. The former is preferable - you'll get a better understanding of what's being done (and it's less work for me!).

Bob a complete software package calculating Ne using several methods is NeEstimator available at <http://www.dpi.qld.gov.au/fishweb/11674.html> cheers and good luck, Greg

I have a program to estimate Ne (and migration rate) from temporal variation of allele frequencies. For details, see my website: <http://www.zoo.cam.ac.uk/ioz/people/wang.htm> Best wishes, Jinliang

Arlequin (<http://lgb.unige.ch/arlequin/>) can get you good theta estimates from populations, from SNPs or from microsatellite data. So, if you happen to have a way to estimate your mutation rate, you can get an idea of the effective population size. Even if you don't know the mutation rate, if there's reason to assume that it's relatively constant throughout your time frame, you can still get relative values of Ne from the thetas. -Mike Wisner

you might look at a program called "Estim" (Vitalis&Couvret, 2001 Mole Ecol Notes). Also, Williamson&Slatkin 1999 Genetics might be a good place to start for entry into that literature. If you do a citation search (to see who has cited this article), there are lots of refs regarding this topic. Cheers, Charles

I found Dr Jinliang Wang's MLNe very useful.

It is available at: <http://www.zoo.cam.ac.uk/ioz/-software.htm> It computes Ne using moment-based and a pseudo-likelihood estimators among

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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>

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## Flea mtDNA

Dear Evoldir members,

I am looking for protocols to extract and amplify -in European fleas from the Ceratophyllidae family-, mitochondrial protein coding regions (cytochrome b gene would be the best) sufficiently variable to detect variability at the intraspecific level.

Could anyone gives me some information, degenerated primers and/or references on the subject?

Many thanks in advance for your help!

Caroline.

Caroline Nieberding

Unité de recherches zoogéographiques

Institut de Zoologie

Quai Van Beneden, 22

4020 Liège

Belgique

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Fax: ++33 4 99 62 33 45

Nieberding Caroline <[caroline.nieberding@ulg.ac.be](mailto:caroline.nieberding@ulg.ac.be)>

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## Fragment analysis

hello all.

my lab is currently trying to setup our 3730xl sequencer to do microsatellite genotyping. we currently only have the 50cm array, and would like to run it 96 wells at a time. abi informs us that 50cm arrays are not supported, and that we would have to upgrade our data collection software (v1.0 to v.2.0) to be able to use the run fragment analysis with 96 wells. on both counts it means paying a huge sum to abi, and we feel we have paid enough to them.

has anyone had any success genotyping microsats on a 3730xl with data collection software v1.0 with 96 wells on a 50cm array? if so, could you please send us some instructions on how to do the spectral calibration to setup the ds-33 matrix set.

thank you for your time and attention.

kind regards,

anders.

– Anders Gonalves da Silva PhD candidate Center for Environmental Research and Conservation Department of Ecology, Evolution and Environmental Biology 1200 Amsterdam Ave. 10th Floor MC 5557 Columbia University New York, NY 10027

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IUCN Tapir Specialist Group  
[www.tapirspecialistgroup.org](http://www.tapirspecialistgroup.org) Instituto de Pesquisas Ecológicas (IPÉ) [www.ipe.org.br](http://www.ipe.org.br)

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## Genealogy correlations

dear evoldir members

some time ago I posted a mail to the list asking for any reference to a /method/software to infer/test correlation between intraespecies trees / genealogies.

I have received several e-mails interested in the answers to the query but so far i have received no answers to

the query itself. Thus, I would like to submit again the same question just in case someone feels that can now contribute to this still open question (at least to us).

thanks a lot

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Santos Alonso

Dpt. Genetics, Phys. Anthop. and Anim. Phys. University of the Basque Country SPAIN

Santos Alonso Alegre <ggpalals@lg.ehu.es>

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## Greenland primulas

Hi everybody

I'm a PhD student working on the phylogeography of *Primula* sect. *Aleuritia* (Primulaceae). Taxon sampling is complete, except for leaf tissues of two species from Greenland (*P. egaliksensis* and *P. stricta*). Is anybody willing to help me in getting this material?

Collecting instructions can be found under following link:

<[http://www.systbot.unizh.ch/institut/-personen/wiss/guggisberg\\_media/-Wanted\\_list\\_Greenland.pdf](http://www.systbot.unizh.ch/institut/-personen/wiss/guggisberg_media/-Wanted_list_Greenland.pdf)>[http://www.systbot.unizh.ch/institut/personen/wiss/-guggisberg\\_media/Wanted\\_list\\_Greenland.pdf](http://www.systbot.unizh.ch/institut/personen/wiss/-guggisberg_media/Wanted_list_Greenland.pdf)

Any

help is welcome!

Thank you in advance

Alessia

\*\*\*\*\* Alessia Guggisberg PhD student University of Zurich Institute of Systematic Botany Zollikerstrasse 107 CH-8008 Zurich SWITZERLAND

Email: [alg@systbot.unizh.ch](mailto:alg@systbot.unizh.ch) Website: <http://www.systbot.unizh.ch/institut/personen/wiss/-guggisberg.htm> Phone: ++41 (0)1 634 84 30 Fax: ++41 (0)1 634 84 03 (secretary) \*\*\*\*\*

Alessia Guggisberg <[alg@systbot.unizh.ch](mailto:alg@systbot.unizh.ch)>

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## Human evolution info

Our students have to conclude their four years biology course by writing a small monography-like concluding thesis/text. One of my students chose to write about human evolution. I happened to give her a small paperback "Why sex is fun - the evolution of human sexuality" by Jared Diamond.

In the meanwhile this particular student made thoughts of his own and she came out with the proposal to write a text primarily about the following species:

1.) *Australopithecus africanus* 2.) *Australopithecus robustus* 3.) *Homo erectus* 4.) *Homo habilis* 5.) *Homo sapiens*

Now she wants to know whether there are particular essays, on-line publications, papers, et cetera, which deal with questions of sexual dimorphism, sexual selection, and evolution of sexuality in general in those already chosen five species, topic of her concluding essay?

with best regards,

Thomas Schlemmermeyer UEMS - Universidade Estadual de Mato Grosso do Sul Unidade Mundo Novo BR 163, km 20,2 ; 79980 - 000 Mundo Novo - MS - Brazil

Thomas

Schlemmermeyer

<[t\\_schlemmermeyer@hotmail.com](mailto:t_schlemmermeyer@hotmail.com)>

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## Insect preservation answers

Thanks to everyone who responded to my inquiry about shipping insects for DNA extraction without the use of ethanol! I've posted most of the responses below. DMSO preservation sounds like something to try in the future, but unfortunately I didn't have time to try it with my weevil larvae. I decided to go with initial preservation in ethanol. Then, just before shipping, pour off the ethanol, cotton stop the vials and place them in a bag with silica gel desiccant. I'm hoping this works. There were a few other suggestions especially worth looking into (ie. RNAlater and FTA cards by Whatman) Thanks again, everybody! Steve

Query: >Does anyone have suggestions for preservatives other than ethanol for >shipping insects to be used in genetic work? (regulations on ethanol are >making it difficult to ship)

Responses: I have successfully carried samples in vials over silica gel to desiccate them. This has produced DNA extractions and PCR bands as good or better than sample from 100% ethanol, although the morpho-

logical features don't preserve well (e.g., setae are lost, wings get bent), if that is important.

Here is a recipe that we used to preserve fish eggs for DNA analysis. This seems to work best with copious amounts of buffer compared to the amount of material to be preserved (We would put about 50-100 fish eggs in a 50mL Falcon Tube). I have not used it for insects but it might be worth experimenting with. DMSO Preservation Buffer, pH 7.5 250mM EDTA (disodium) 20% DMSO saturated NaCl to make 1 liter 93.05 g EDTA 200 ml DMSO ~ 200 g NaCl pH to about 8.5 before adding NaCl to get the EDTA into solution (we use NaOH). Add the NaCl (warming helps salt go into solution) pH to 7.5 (we use HCl)

I have collected insects in the field straight into silica gel. These were then used for molecular analyses, but I only amplified a rather short bit of mitochondrial 12S. I switched to 100% ethanol shortly after so did not do anything more with this material. But I did successfully extract the DNA after storing in silica gel at -20 for several months. Also the insects I work with are small - 2-3mm - it may be different with larger insects.

I don't know how far you are shipping the insects. However, I did a lot of genetics work on fleas here at northern arizona university and I stored them for long amounts of time in a -80 freezer without any liquid. I would think that if you shipped them on dry ice, they would survive the journey fine.

Simple dessication seems to work quite well in terms of preserving insect DNA. I did a project on butterflies using museum specimens and was able to amplify mtDNA from specimens that were up to 100 years old. However, some of the more recent specimens (~20 years) did not amplify at all. I suspect it has a lot to do with the speed at which specimens are preserved. If a freshly collected insect is killed and dried rapidly, there is less opportunity for degradation.

I know what you mean...shipping regulations have begun to make things difficult for us. Lately, I've been shipping insects for genetic research by pouring off the excess EtOH from each specimen vial, and shipping the vials in a styrofoam cooler with icepacks. My specimens are all kept at -80, and remain frozen until time of shipping; even after the excess EtOH is removed, the specimen tissues are saturated with ethanol, and so seem to be fine if shipped via overnight delivery and kept cold. It might be overkill, but I also tend to coordinate closely with the recipient, telling them exactly when the specimens are shipped, when to expect delivery, and providing shipment tracking numbers. So far, this has worked well for us.....

Maybe DNAzol could be useful. But we haven't tried it yet in our analysis.

FTA cards made by Whatman will likely work (Whatman catalogue pages 116-119 for products and an outline of the procedure). They are also extremely easy to work with after sample collection, eg shipping, storage, extraction for PCR. I have not yet used them myself (but plan to soon); a colleague just tried them out (on tomatoes, but these cards are VERY versatile) and was very satisfied with the results.

