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# E v o l D i r

May 1, 2004

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

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## 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](mailto:Golding@McMaster.CA).

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

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



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## Conferences

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### Brisbane AncientDNA Jul12-17 2

The 7th International Conference on Ancient DNA and Associated Biomolecules is being held in Brisbane, Australia from the 12th to the 17th of July 2004. This conference brings together experts in the fields of genetics, microbiology, microscopy, biochemistry, human and other evolutionary biology, palaeontology, medicine, criminal and wildlife forensics.

If you would like to be a part of this conference DNA7 is now accepting abstracts for all sessions, including population genetics, disease and forensics. Abstracts will be accepted until the 30th of April of 2004.

Submit your Abstract Now to [abstracts.dna7@uq.edu.au](mailto:abstracts.dna7@uq.edu.au)

For further information about the conference please visit the conference website at <http://dna7.ansoc.uq.edu.au> or e-mail enquiries.dna7@uq.edu.au

Regards Tamara Brown

DNA7 Conference Committee Archaeological Science Laboratory School of Social Science & School of Biomedical Sciences The University of Queensland

Lab: (61)(07) 3365 7252 Mobile: (61) 0408 308 215  
e-mail: [t.brown@uq.edu.au](mailto:t.brown@uq.edu.au)

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### CornellU EGLME Apr24 2

Deadline for Abstracts, April 9. Late registrations for participation accepted.

CALL FOR PAPERS

EGLME VIII

Eighth Eastern Great Lakes Molecular Evolution Meeting

<http://www.ars-grin.gov/gen/eglme> Saturday, April 24, 2004 8:30am - 5:00pm

G10 Biotechnology Building Cornell University Ithaca, NY

The 2004 Eastern Great Lakes Molecular Evolution Meeting (EGLME VIII) will be held on Saturday, April 24, 2004 in room G10 of the Biotechnology Building at Cornell University in Ithaca, NY. Registration, coffee, and poster setup will begin at 8:30 A.M., the first talk at 9:30, with the meeting ending around 5 pm.

EGLME is a forum for faculty, postdocs, grad students, staff, and undergrads to share their work on molecular evolution (broadly defined, including studies of the molecular evolutionary biology or molecular population genetics of any trait in any organism). In the interest of stimulating interaction and discussion among all participants, there will not be concurrent sessions. (We anticipate 18 talks and 30-50 posters.)

There is a link to the abstract submission form at the EGLME VIII website (deadline: April 9, 2004).

Talks will be selected from submitted abstracts, and will be of 15 - 20 minutes duration. Selection will be made by the organizing committee based on the submitted abstract, with attention given to timeliness and general interest of the work. An effort will be made to have as many labs represented as possible. Individuals submitting requests to give talks will be informed by April 16, 2004 as to whether they have been selected to give a talk.

Those not chosen for talks will be strongly encouraged to present a poster on their work. Posters will be available all day, with a mid-day poster session set aside.

In addition, we are considering a computer software demonstration. If you have software relevant to the study of molecular evolution that you would like to demo, please email the organizers.

Registration: online at <http://www.ars-grin.gov/gen/eglme> Registration Fee: None (and we anticipate lunch will be covered by sponsors as well)

Lunch (including a vegan option) will be available on site for all preregistered participants. There may or may not be a small fee for lunch, depending on sponsorship.

There is no charge for parking on the Cornell Ithaca campus on the weekend; however please do not park in service or handicap spots unless you have the necessary permit.

Whether you plan to attend the meeting or simply want to stay on the mailing list, please complete the online registration form at the EGLME VIII website no later than April 9, 2004 at 5:00pm, Eastern time.

Please feel free to duplicate and distribute copies of this notice to anyone interested in attending the meeting, particularly students and faculty who are new to these meetings or to the field of molecular evolution.

A schedule and additional details on the meeting will be available online no later than April 16th at the EGLME VIII website.

Links to information about travelling to Ithaca, maps of the Cornell campus, and links to descriptions of research and educational activities at the USDA-ARS Plant Genetic Resources Unit in Geneva, NY and Cornell University can also be found on the EGLME VIII website.