I've shipped mammals that were collected in ethanol by draining most of the ethanol but leaving the samples soaked in the stuff. I have to add that we were transporting them in our luggage, so it didn't take long before we could add new ethanol. We experienced no trouble, but regulations or baggage checks in e.g. the US might be stricter.

Just the usual suggestions of dry ice or extract & ship the DNA.

An excellent alternative to ethanol for preserving insects (either for shipment or long term storage) is salt-saturated DMSO (usually 20-30% salt content).

we've had good luck with insects in RNA later, though I don't know what, if any, shipping restrictions there might be on it. I've also been interested

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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>

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## Isogenic plant lines

Hello everyone,

Does anyone know of near-isogenic lines of plant species that are native to the eastern US?

Thank you, Mary Ellen Czesak [maczesak@vassar.edu](mailto:maczesak@vassar.edu)  
[maczesak@vassar.edu](mailto:maczesak@vassar.edu)

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## JMS memorial June26

A celebration of the life and work of John Maynard

Smith.

A memorial will be held for JMS at 4pm on Saturday 26th June 2004, in the Meeting House at the University of Sussex.

All are welcome to join us to celebrate John's life and his remarkable contribution to biology.

It would be helpful to know how many people to expect, so please reply to this email (CSE@sussex.ac.uk) if you think you will attend. We will then email further details about the event to you, as they become available.

Centre for the Study of Evolution, School of Life Sciences, University of Sussex, Falmer, Brighton, BN1 9QG, UK

[www.biols.susx.ac.uk/CSE](http://www.biols.susx.ac.uk/CSE) CSE@sussex.ac.uk fax: +44-1273-678 433

Centre for the Study of Evolution  
<CSE@sussex.ac.uk>

So that we can gauge the number of people expected, if you think you will attend please send a reply to this email (CSE@sussex.ac.uk) , or go to <http://www.biols.susx.ac.uk/CSE/members/jms/jmsmemorial.htm>.

If you would like to contribute anecdotes, stories, and personal recollections of John's life and work to be displayed at the event, please go to the CSE website at <http://www.biols.susx.ac.uk/CSE/members/jms/-jmsmemorial.htm> . Centre for the Study of Evolution, School of Life Sciences, University of Sussex, Falmer, Brighton, BN1 9QG, UK

[www.biols.susx.ac.uk/CSE](http://www.biols.susx.ac.uk/CSE) CSE@sussex.ac.uk fax: +44-1273-678 433

Centre for the Study of Evolution  
<CSE@sussex.ac.uk>

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### Jeffery probe labels

Hi everyone,

Does anyone know of a way i could fluorescently label Jeffery's 33.6 and 33.15 probes? I am using them in a parentage study in a bird species (Longtailed Wagtail) with Southern Blotting techniques.

Thanks Kate Meares 201302042@nu.ac.za or k8meares@yahoo.com

Hello everybody,

I am working on citb gene in liolaemus lizards, and I would like to estimate divergence times between my species (there is not fossil record) Has anybody notice about the molecular clock in lizard mt DNA, and much better, about the cit b divergence rate?

thanks a lot

Beatriz López

Beatriz Lopez <blopez@abulafia.ciencias.uchile.cl>

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### John MaynardSmith Memorial

A celebration of the life and work of John Maynard Smith. University of Sussex, 4pm Saturday 26th June 2004.

All are welcome to join us to celebrate John's life, and his remarkable contribution to biology. Speakers will include Richard Dawkins, Paul Harvey, Alexey Kondrashov, Bruce Levin and Robert May.

Refreshments will be served from 3pm in the Meeting House. The programme will begin at 4pm and drinks will be served after the event at 5:30 pm.

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### Mangrove extraction protocols

Has anyone extracted DNA from mangrove propagules and, does anyone know of a published procedure? Thank you,

Greta Goranova mgoranova@clarku.edu

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### Multiple matings



Dear colleagues,

I am investigating an ant species where I suspect that the queen has mated more than twice. I suspect this from preliminary microsatellite analyses of the contents of the spermathecae. The question then arises as how to statistically verify that this is the case - does anyone know a (maximum likelihood/bayesian/other) program that will estimate the number of males that a single female has mated with (without having to genotype her progeny).

Many thanks in advance, Andrea.  
a\_makrantonih@hotmail.com

intra-individual (within individual) variation, sequencing of individual colonies is necessary. In this situation, what other ways could be taken for sequencing of individual colonies, if *E. coli* prove not to be the problem? If anybody could help, please kindly send me a message to carlzyu@hsrl.rutgers.edu

Thank you very much!

Carl

HSRL Rutgers University carlzyu@hsrl.rutgers.edu

Ziniu Yu <carlzyu@vertigo.hsrl.rutgers.edu>

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## Mutation Rate estimation

Dear Evoldir members,

Does anyone know a program to estimate mutation rate using sequence data of related individuals? Any suggestion is welcome! Best regards.

Cristina Santos

Cristina Santos PhD student University Autònoma of Barcelona Spain Cristina.Santos@uab.es  
Cristina.Santos@uab.es

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## PCR cloning

Hi! Everybody,

Here I have a question to ask for your help. One of my friends met a problem in PCR product cloning which he never met before. He inserted PCR products into T-vector and transformed *E. coli*, then plated on solid media, no problem. But when white colonies were picked into liquid media for culture, these *E. coli* seem did not grow at all. When transferring white colonies into other plates, it was ok. He checked media, antibiotics etc, seems no problem. He also tried other people's media by picking white clones into their liquid media, the same thing happened, no growth. It seems *E. coli* had problem. But the cells grew well before transformation. Does anybody meet this kind problem before? What could be the causes for the problem?

He is working on ITS of invertebrate species. To check

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## PCR cloning answers

Dear Members, Thank you very much to everyone who replied to my inquiry about PCR cloning problem. Because some people have shown interest in the answers to my inquiry, I have made a summary list of the messages I received below. Basically, all responses suggested the same strategy: do PCR on individual colonies and then sequence the PCR product directly. My friend and I were hoping to get suggestion/advice from experienced follows before we go on. Once again, thank you all who responded to my inquiry, I appreciate it.

Best,

Carl HSRL,Rutgers University carlzyu@hsrl.rutgers.edu

My initial inquiry:

One of my friends met a problem in PCR product cloning which he never met before. He inserted PCR products into T-vector and transformed *E. coli*, then plated on solid media, no problem. But when white colonies were picked into liquid media for culture, these *E. coli* seem did not grow at all. When transferring white colonies into other plates, it was ok. He checked media, antibiotics etc, seems no problem. He also tried other people's media by picking white clones into their liquid media, the same thing happened, no growth. It seems *E. coli* had problem. But the cells grew well before transformation. Does anybody meet this kind problem before? What could be the causes for the problem? He is working on ITS of invertebrate species. To check intra-individual (within individual) variation, sequencing of individual colonies is necessary. In this situation, what other ways could be taken for sequencing of individual colonies, if *E. coli* prove not to be the problem? If anybody could help, please kindly send me

a message.

Answers:

(1) That's a strange situation indeed! If the bacteria simply refuse to grow in liquid culture, then it should still be possible to sequence clones. I have had generally good success with PCR amplification and sequencing of single colonies of bacteria using primers from the T-vector that flank the insert site. To get the template DNA, transfer part of the colony into 50 uL of water in a microcentrifuge tube, and vortex.

(2) I would suggest that you PCR directly from the individual colonies growing on the solid media (either with ITS or vector primers) to amplify the ITS copy that has been inserted. If you use a cocktail stick to LIGHTLY touch a single colony and then drop that into a PCR mix, stir gently and remove it should amplify fine. Then just clean-up the PCR product and sequence. If you want to be able to return to these specific colonies at a later date (but within a few weeks), then streak out the individual white colonies onto new solid media, label them and grow them up overnight before you begin to PCR from them.

(3) You do not have to culture the bacteria. You can just do PCR directly from individual colonies, and then sequence the products. People routinely do this in my lab. You can use universal M13 sequencing primers as PCR and sequencing primers.

(4) I had a problem when I started my phd in that someone had done some cloning but the clones were old and had died. As you know it's expensive to clone, so I tried to sequence these anyway, and had good success. Firstly I scraped a small amount of dead cells from the plate and carried out a PCR using universal M13 primers and ran them out on a gel. Most clones I tried PCR'd successfully. I then did a 1:100 or 1:200 dilution and re-PCR'd in the same way. I then carried out a normal clean-up (Wizard preps) and sequenced as per a normal sample.

(5) I would pick colonies, dilute them and use them as a template for PCR and then sequence the PCR product directly.

(6) I have not experienced the problem you are describing but I can tell you a way to get out of growing the clones up in broth prior to sequencing. We directly sequence clones by the method I have attached. It has saved us a great deal of time when we have had hundreds of clones to sequence.

(7) Why not do PCR on clones, and sequence the PCR product? (just set up a PCR as usual, with internal or universal primers, and stick a pipette tip into a colony

to pick up some bacteria, place the tip into the PCR cocktail and pipette up and down a few times to get bacteria into the tube, put on thermocycler with normal conditions, except increase the denature time before the first cycle. I think that Invitrogen recommends 10 minutes at 95C at the beginning of the first cycle to denature some enzymes in the bacteria. Your friend should check the literature of the cloning kit he is using (if using a kit) to see if they have a recommendation. Then you use a kit to purify the PCR rxn and sequence. He can sequence several clones in this way.

(8) Since you need only a small amount of DNA for sequencing, and since the colonies do grow well on plates, I'd suggest that you simply try patching the white transformants out on plates, then scraping the mass off of plates into P1 or GTE or your normal miniprep suspension buffer. One thing that you should be aware of: growth on normal agar inhibits

— / —

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>

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## PCR inhibition

Hi everyone,

I have a problem doing PCRs on mtDNA extracted from lion dung. I did lots of (hotstart) PCRs on dung samples and never had problems. Now, I have got lots of clean DNA from one sample (big pellet), but I am unable to do a PCR on it. I think because there are too much small DNA fragments (<50 bp) competing with the primers for TAQ. After PCR these fragments are very clearly visible with EtBr staining. I first confused it with primer dimers. Diluting does not work, as I will then also dilute my mtDNA.

My question: is there a convenient way to separate small fragments (<1000 - < 50 bp) from the rest of the DNA sample)?

Kind regards, Dr. Pim van Hoof University of Antwerp  
 pim.vanhoof@ua.ac.be pim.vanhoof@ua.ac.be

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## PCR primer kits

Hi,

Does anyone know of a source for PCR primer kits for Anopheles mosquitoes (or other Diptera for that matter) that I could use to amplify genes from Chironomidae? I'd like to get as many nuclear genes as possible. I appreciate any suggestions, and also I apologize if you get this message more than once.

Thanks, Sean

Sean F. Werle <swerle@ent.umass.edu> Organismic and Evolutionary Biology Morrill Science Center, UMass, Amherst

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## Pandit database

We are pleased to announce the release of Pandit version 12.0, freely available via <http://www.ebi.ac.uk/-goldman-srv/pandit>. Pandit is a collection of multiple sequence alignments and phylogenetic trees covering many common protein domains. For each of 7226 families, the data available includes:

- \* a protein sequence multiple alignment,
- \* a corresponding nucleotide sequence alignment
- \* inferred phylogenetic trees derived from each alignment

We can imagine many uses for this database, but we are particularly optimistic that it will help in the devising of improved mathematical models of amino acid and codon sequence evolution and for investigation of the effects of selection on protein sequence evolution.

Pandit is derived from the Pfam database of protein family alignments and HMMs (<http://www.sanger.ac.uk/Software/Pfam>).

Nick Goldman

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

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## Paup problem

Hello everyone

I'm trying to make a DNA-sequence based phylogenetic reconstruction under the last version of PAUP(4.0b10) and I have a little problem. When I choose the Maximum Likelihood criterion with Bootstrap as resampling method and full Heuristic as type of search the program does not allow me to save as many best scored trees as I want (the option "keep N best trees" is unavailable, the "best tree only" option is the only one available, hence only saves the best tree). May be I'm assuming search options so the program doesn't allow me to choose this option. Any helpful comment will be appreciated.

Thank you all. Best for everyone

Javier Sánchez-Fontenla PhD Student. Spain

[javisan@ceab.csic.es](mailto:javisan@ceab.csic.es)

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## Proceedings Evol Symposium

Dear EvolDir members,

Proceedings of International Symposium "Evolutionary ideas in biology" are being published. More information is available at: <http://ibss.febras.ru/evolut/evolut.pdf> Sincerely, Dr. Alexei Kryukov Laboratory of evolutionary zoology and genetics, Institute of Biology and Soil Science Far East Division Russian Academy of Sciences Vladivostok 690022, Russia [kryukov@ibss.dvo.ru](mailto:kryukov@ibss.dvo.ru)

Alexei Kryukov <[kryukov@ibss.dvo.ru](mailto:kryukov@ibss.dvo.ru)>

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## Program updates

Dear all,

Updated versions of Modeltest, TCS, GeoDis, SNPsim and Collapse are available from <http://darwin.uvigo.es>

Programs like ParsProb, Matrix or Chiperm are discontinued, as they have been superceded.

Cheers,

David.

– David Posada Facultad de Biología Campus Lagoas-Marcosende Universidad de Vigo Vigo 36200, Spain

Phone: +34 986 812038 Fax: +34 986 812556 Email: dposada@uvigo.es Web: darwin.uvigo.es

David Posada <dposada@uvigo.es>

## Pseudogene phylogeny answers

Dear Members,

Thank you very much to everyone who replied to my inquiry. Because I received a number of requests for responses, I have compiled them below.

I hope that I received all of your replies. Our server was hit by a virus soon after I posted my question and was shut down for several days. My apologies to those who replied but are not listed.

Thanks again, Deb

My initial query:

I have a set of mitochondrial sequences and their corresponding nuclear pseudogene sequences from several vole species that I would like to use to construct a phylogeny. I have compared mitochondrial cytochrome b sequences to their nuclear pseudogenes and have found that the mitochondrial sequences are evolving more rapidly. Rather than constructing a tree for each sequence type and comparing the resultant topologies, I would like to incorporate them all into one tree but am not sure of methods that will account for the differences in their modes of evolution. I understand how to find appropriate models of substitution for a particular set of sequences using software like PAUP\* and Modeltest. I am also aware of partitioning models along sequences as with Mr. Bayes software. However, is there a way to incorporate different, appropriate models to accommodate the extreme differences in evolution between mitochondrial and nuclear sequences?

Responses:

A long time ago, before the advent of computers (well, 1996 anyway!) I was confronted with a similar situation. This is not a direct answer to

your question because I took a different approach to what you are suggesting, but you might find it interesting to compare the nuclear and

mtDNA suites of sequences in some of the same ways that I did. You can download Sunnucks, P., & Hales, D.F. (1996) Numerous transposed sequences

of mitochondrial cytochrome oxidase I-II in aphids of the genus Sitobion (Hemiptera: Aphididae). *Molecular Biology & Evolution* 13: 510-524.

>From my website at <http://www.latrobe.edu.au/-genetics/staff/sunnucks/homepage/research2.htm>

Try Ziheng Yang's program PAML. You can paste different genes end to = end in your alignment, assign them different models of sequence evolution and then construct a single tree.

— You might try a log-det transformation

When I tried to resolve this issue a few years ago, using PAUP\* and PAML, I could find nothing that would partition branches into different models of evolution. I still constructed a phylogeny, but more to illustrate the data than to be trusted. I found that parsimony methods came out with the worst trees, the pseudogene branches (which should have been relatively short)

were similar in length to the faster evolving mtDNA and this changed the

tree topology. Maximum likelihood trees with neighbour joining starting trees were better. In the end I chose to use a relatively undetailed model of evolution (e.g. HKY85-type parameters), but erred on the side of using the mtDNA-like parameters, because these changes were more common than nuclear ones. The nuclear mode of evolution would mostly have occurred in the terminal branches, and would therefore be less important for reconstructing ancestral states, or for determining general topology.

— The program by Mark Pagel and Andrew Meade, A phylogenetic mixture model for detecting pattern-heterogeneity in gene sequence or character-state data, will be available soon from Mark Pagel's website: = <http://www.ams.rdg.ac.uk/zoology/pagel/> —

The software Hy-Phy allows you to do this sort of thing. The web site is

<http://www.hyphy.org/=20>

You could try it by performing an analysis with modeltest for each sequence (gene, locus, etc.) in order to

check what is the “best model” that fits your data. Then, perform the combined analysis of all the sequences following Yang models for combined analysis with the more inclusive model (the most general model fitted to some of the sequences), incorporating the differences in rates among loci (there is a variable in the control file than accounts for it). You must perform a separate analysis (considering separate estimations for each loci) as well, and try to see if the topologies are concordant. You must remember that genes are not merely markers and that they can tell you about their own histories. Then, for the combined analysis to be useful, the tree that underlies each data set (each gene) must be the same, even when the relative rates of evolution and the rest of the parameter values are not the same for all of them.

Yang: Yang, Z. 1996. Maximum-Likelihood Models for Combined Analyses of Multiple Sequence Data. *Journal of Molecular Evolution* 42: 587-596.

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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>

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### Relative rate test

Dear Evoldir members,

We are performing a relative rate test (on protein coding sequence) using two sequences (ca. 15% diverged) versus a more divergent outgroup (ca. 25% diverged). We are using the HyPhy computer package using the following settings:

Goldman-Yang 1994 codon based model  
Synonymous/non-synonymous rates independent  
Gamma distribution with 4 rate classes

There are 4 independent parameters which are: -  
mu = non-synonymous rate - R = synonymous/non-synonymous ratio for the branch - kappa = transition/transversion ratio - alpha = the shape parameter for the gamma distribution

The final option is constraining either R, mu, or all parameters.

I would basically like to know when it is appropriate to constrain each of these three different options.

Thanks for your help! Tracy Marsters

Please reply to: <c.van-oosterhout@hull.ac.uk>

C.Van-Oosterhout@hull.ac.uk

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### SOLID for LIMBS

Hi

We are looking at a lab management systems for our DNA and Genomics facility. Specifically we are considering a product that uses SOLID as database. I had never heard of SOLID before and was wondering if anybody has feedback to give on it. Please email me directly, thanks!

Helaman Escobar DNA Sequencing & Genomics Core  
University of Utah dna@cores.utah.edu

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### Salmonid primers

Dear Colleagues

In an ongoing parentage study of hybridization between *Salmo marmoratus* and *Salmo trutta* in Slovenia we are in need of extra microsatellite loci to increase the confidence of our data. This is first and foremost due to the fact that the marble trout involved in the study show very low levels of polymorphism. We would therefore kindly ask you to take a look at the attached file which contains the names of loci that we have already screened for variation. If you have loci in your lab which are not on the list below, we would be pleased if you could send us a few aliquots of primer to test on our trout.

Thanks in advance

Best regards

Patrick Berrebi and Torben Meldgaard

Listing of the 62 loci already tested (*Salmo* and *Onchorhynchus*)  
MST85 Omm1070ARS Omm1090ARS  
Omm1105ARS Omm1107ARS Omm1108ARS  
Omm1138ARS Omm1164ARS OMM1172ARS  
Omy1Fgt1TUF omy11DIAS omy12DIAS omy13DIAS  
omy15DIAS omy17DIAS omy18DIAS omy20DIAS  
omy21DIAS omy22DIAS omy3DIAS Omy77  
omy9DIAS omyIgM(DIAS) Onem10 Onem14 Onem2



Onem9 Ots107 Sfo1 Sfo12 Sfo18 Sfo23 Sfo3 Sfo8  
 Ssa197 Ssa1DIAS Ssa202 Ssa2DIAS Ssa3DIAS  
 Ssa4DIAS Ssa5DIAS Ssa6DIAS Ssa7DIAS Ssa85  
 Ssa8DIAS SsaT47LEE SSLEEI84 SSOSL20 SSOSL311  
 SSOSL417 SSOSL438 SSOSL439 SSOSL85 Str12 Str24  
 Str43 Str58 Str591 Str593 Str79 StrBS131INRA T3-13

Patrick BERREBI UMR 5119 "Ecosystèmes La-  
 gunaires" Equipe EFEP (Écologie Fonctionnelle et  
 Evolution des Poissons) Université Montpellier II CC  
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 (France)

Tel. France 04 6714 3732 - International 33 4 6714 3732  
 Fax. France 04 6714 3719 - International 33 4 6714 3719  
 <<http://www.univ-montp2.fr/serveurs/ecolag.html>>

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### SequenceAlignment citations

Dear EvolDir readers,

Since June last year (when my new website went up),  
 over 1200 people have downloaded Se-AL, my manual  
 sequence alignment editor for the Macintosh:

<http://evolve.zoo.ox.ac.uk/software/seal/> I originally  
 wrote this program for my own use and so it is much  
 less polished than I would have liked. Unfortunately I  
 haven't had time to update this program or even fix a  
 number of bugs that I am aware of. Now we have plans  
 to get funding to produce a successor to Se-AL (and  
 the similar tool for PC, BioEdit) which will be cross-  
 platform. In order to do this I need to compile a list  
 of papers that cite Se-AL. Unfortunately as there is no  
 paper describing Se-AL, it is difficult to do this directly  
 from the publication indices.

If any reader of EvolDir has cited Se-AL in their papers,  
 I would be immensely grateful if they could drop me an  
 email with a citation or citations of these papers.

Finally, if any really enthusiastic Se-AL users wishes to  
 email me a letter of support for further development,  
 these could be used to support the funding application.

Many thanks, Andrew

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Andrew Rambaut, EMAIL - an-  
 drew.rambaut@zoo.ox.ac.uk Zoology Department,  
 WWW - <http://evolve.zoo.ox.ac.uk/> University of  
 Oxford, TEL - +44 1865 271261 South Parks Road,  
 Oxford, UK FAX - +44 1865 271249

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### Software MEGA 3 TestRelease

Dear Colleague: We are pleased to make available an  
 advanced beta test release of MEGA version 3 (test  
 release 5). You can download MEGA3 from [http://-  
 www.megasoftware.net/mega3](http://www.megasoftware.net/mega3) .

What's new in MEGA3? 1. Alignment system (a)  
 Manual alignment of DNA and proteins (b) automatic  
 translation/untranslation (codon alignment) (c) Inte-  
 grated ClustalW. (d) Import sequencer and other for-  
 mat data (e) save alignment sessions 2. Web data  
 mining (a) Integrated web-browser (b) One-click se-  
 quence retrieval from GenBank/BLAST 3. Sequence  
 Trace File Editor (a) Intuitive display (b) Manual edit-  
 ing of sequencer trace file (c) Launching BLAST from  
 sequencer trace files (d) trace file printing. 4. Enhanced  
 Tree Explorer (a) Ability to read/write newick format  
 files (b) Add images to groups and taxa. 5. Expanded  
 distance calculations (a) LogDet, JTT, Dayhoff models  
 (b) Relaxation of the homogeneity assumption

A comprehensive list of MEGA's features can be  
 found on the MEGA 3 website at the follow-  
 ing address: [http://www.megasoftware.net/mega3/-  
 features.html](http://www.megasoftware.net/mega3/-features.html) We appreciate your willingness to test  
 drive this version. Please send your comments and bug  
 reports to us at the earliest possible date to allow us  
 to release MEGA3 for use in research and teaching. In  
 the meantime, please do not publish results from this  
 test version, unless you have checked them with the full  
 release of MEGA2 or with other suitable programs.

With best wishes,

Sudhir Kumar, Koichiro Tamura, and Masatoshi Nei  
 MEGA Software Development Team

---

### Software Modeltest

Dear Modeltest users,

An updated version of Modeltest is now available from  
<http://darwin.uvigo.es> Cheers,

David.

- David Posada Facultad de Biología Campus Lagoas-

Marcosende Universidad de Vigo Vigo 36200, Spain  
 Phone: +34 986 812038 Fax: +34 986 812556 Email:  
 dposada@uvigo.es Web: darwin.uvigo.es

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## Starch Montpellier

Dear colleague,

If you need HYDROLYSED STARCH for electrophoreses (mainly allozymes)

The University Montpellier 2 (France) produces a starch which has been used for more than 100 papers published by the labs : - Genome, Populations, Interactions (CNRS UMR 5000), University Montpellier 2 - Genetique et Environnement (ISEM CNRS UMR 5554), University Montpellier 2 - Ecosystemes Lagunaires (CNRS ERS 2011), University Montpellier 2 and several other French and European laboratories.

You can order by fax You can ask for a free sample of 100g

The prices, shipping included : France 76 euros HT /Kg  
 Europe 84 euros /Kg Non European country : 92 euros /Kg

We produce also basic systems for horizontal electrophoresis, ask for description and prices

Please, use the address and references given below

Patrick BERREBI UMR 5119 "Ecosystèmes Lagunaires" Equipe EFEP (Écologie Fonctionnelle et Évolution des Poissons) Université Montpellier II CC 093. Place E. Bataillon 34095 Montpellier Cedex 5 (France)

Tel. France 04 6714 3732 - International 33 4 6714 3732 Fax. France 04 6714 3719 - International 33 4 6714 3719 <<http://www.univ-montp2.fr/serveurs/-ecolag.html>> berrebi@univ-montp2.fr

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## Sturgeon specialist

Daer Sir or Madam

I am a research staff in molecular genetics group of National Research Center for Genetic Engineering and

Biotechnology (NRCGEB), Iran. I am using a variety of DNA markers (RFLP, RAPD, SSR, SCAR, AFLP, SSCP and etc), DNA sequence data and advanced statistical methods to answer a number of different questions related to biodiversity, conservation, phylogenetics and population genetics in a variety of animal (especially fishes) and plant (especially olive) species in Iran. I have a question. Dear Professor would you like to design a research program on the Sturgeon fishes (Acipenseridae) in the Caspian Sea? (of course in field of biodiversity and population genetic). If you are agree I will have more information about the project.

Sincerely Yours,

S.M. Samaee

National Research Center for Genetic Engineering and Biotechnology (NRCGEB). P.O.Box: 14155-6343, Tehran, Iran. Postal Cod: 1417864411 Fax: (+98) 21 6418304 or 6419834 E-mail: samaei@nrcgeb.ac.ir samapharma@yahoo.com

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## Urosaurus primers

I wish to inquire if there is anyone out there who is working on developing primers for the lizard *Urosaurus ornatus* or related lizards. These could be from the genera *Uta*, *Uma*, *Callisaurus*, *Cophosaurus*, *Holbrookia*, *Petrosaurus*, *Phrynosoma*, or *Sceloporus*. These primers will be used for a paternity analysis in a field selection study. Any assistance or leads would be much appreciated.

Best,

Paul Hamilton

<<mailto:phamilton@asu.edu>> phamilton@asu.edu

<<http://www.lizardchasers.org/>>

[www.lizardchasers.org](http://www.lizardchasers.org)

Paul Hamilton Arizona State University School of Life Sciences Tempe, Arizona 85287-4601

mailing address: Arizona State University , West Campus Department of Life Sciences 4701 W Thunderbird Rd. Mail Code 2352 Glendale AZ, 85306 602 363-0331

Paul Hamilton <[phamilton@asu.edu](mailto:phamilton@asu.edu)>

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## Wild Arabidopsis collection

Dear Colleagues,

I am organizing an effort to collect seeds of *Arabidopsis thaliana* with ecological information about the local habitat. Initially this effort was focused on North America just because that is where most of us are based. Currently, this has been expanded to at least coordinate with efforts in Europe and Central Asia. This project is still in the planning stages, although we have been starting to collect. This collection will differ from the current ecotypes as it will have information about the local site and plants and it will have multiple maternal sibships. I also have a list serv for this effort and related matters. If you are interested in participating in the effort contact me (dlbyer2@ilstu.edu) to be added to our list serv. cheers, Diane

Diane L. Byers Assistant Professor in Evolutionary Biology Behavior, Ecology, Evolution, and Systematics Section Department of Biological Sciences Campus Box 4120 Illinois State University Normal, IL 61790 309-438-8167 fax 309-438-3722 e-mail dlbyer2@ilstu.edu <http://www.bio.ilstu.edu/byers/>

Diane Byers <dlbyer2@ilstu.edu>

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## cDNA genomic alignment

Hello EvolDir

Does anyone know of a program that takes genomic DNA (i.e. with non-coding DNA regions) and cDNA as inputs, and gives aligned outputs (i.e. with exons and introns)? Seems like many people are encountering this problem, and the number will only increase. I can

think of several ways a program could do this, but I have no idea how to code it.

On the same note, does anyone have a program that takes a multi-fasta file and aligns all the sequences using tblastx rather than the clustal algorithm?

Cheers and thanks for any help,

Chris

Christopher West Wheat, Ph. D.

Max Planck Institute of Chemical Ecology Department of Genetics and Evolution Hans Knoll Str. 8 07745 Jena, Germany

home phone: 49-(0)3641-666185 work phone: 49-(0)3641-571415 fax : 49-(0)3641-571402

cwheat@ice.mpg.de cwheat@ice.mpg.de

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## mtDNA nuclear markers

Dear everybody,

I am interested to know if it is possible to combine mitochondrial (RFLP) and nuclear (microsatellite) marker data for constructing phylogenetic trees. If so, would it be reasonable to include the mtDNA as four (identical) loci, in order to compensate for the differences in effective size of nuclear and maternally inherited loci.

Many thanks in advance!

8) Anni

Anni Tonteri Ph.D. student Department of Biological and Environmental Sciences Division of Population Biology P.O. Box 65 00014 University of Helsinki FINLAND

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8) Anni

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## PostDocs

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### ArizonaStateU EvolBioinformatics

#### POSTDOCS in EVOLUTIONARY BIOINFORMATICS

Applications are invited for RESEARCH AND DEVELOPMENT POSITIONS in the computational biology laboratory of Dr. Sudhir Kumar at Arizona State University. Successful candidates must have expertise in one of the following five areas: (1) comparative analysis of DNA and protein sequences, (2) development of statistical or computational methods for molecular evolutionary analysis, (3) computer simulations in molecular phylogenetics, (4) building developmental gene interaction networks from data-mining, and (5) biological software and database development. Candidates must have a Ph.D. in a related discipline. Preference will be given to candidates with research programs that emphasize theoretical, informatics, and/or empirical analysis of data from animals. Successful candidates will have flexible start dates beginning immediately or later in the year. All initial appointments will be for one year and will be renewable for additional years contingent upon satisfactory performance and availability of funds. Applicants must submit a cover letter indicating his/her area of expertise; a brief statement of research interest, a complete curriculum vitae; and names, addresses, and telephone numbers of two references to: Sudhir Kumar, School of Life Sciences, Arizona State University, PO Box 874501, Tempe, AZ 85287-4501. E-mail: [s.kumar@asu.edu](mailto:s.kumar@asu.edu); FAX (480) 965-6899; Telephone: (480) 727-6949; Web sites: Kumar Laboratory (<http://www.kumarlab.net>), Center for Evolutionary Functional Genomics (<http://www.azbio.org/efg>), School of Life Sciences (<http://sols.asu.edu/geb>). Review of applications will begin starting June 15, and

thereafter on the first and 15th of each month until the positions are filled. Arizona State University is an Affirmative Action/Equal Opportunity Employer

— Dr. Sudhir Kumar, Director Center for Evolutionary Functional Genomics Arizona Biodesign Institute Associate Professor, School of Life Sciences Life Sciences A-351 Arizona State University Tempe, AZ 85287-4501 Tel: (480)-727-6949 (office) (480)-727-6947 (lab) Fax: (480)-965-6689 Email: [s.kumar@asu.edu](mailto:s.kumar@asu.edu) Software: <http://www.megasoftware.net/>

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### Austria Drosophila Gene expression

Postdoctoral position available

Evolution of male biased gene expression in Drosophila

This position is available for 18 months in the laboratory of Christian Schlotterer. Applicants should have a background in molecular evolution and/or population genetics. Candidates familiar with molecular techniques (expression profiling, sequencing, cloning) and genomic databases are particularly encouraged to apply.

The successful candidate will have close interaction with bioinformaticians, population geneticists and developmental biologists in the group.

Current members of the laboratory come from Austria, France, Germany, Italy, India and Scotland. The laboratory operates bilingually, allowing non-German speaking researchers to integrate easily.

Vienna provides a stimulating scientific environment with a number of research groups focusing on population genetics and evolutionary biology: Reinhard

Burger, Ulf Dieckmann, Dustin Penn, Karl Sigmund, Peter Schuster and Claus Vogl. Apart from good science, Vienna also offers an active cultural life (2 operas, 2 world class concert houses, numerous museums and the famous coffee houses), excellent public transport, excellent schools, numerous museums, and attractive outdoor recreation opportunities (alps are close by and you can sail within the city area!). <http://www.virtourist.com/cgi-bin/search.pl?Range=All&Format=Standard&Terms=vienna&Submit=Post>

Further questions and applications should be directed to Christian Schlotterer (Christian.schlotterer@vu-wien.ac.at). The position is available immediately; however, the starting date is flexible.

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### CollegeWilliamMary EvolEndocrinology

Postdoctoral Position, Evolutionary Neuroendocrinology, College of William and Mary (Available September 2004 until filled)

A research/teaching postdoctoral position is available, renewable annually for up to five years, to investigate the evolution of complex neuroendocrine pathways. Applicants should have a PhD prior to September 2004 and experience in one or more of these areas: neuroendocrinology, behavior, evolutionary biology, physiology, or cell and molecular biology. The successful candidate will conduct collaborative research, assist in managing a research laboratory of undergraduate and master's level research students, and teach one course annually, preferably comparative physiology, each spring semester. The research focus is on the contribution of genetic variation and phenotypic plasticity to the evolution of a complex neuroendocrine pathway. This pathway integrates photoperiod and other environmental information to regulate reproductive, physiological and behavioral responses to seasons. More details on the research are available at: <http://faculty.wm.edu/pdheid>. The College of William and Mary is a Public Ivy<sup>1</sup> with 5500 undergraduate enrollment, nationally competitive undergraduates, and a strong research tradition. This postdoctoral position is particularly good experience for individuals wanting to develop skill at balancing teaching and research while working at a selective undergraduate institution. Starting salary will be \$35,000 plus benefits. Please send curriculum vitae, a brief description of research interests/experience, and the names and contact informa-

tion of three references to: Dr. Paul Heideman, Chair-elect, Department of Biology, P.O. Box 8795, College of William and Mary, Williamsburg, VA 23187-8795; e-mail: [pdheid@wm.edu](mailto:pdheid@wm.edu). Applications from minorities, women, or non-US citizens are encouraged. The College of William and Mary is an Affirmative Action/Equal Opportunity Employer.

[gwgilc@wm.edu](mailto:gwgilc@wm.edu) [gwgilc@wm.edu](mailto:gwgilc@wm.edu)

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### CornellU InsectImmunity

#### POSTDOCTORAL POSITION

A postdoctoral position to study the evolutionary genetics of insect immunity is available in the laboratory of Brian Lazzaro at Cornell University. Work in the lab is primarily focused on antimicrobial responses in *Drosophila* and antimalarial responses in *Anopheles*. The *Drosophila* project involves using population and quantitative genetic approaches to characterize genes contributing to phenotypic variation in resistance to environmental microbes. The *Anopheles* project uses molecular evolutionary and population genetic approaches to infer selective pressures placed on mosquito immune response genes by malaria parasites. The applicant may work in either or both systems, tailoring project details to fit their background and interests.

Applicants should have a strong background in population genetics, molecular evolution, ecological genetics, or a related discipline. Applications should include a CV, a brief statement of research interests and experience, and contact information for three references. Support for this position is available immediately, but start date is flexible.

Applications and informal inquiries may be directed to:

Brian P. Lazzaro, Ph.D. Department of Entomology Cornell University Ithaca, NY 14853 email: [BL89@cornell.edu](mailto:BL89@cornell.edu) [http://www.entomology.cornell.edu/Faculty\\_Staff/Lazzaro/](http://www.entomology.cornell.edu/Faculty_Staff/Lazzaro/)

Cornell is an Affirmative Action/Equal Opportunity Employer.



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## FloridaStateU TheoEvolGenetics

Postdoc in theoretical evolutionary genetics: A post-doctoral research position is available at Florida State University to work with Drs Thomas F. Hansen and David Houle on an NSF-funded project entitled "Evolvability and constraints in fly wings". The project studies the genetic basis of evolvability through various theoretical models, and by using the remarkably conservative wing shape in *Drosophilid* flies as a model system. We seek an applicant to work with us either on the theoretical part of the project, or on a combination of the theoretical and experimental /empirical parts. We are quite flexible in regard to the exact topic of work for the postdoc. The project offers the opportunity to work on the interface between theory and experiment in an interactive research group already including two faculty, two postdocs, and a number of graduate and undergraduate students. Applicants should have an interest in broad and conceptual issues of evolutionary biology and population genetics including the relationship between genotype and phenotype and the role of constraints in evolution. We are looking for expertise in one or more of the following areas: Theoretical or computer modeling, multivariate statistics, developmental genetics, modeling of gene-regulatory networks, and population/evolutionary genetics. The position is available immediately. Funding is guaranteed for two years with a salary of \$28,000-\$30,000 per year depending on experience.

For more detail see our respective lab pages (<http://bio.fsu.edu/~dhoule/>) and (<http://www.bio.fsu.edu/faculty-hansen.php>). Many of the ideas in the project are discussed in:

Hansen, T. F. & Houle, D. 2004. Evolvability, stabilizing selection, and the problem of stasis. In Pigliucci, M. & Preston, K. (Eds). *Evolutionary biology of complex phenotypes*. Oxford University Press. Pp. 130-150. (A preliminary version is available on our web pages).

Florida State University has a dynamic and expanding group of some 20 ecologists and evolutionary biologists, including recent hires of computational biologists: Dave Swofford, Gavin Naylor, Peter Beerli, and Fredrik Ronquist. The atmosphere is collegial and interactive. For more information, see the Ecology and Evolution group's web site (<http://www.bio.fsu.edu/>). Tallahassee offers cheap living, warm weather, and the many

opportunities for outdoor recreation in the surrounding area.

To apply, contact Thomas Hansen ([thomas.hansen@bio.fsu.edu](mailto:thomas.hansen@bio.fsu.edu)) or David Houle ([dhoule@bio.fsu.edu](mailto:dhoule@bio.fsu.edu)) with a letter detailing your expertise and interest in the position, a Curriculum Vita, and the names of three references that we may contact.

Thomas F. Hansen Florida State University Department of Biological Science, Conradi Building, Tallahassee, FL32306 USA Phone: +(850)-644-4779 Email: [thomas.hansen@bio.fsu.edu](mailto:thomas.hansen@bio.fsu.edu) Fax:+(850)-644-9829 Fax:+(850)-644-9829

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## HalleGermany AnimalPopGenet

The department of community ecology at the UFZ Centre for Environmental Research Leipzig-Halle will fill a position of a Postdoctoral Fellow starting 1 September 2004. The position is for a period of three years. The department of community ecology is an interdisciplinary botanic-zoological group with emphasis on e.g. biodiversity, population structure in the landscape context, fragmentation, conservation genetics, biological invasions, microevolution, population biology and macroecology. The applicant will work in the area of animal population genetics and phylogeography. We expect the applicant to develop research projects integrated in the departments activities linked e.g. to current analyses of genetic population structure of phytophage, parasite- and parasitoid complexes and phylogeographic studies. Minimal requirements are a finished PhD thesis in biology with population genetic or phylogeographic background, experience with molecular markers and automated sequencers and international publication record. Experience with one or more of development of microsatellite markers, analyses of subfossil DNA is desirable as is grant success. The candidate cannot be older than 35 years of age, possess a valid university degree in the above mentioned or closely related fields and must have completed his Ph.D. within the last 5 years. The place of work is Halle/Saale, Germany. Salary will be according to the appropriate civil service level (BAT-O). Physically handicapped persons will be favoured if they are equally qualified. To increase the share of women in science and research women are explicitly encouraged to apply. For further information please contact: Dr. Durka,

Tel. +49 (0)345-5585 314, e-mail: walter.durka@ufz.de <mailto:walter.durka@ufz.de> Recruitment advertising of the UFZ take place both in the press and in the internet (<http://www.ufz.de> <<http://www.ufz.de>>). Candidates should send their application with CV, list of publications and references under the code digit 26/2004 until 15 June 2004 to the Personnel Department, No.: P.O. Box 500136, D-04301 Leipzig, Germany

cally challenging research with models that are highly relevant for population biology.

Applications including a short CV and two letters of reference should be submitted by 30 June 2004 to Dr. Otso Ovaskainen by email, [otso.ovaskainen@helsinki.fi](mailto:otso.ovaskainen@helsinki.fi).

Further information: Otso Ovaskainen ([otso.ovaskainen@helsinki.fi](mailto:otso.ovaskainen@helsinki.fi), phone +358 9 191 57924), Metapopulation Research Group, Department of Biological and Environmental Sciences, PO Box 65 (Viikinkaari 1), 00014 University of Helsinki, Finland.

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## Helsinki MathEcol

### POST DOC POSITION IN MATHEMATICAL BIOLOGY IN HELSINKI, FINLAND

A two-year post doc position (with a possibility for a one year extension) on mathematical biology is available from August 2004 onwards in the Metapopulation Research Group ([www.helsinki.fi/science/metapop](http://www.helsinki.fi/science/metapop)), Department of Biological and Environmental Sciences, University of Helsinki, Finland. Monthly salary is ca. 2400 EUR. The PhD project is aimed at developing mathematical methods for the analysis of spatial and stochastic multi-species population models.

While theoretical ecologists have developed various approaches to understand the roles that space and stochasticity play in ecological systems, these approaches (including simulations, pair-approximations, and spatial moment equations) have been at least partly based on heuristic arguments. We aim at developing a new general framework for the analysis of stochastic and spatial systems, which is based on the theory of distributions (to account for space) and on a systematic perturbation expansion (around a mean-field model) of the underlying stochastic differential equations (to account for noise). As a starting point, we have applied the method to a Markov process that represents a single-species metapopulation inhabiting an infinitely large dynamic landscape. The results, which characterize the spatio-temporal correlation structure of the stationary state in an asymptotically exact manner, are among the first mathematically rigorous results in theoretical ecology that relate to a stochastic model with a non-trivial spatial structure.

The available project aims at applying the above described modeling framework to multi-species models, such as competition models and host-parasitoid models. The project provides an excellent opportunity for a post doc who is interested in pursuing mathemati-

Job Description: An EU funded post-doctoral position in insect dispersal is available immediately for a 2 year study involving dispersal studies of the European corn borer, *Ostrinia nubilalis* (Lepidoptera: Crambidae). The successful applicant will receive a one-year appointment with good chances for a second year renewal. This appointment includes a salary (around 2,000 euros per month), healthcare benefits, and a research/travel allowance. This position is funded by an EU project entitled "Protecting the benefit of Bt-toxins from insect resistance development by monitoring and management". The aim of this project is the management of Bt maize (maize producing a toxin of *Bacillus thuringiensis*) in order to avoid the evolution of resistance in natural populations of the European corn borer (ECB). A significant part of this project requires the investigation of individual dispersal at a fine geographical scale. Beyond the framework of the EU project, the post-doc fellow will be involved in evolutionary studies on *Ostrinia nubilalis* related to host plant adaptation and sympatric speciation and/or ecological studies aimed at integrating the ECB-maize interaction into a broader, community-wide perspective.

Job location: Center for Biology and Management of Populations (CBGP), Montpellier (France). The successful candidate will join the Population Genetics team which includes 10 evolutionary biologists (Arnaud Estoup, Jean Marie Cornuet, Réjane Streiff, Jean Francois Cosson.). For more information on the CBGP, please visit the web site at <http://www.ensam.inra.fr/-CBGP/>. Required experience: mark-recapture experiments, theoretical skills on the analysis and modeling of insect dispersal, field surveys including GPS and mapping techniques. A background in landscape ecology and/or community ecology would be a plus. The appli-

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## Montpellier InsectDispersal

cant must be physically fit (i.e. able to work long days in steep terrain), able to supervise a field crew and field experiments.

Application : a Ph.D. is required; to apply, submit electronically (1) CV, (2) copies of recent publications (maximum of three), (3) a statement of research interests (4) the names and addresses of three individuals to Denis Bourguet (bourguet@jouy.inra.fr) and Sergine Ponsard (sergine.ponsard@cict.fr). Review of applications will start 1st of June 2004 and continue until the position is filled.

Denis Bourguet <bourguet@ensam.inra.fr>

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## Montpellier Phyloinformatics 2

Open post-doctoral position, starting September 2004, Montpellier - FRANCE

“Phylogenomics, supertrees, supermatrices”

The recent increase in the number of DNA, RNA, and protein sequences available for a variety of organisms helps to understand complex questions of evolutionary biology in a phylogenetic framework. Ambitious Tree of Life projects are now set up, with the aim of reconstructing the evolutionary history of very large species sets using numerous genes. The genes can be analyzed separately to produce the gene trees, which are then combined into a “supertree” describing species evolution. Alternatively, the genes can be assembled into a supergene or “supermatrix”, which is then analyzed to obtain the final species tree.

The candidate will work on supertree and supermatrix approaches. Various methods will be envisaged (combinatorial, probabilistic, bayesian) and compared using both simulations and real data sets at a genomic scale (bacteria, eukaryotes, mammals).

Contact (URGENTLY!):

Emmanuel J. P. DOUZERY - douzery@isem.univ-montp2.fr <http://www.isem.univ-montp2.fr/PPP/-PHYLMOL.php> (Go to Research > Phyloinformatics > Supertrees)

Olivier GASCUEL - gascuel@lirmm.fr <http://www.lirmm.fr/~w3ifa/MAAS/> Olivier GASCUEL <gascuel@lirmm.fr>

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## Montpellier Phyloinformatics 3

Open post-doctoral position, starting September 2004, Montpellier - FRANCE

“Phylogenomics, supertrees, supermatrices”

The recent increase in the number of DNA, RNA, and protein sequences available for a variety of organisms helps to understand complex questions of evolutionary biology in a phylogenetic framework. Ambitious Tree of Life projects are now set up, with the aim of reconstructing the evolutionary history of very large species sets using numerous genes. The genes can be analyzed separately to produce the gene trees, which are then combined into a “supertree” describing species evolution. Alternatively, the genes can be assembled into a supergene or “supermatrix”, which is then analyzed to obtain the final species tree.

The candidate will work on supertree and supermatrix approaches. Various methods will be envisaged (combinatorial, probabilistic, bayesian) and compared using both simulations and real data sets at a genomic scale (bacteria, eukaryotes, mammals).

Contact (URGENTLY!):

Emmanuel J. P. DOUZERY - douzery@isem.univ-montp2.fr <http://www.isem.univ-montp2.fr/PPP/-PHYLMOL.php> (Go to Research > Phyloinformatics > Supertrees)

Olivier GASCUEL - gascuel@lirmm.fr <http://www.lirmm.fr/~w3ifa/MAAS/> -----

LIRMM, 161 rue Ada, 34392 - Montpellier - FRANCE  
Tel. (33 or 0 from France) 4 67 41 85 47 Fax. (33 or 0 from France) 4 67 41 85 00 <http://www.lirmm.fr/~w3ifa/MAAS/> gascuel@lirmm.fr

Emmanuel J. P. DOUZERY - Maitre de Conférences Lab. de Paleontologie, Paleobiologie et Phylogénie CC064 (RDC bat. 22) Institut des Sciences de l'Evolution (UMR 5554 CNRS) Université Montpellier II - Place E. Bataillon 34 095 Montpellier Cedex 5 - France

Tel. = 33 4 67 14 48 63 / Fax = 33 4 67 14 36 10 e-mail = ed@isem.univ-montp2.fr

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## Munich TheoPopGen

Postdoc position Theoretical population genetics  
 “Interactions in evolutionary processes” Ludwig-  
 Maximilians-Universität (LMU) Munich

### PROJECT

An Emmy Noether research grant from the German Research Foundation (DFG) has been awarded to study the role of epistasis (gene interactions) and gene-environment interactions in evolutionary processes. The overall goal of the project is to understand how past evolution and environmental factors shape the boundary conditions under which further evolution occurs. Questions are asked on the molecular and the quantitative genetic level and include the following:

\* Molecular population genetics: How does epistasis affect rates of evolution? Adaptation after rapid environmental changes: How do footprints of selection look like if selected alleles are taken from the standing genetic variation? What is the distribution of selection coefficients of adaptive substitutions in this case? (Collaboration with Wolfgang Stephan and Allen Orr)

\* Multilocus models of quantitative genetics: How does epistasis affect the genetic variation in mutation-selection balance? How does the genetic architecture of complex traits evolve? What maintains evolvability of these traits? Is there a tendency for the evolution of genetic robustness? What are the evolutionary consequences of genetic robustness? Is there selection for modularity of the genotype-phenotype map? (Collaboration with Gunter Wagner and Thomas Hansen)

\* Potential further topics include: Measurement of epistasis from QTL data, Evolution of genetic buffering, genetic differentiation, and phenotypic plasticity in structured environments, Evolution of mutational buffering in clonal populations

... and there is a lot of room for your own ideas and suggestions.

Problems are addressed by analytical approaches, simulation studies and data analysis. Contacts and collaborations have been established with:

Ellen Baake, Bielefeld Univ. Arjan De Visser, Wageningen Univ. Wilfried Gabriel, Munich Thomas Hansen, FSU at Tallahassee Beate Nuernberger, Munich Allen Orr, Rochester Wolfgang Stephan, Munich Michael

Turelli, UC Davis Gunter Wagner, Yale

### QUALIFICATIONS

The most important prerequisite is high motivation and an interest in population genetic modeling.

A PhD in evolutionary biology, physics, or mathematics and at least basic knowledge in population genetics and the relevant mathematical methods is required for this position. Applicants with a biological background should have experience in population genetics, molecular evolution, or a related field. Highly qualified applicants with background in mathematics (stochastic processes) or theoretical physics (many particle systems) are also encouraged to apply. Computer skills (C++, Mathematica, etc) are helpful, but not mandatory.

### APPLICATION

Informal inquiries and full applications (including CV, publication list, experience, qualifications, and address/phone/email of two references) should be sent by e-mail (or regular mail, see address below) in English or German to Joachim Hermisson ([hermisson@zi.biologie.uni-muenchen.de](mailto:hermisson@zi.biologie.uni-muenchen.de)). Disabled applicants will be privileged if equally qualified. The position is funded for one year with extension possible (up to two years). It is available immediately, but the starting date can be negotiated. Salary will be according to BAT IIa, which is about 36.000 - 42.000 Euro per year before tax (depending on age, marital status etc).

The department “Biologie II” of the LMU Munich offers an excellent research environment and a strong scientific background in evolutionary biology, with a particular strength in theoretical population genetics. Main research fields are molecular population genetics (groups of W. Stephan and J. Parsch) and evolutionary ecology (W. Gabriel and S. Diehl). Language in lectures and seminars is English.

— Dr. Joachim Hermisson, Department Biologie II, LMU Munich, Luisenstr. 14, D-80333 Munich, Germany, Tel: +49-89-5902-290, e-mail: [hermisson@zi.biologie.uni-muenchen.de](mailto:hermisson@zi.biologie.uni-muenchen.de) <http://www.zi.biologie.uni-muenchen.de/institute/zi/-abt/ln/evolutionsbiologie/>

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**NorthCarolinaStateU**  
**DiseaseModels**

North Carolina State University– Vector/disease models

Postdoctoral Fellowship

Vector/disease models: We need an evolutionary biologist with experience in computer simulation modeling (C++ preferred) to work on an NIH-funded project. The project is aimed at developing spatially explicit models of mosquito population dynamics/genetics that can contribute to assessment of risks and benefits associated with a number of strategies for releasing transgenic mosquitoes to reduce the incidence of human disease. The fellowship is for 3 years. In addition to working on model development and testing, the person in this position will collaborate in an interdisciplinary group composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries, in efforts to develop novel transgenic strategies for disease reduction. The person in this position will develop a user-friendly version of the model and will work with the PI in organizing an NIH-funded workshop to teach other researchers to use the model. There will be an opportunity for some empirical research (if desired), and for interactions with other members of the lab working on other evolutionary and modeling research.

An overview of the area of research and an entry point to relevant literature can be found in “Gould, F., and P. Schliekelman. 2004. Population genetics of autocidal control and strain replacement. *Ann. Rev. Entomol.* 49: 193-217”.

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

To apply: Send to Fred\_Gould@NCSU.edu 1) A one or two page letter of intent. 2) CV. and 3) Names of 3-4 references. Closing date for applications is August 1, 2004, or until a suitable candidate is found.

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## Rotterdam bioinformatics

Post-doc or PhD student in Biostatistics / Bioinformatics

A Post-doc or Ph.D. student position is available in the newly established Department of Forensic Molecular Biology at the Erasmus MC University Medical Centre Rotterdam, The Netherlands. You will be working on theoretical population genetic and bioinformatic issues in projects investigating human individual and population differences with the future aim of predictive use in forensic identification. You have a strong background in statistics /biostatistics /bioinformatics (PhD/MS) with experience in theoretical population genetics (data analysis, data modeling, model development). Programming skills as well as experience in data mining are needed and skills in data management are a plus. You are highly motivated, scientifically creative and able to work independently. Biologists with a strong background in theoretical population / medical genetics (PhD/MS), who are able to work independently on statistical issues are encouraged to apply as well.

As Post-doc you will officially be appointed by the Netherland Forensic Institute (NFI), fulltime for a period of two to three years, place of work is Erasmus MC. The gross monthly salary, depending on qualifications and experience, is a maximum of ? 3.458,88 (scale 10) full-time. The conditions of employment are in accordance with the ARAR. As PhD student you will be appointed by the Erasmus University Rotterdam, full-time for a period of four years, place of work is Erasmus MC. The gross monthly salary will be ? 1.702 gross in the first year up to ? 2.283 gross in the fourth year. The conditions of employment are in accordance with the Collective Bargaining Agreement for Dutch Universities.

Please send your application with CV, a description of research interests, publication list and names and contact information for three references to Prof. Dr. M. Kayser, Department of Forensic Molecular Biology, Erasmus MC University Medical Center Rotterdam, Medical-Genetic Cluster, PO Box 1738, 3000 DR Rotterdam, The Netherlands, or by e-mail to [m.kayser@erasmusmc.nl](mailto:m.kayser@erasmusmc.nl).

– Manfred Kayser, Dr. rer. nat. habil. Dipl.-Biol. Professor of Forensic Molecular Biology Erasmus MC - University Medical Centre Rotterdam Department of Forensic Molecular Biology PO Box 1738, 3000 DR Rotterdam, The Netherlands

Phone: ++31-10-46380-73: secretary -72 E-mail: [m.kayser@erasmusmc.nl](mailto:m.kayser@erasmusmc.nl)

Manfred Kayser <[m.kayser@erasmusmc.nl](mailto:m.kayser@erasmusmc.nl)>



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## UArizona GenomeEvol

### GENOME EVOLUTION UNIVERSITY OF ARIZONA

We have two Postdoctoral Research positions available in the lab: one to conduct bioinformatic and computational studies on bacterial genomes (including analyses of complete genome sequences and of gene expression and proteomic data), and the other to conduct experimental studies on the processes gene transfer and degradation on the evolution of bacterial genomes.

Applicants could have skills in any of several areas of evolutionary, molecular, microbial or computational, biology and/or genetics, and we encourage applicants from any of these fields.

The position is available immediately; however, the starting date is very flexible. Salary (in the range of \$35K to \$45K, plus benefits) will be commensurate with experience.

If interested, please send your curriculum vita and the names of at least two referees to:

Howard Ochman Department of Biochemistry 233 Life Sciences South University of Arizona Tucson, Arizona 85721 USA 520-626-8355 (phone) 520-621-3709 (fax) hochman@email.arizona.edu

If you have questions regarding either of these positions, please contact me via e-mail. Also, I will be at the ASM meeting (New Orleans, May 23 - 27) and the SMBE Genomes and Evolution meeting (Penn State, June 17 -20), and I would be happy to speak with you then.

Howard Ochman <hochman@email.arizona.edu>

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## UCLA AvianPopStructure

### POSTDOCTORAL POSITION AVIAN POPULATION STRUCTURE, CONNECTIVITY, CONSERVATION, AND EVOLUTION

A postdoctoral position is available in the Department of Organismic Biology, Ecology, and Evolution and the

Center for Tropical Research, Institute of the Environment at UCLA. The position is available for one year with the possibility of renewal.

We are seeking a broadly trained evolutionary biologist with a strong background in the application of molecular genetic techniques to natural populations, preferably in birds. The successful candidate's primary responsibility will be to investigate the population genetic structure and connectivity of Neotropical migrant birds and to assist in expanding the Center's research activities in avian evolution and conservation. In addition, the postdoctoral fellow will have the opportunity to explore broader questions relating to population diversification and microevolutionary processes. The fellow will be expected to interact and collaborate with postdoctoral researchers and graduate students working on other projects. Other Center projects include: 1) investigations of the mechanisms of speciation, 2) avian phylogenetic structure and disease, and 3) seed dispersal and forest regeneration. We are particularly interested in individuals with experience in working at the intra-specific level and with broad knowledge of molecular genetic techniques, especially the application AFLPs. Interested candidates should send a CV, a brief description of research interests, and names and contact information for three references to:

Thomas B. Smith Professor, OBEE Director, Center for Tropical Research Institute of the Environment University of California, Los Angeles 1609 Hershey Hall Box 951496 Los Angeles, CA 90095-1496 USA <http://www.ioe.ucla.edu/ctr> tbsmith@ucla.edu Phone: (310) 206-6234 Fax: (310) 825-5446

"Thomas B. Smith" <tbsmith@ucla.edu>

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## UCollegeLondon EvoDevo

University College London Post Doctoral Research Fellow

Department of Biology

Post doctoral Research Fellow in Evolution of Development

Stasis and change in the regulation of a master gene and the evolution of morphological novelty in the arthropods.

Applications are invited for a three-year, BBSRC-funded post in the department of Biology.

The research will involve cloning of genes from the model crustacean *Parhyale hawaiiensis*, whose homologs in *Drosophila* are involved in the regulation of expression of the leg-promoting gene, *Distal-less* (*Dll*). These *Parhyale* genes will be assayed for a role in *Dll* regulation using *in situ* hybridisation, RNA interference and using reporter constructs introduced into flies and *Parhyale*. Experience of molecular biology is essential, knowledge of *Drosophila* genetics, in particular transgenesis, highly desirable as is an interest in animal evolution.

For further details of the project contact Dr Max Telford at [ucbtmax@ucl.ac.uk](mailto:ucbtmax@ucl.ac.uk) or at the address below. The position is funded at Point 6 on the University 1A scale. Starting salary currently £22,445 including London allowance of £2,134.

Please apply in writing with a current CV and the names of 3 referees to:

Dr Max Telford, Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT

The closing date for applications is Thursday, 10th June 2004.

UCL Taking Action for Equality

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## UUtah Solanaceae

Searches reopened for two postdocs at the University of Utah.

One postdoctoral position is available on an NSF-funded project to investigate systematic relationships in the spiny *Solanum* clade (*Solanaceae*). This group, largely equivalent to *Solanum* subgenus *Leptostemonum*, includes about 450 species and is the largest subgenus in *Solanum*. Responsibilities include generation of molecular data for phylogeny reconstruction (mainly sequences of chloroplast and nuclear genes); maintenance and analysis of living greenhouse collections of *Solanaceae*; data analysis, presentation, and publication; training and supervision of undergraduate lab assistants; and oversight of routine lab activities. Candidates should have a Ph.D. and experience in molecular systematics of plants; experience with *Solanaceae* is preferred but not required. This position is available for one year beginning immediately and renewable for up to two years.

The second postdoctoral position is available on an internationally collaborative project to produce a global monograph of the genus *Solanum* (*Solanaceae*). The project is one of four Planetary Biodiversity Inventory programs funded by NSF in collaboration with the ALL Species Foundation. *Solanum* includes between 1000 and 2000 species and is one of the largest genera of angiosperms. The species level taxonomy, including images, keys and specimen data, will be made available over the Internet. Responsibilities include monographic taxonomy of selected species groups of *solanums*; specimen and image databasing and manipulation; field work for the collection of herbarium, seed and silica gel samples; generation of molecular data for phylogeny reconstruction (mainly sequences of chloroplast and nuclear genes); maintenance and analysis of living greenhouse collections of *Solanaceae*; data analysis, presentation, and publication; training and supervision of undergraduate lab assistants; and oversight of routine lab activities. Candidates should have a Ph.D. and experience in plant systematics, field work and with working in a team; experience with *Solanaceae* is preferred but not required, as is experience with molecular systematics and a variety of methods of data analysis. This position is available for one year beginning immediately and extendable for up to five years.

Electronic submission of applications is encouraged.

Review of applications will begin immediately and continue until a suitable candidate is chosen. Applicants should submit a statement of interest and description of past experience, a curriculum vitae, and contact information (names, email addresses, and phone numbers) of three references to:

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 USA E-mail: [bohs@biology.utah.edu](mailto:bohs@biology.utah.edu) Phone: (801) 585-0380

Information on the Biology Department at the University of Utah is available at [www.biology.utah.edu](http://www.biology.utah.edu) The University of Utah is an Equal Opportunity Employer.

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 (801) 585-0380

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## UZurich SpermBiology

Postdoc, Sperm biology

A postdoctoral position is available in the Zoological

Museum of the University of Zürich, Switzerland. The successful applicant will join a group working on the biology of sperm in the yellow dung fly. The research will be on the integration of evolutionary and physiological perspectives but the exact details will be arranged in collaboration with the successful applicant. Applications will be particularly welcome from two research directions: a) candidates able to integrate biological data into mathematical models of sperm movement and transport, and b) candidates interested in the physiological or microanatomical processes of sperm transport and function in insects.

Applicants must have a PhD. Good computing or quantitative biological skills and publications in international journals are essential. Knowledge of German would be advantageous. The position is available for two years, with two possible extensions of one year. The position is available from July 1, 2004, but later dates are acceptable. For inquiries contact [pward@zoolmus.unizh.ch](mailto:pward@zoolmus.unizh.ch).

Please send a curriculum vitae, list of publications and summary of research interests, in a single file by e-mail, by 28th June to [zmdirektion@zoolmus.unizh.ch](mailto:zmdirektion@zoolmus.unizh.ch) or Prof Ward, Universität Zürich, Zoologisches Museum, Winterthurerstr. 190, 8057 Zürich.

– Prof Paul I Ward Direktor Zoologisches Museum der Universität Zürich Winterthurerstrasse 190 CH 8057 Zürich Switzerland Phone +41 1 635 4760 Fax +41 1 635 4780

Direktionssekretariat: Rosemarie Keller Mail: [kellerro@zoolmus.unizh.ch](mailto:kellerro@zoolmus.unizh.ch) Phone +41 1 635 4761

Paul Ward <[pward@zoolmus.unizh.ch](mailto:pward@zoolmus.unizh.ch)>

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## Yale DiseaseEvol

A post-doctoral position is available at Yale Medical School in the Department of Epidemiology and Public Health to model the evolution and epidemiology of infectious diseases. The precise project is flexible, but possible projects may include population genetics of disease resistance, evolution of virulence, spatial dynamics of disease transmission, vector-borne diseases and control of emerging diseases.

This position will require an independent and motivated individual who has published in epidemiology, population biology and/or population genetics. Mathematical and/or computational modeling skills are essential. Applicants should have received their PhD prior to taking up the appointment.

Funding is available for one year, but can be renewed, depending on performance. The salary is according to NIH pay scale, i.e. \$35,568 to 41,496 per year, commensurate with experience.

Closing date: Open until filled.

To apply please send CV, brief statement of research interests and contact information for two academic referees to Dr. Alison Galvani at [agalvani@nature.berkeley.edu](mailto:agalvani@nature.berkeley.edu)

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## WorkshopsCourses

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**Barcelona Morphometrics May18-20**

Dear Colleagues

This is an invitation to the course: Introduction to Geometric Morphometrics. The course will be held at the Universitat Autònoma de Barcelona, in Barcelona (Spain), from 18 to 20 May.

Morphometrics is the study of shape variation in organisms and its covariation with other variables. While the traditional approaches are based on sets of distances measurements, the geometric morphometric, uses landmark coordinates to capture the shape of the study object and provides more powerful statistical tests for differences in shape. This new method is needed and used whenever we need to describe and compare shapes of organisms or the shapes of particular structures. It could be used for studying geographical effects, developmental stages, genetic effects, environmental effects etc. Thus it is useful for a broad category of students in the fields of ecology, evolution, systematics, genetics, medicine etc. Since it is a powerful tool in many areas in biology it is very useful for inter disciplinary research.

The aim of this course is to provide a comprehensive introduction in this area of research including both theoretical and practical aspects.

Teachers: R. González-José (Universitat de Barcelona) and Silvina Van der Molen (Universitat Autònoma de Barcelona)

For further information please contact Silvina Van der Molen by e-mail (sildermolen@hotmail.com) or by phone (+34 93 581 2618 / 610924577)

Sil Van der Molen <sildermolen@hotmail.com>

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## Switzerland Pollination Sep15-19

Seminar

15 -19 September, 2004 / La Fouly, Swiss Alps

?POLLINATION BIOLOGY: NEWS AND PERSPECTIVES?

Organizers: Luc Gigord, Jérôme Goudet, Ian Sanders & Nicole Galland

Theme: Plants are fundamentally different from animals in many life traits. In particular, they cannot move around to search for a partner or mate. How do plants overcome this problem? As a consequence, most

flowering plants rely on animals (insects, birds, mammals or reptiles) to ensure male gamete transfer (pollen) to female receptacle organs. Not only is pollination biology economically important, generating up to \$20 billion annually, but offers the possibility to study a number of evolutionary and ecological approaches such as hybridisation, population genetic structure, animal behaviour, co-evolution, mimicry, adaptive radiation and speciation. These topics will be treated by several internationally renowned scientists. PhD students and postdocs will have the opportunity during the workshop of developing, discussing and presenting their own research and ideas as well as working together in groups on particular topics of interest.

Invited experts:

Pr. Jon ÅGREN ? University of Uppsala ? Sweden  
 Prof. Chris ECKERT ? Queen's University - Canada  
 Dr. Finn KJELLBERG (DR CNRS) ? University of Montpellier ? France  
 Pr. Susan MAZER ? University of Santa-Barbara ? USA  
 Dr. Jacqui SHYKOFF (DR CNRS) ? University of Paris XI ? France  
 Pr. Douglas SCHEMSKE ? Michigan State University ? USA

Completed forms should be returned to Mrs F. Pham, Département d'Ecologie et Evolution, Bâtiment de Biologie, CH-1015 Lausanne (Tel. 021/692.41.60, Fax. 021/692.41.65, Email: francoise.pham@ie-zea.unil.ch).  
 New deadline for registration: May 15, 2004.

The seminar is free for students from the University of Berne, Geneva, Fribourg, Lausanne and Neuchâtel. Participation about 250 CHF (161 EUROS) for participants from anywhere else. This price includes registration fees, accomodation and food.

----- Registration Form <<Pollination Biology>>  
 September 15-19, 2004

Name:

First name:

University:

Academic position:

Professional address:

Tel.:

Fax.:

Email:

Title of the proposed talk (20 minutes):

Date:

Signature:

Luc Gigord <Luc.Gigord@ie-bsg.unil.ch>

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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto: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](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto: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](mailto: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](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains one of the keywords “Conference, Grad, Job, Other:, Postdoc, Workshop” and then the message stands a better chance of being correctly parsed.

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. So 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<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.