For general questions, please contact:

Sharon Walburn

swalburn@pgru.ars.usda.gov voice (315) 787-2244 or (607) 254-9244 fax (315) 787-2339 or (607) 254-9339

Organizing Committee: Chip Aquadro, Angela Baldo, Andy Clark, Steve Kresovich, Joanne Labate, Brian Lazzaro, Ross Macintyre, Heidi Schwaninger

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## Denmark SocialInsectEvol Sep2-6

Dear All,

The closing symposium of the EU-funded research training network INSECTS (INtegrated Studies of the EConomy of InsecT Societies) will be held in Helsing, Denmark, 2-6 September 2004.

This meeting is open to EVERYONE who is interested in social insects or the evolution of social systems, whether or not they are a member of the INSECTS network (This point was perhaps not emphasized enough when the symposium was announced), and we hope to make it a key event for social insect research, particularly in Europe, as well as emphasizing the parallels between social insects and other social systems.

The scientific program will include approximately 50 talk slots (20 minutes each), the vast majority of which are open to all participants. In addition there will be plenary talks by INSECTS group leaders (Johan Billen, Koos Boomsma, Jürgen Heinze, Graeme Jones, Laurent Keller, Pekka Pamilo, Francis Ratnieks, Paul Schmid-Hempel, Lotta Sundström and Stefano Turillazzi) and invited speakers from outside the network (Those confirmed so far are Eric Bonabeau and Stuart West).

Registration for the meeting opened on the 1 April 2004, and is via the symposium web site:

<http://www.zi.ku.dk/eunet/helsingor/index.html> The closing date for abstract submission is 1 June 2004, and the final deadline for registration is 25 June 2004.

The cost of the meeting is DKK 4400 per person, which covers all costs including registration, conference materials, accommodation, all food for the meeting, the symposium banquet and a half-day excursion to the royal castles of Frederiksborg and Fredensborg.

For more details, and to register, please see the symposium web site:

<http://www.zi.ku.dk/eunet/helsingor/index.html> The first announcement of the meeting can be downloaded as a colour PDF poster from the web site, and a similar

poster of the second announcement should be available in the next few days.

If you would like any additional information about the meeting, please contact INSECTS@bi.ku.dk. If you would like to receive priority information on the symposium, please consider joining the INSECTSmail mailing list (details available at <http://www.zi.ku.dk/eunet/-index.html> and from the symposium web site), which you can do by simply sending an e-mail message to INSECTS@zi.ku.dk asking to join.

- David Nash -

—————David Nash—————

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21323; Fax: +45 353 21250; e-mail: DRNash@bi.ku.dk

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### FortCollins SSBSEASN Jun26-30 4

Evolution Conference: Undergraduate Scholarships in  
Plant Biology and Evolutionary Developmental Biology

Applications are invited for undergraduate students to obtain funding to attend the Evolution 2004 conference (June 26-30, Fort Collins, CO, see: <http://evolution04.biology.colostate.edu/>). Students selected will present a poster describing their research, and will participate in a series of undergraduate activities at the conference (including meetings with faculty mentors and a talk on getting into and succeeding in graduate school). Registration and accommodation will be provided, and successful applicants will be reimbursed for legitimate travel expenses. Preference will be given to students who have conducted research related to the topic of the symposium "Regulatory genes and the evolution of plant phenotype" and to U.S. minorities who are traditionally under-represented in the biological sciences. Applications, comprising a statement of research interests, a CV, and a letter of support from a supervising faculty member, should be sent to David Baum (dbaum@wisc.edu) by May 1.

reevesp@lamar.colostate.edu

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### Harvard ErnstMayrCentenary May10

Ernst Mayr Centenary at Harvard's Museum of Comparative Zoology

On behalf of the Museum of Comparative Zoology (MCZ) at Harvard University, I am pleased to invite you to a public celebration of Professor Emeritus Ernst Mayr's 100th birthday at the MCZ on Monday, May 10, 2004. This all-day event will recognize both this important milestone and Professor Mayr's manifold contributions to evolutionary biology and many related fields. It will feature a series of invited presentations by distinguished scholars, including many of Professor Mayr's collaborators, colleagues, and former students.\* Festivities will end with a late-afternoon reception in Romer Hall of the Museum's public galleries. Professor Mayr and his family, as well as a number of distinguished guests from both within and outside Harvard, will attend. Admission is free and open to the public.

Details regarding the event are available at <http://www.oeb.harvard.edu/mayr.centenary/>; additional information will be posted over the coming weeks. Please address all questions to Molly Devanney (mdevanney@oeb.harvard.edu; 617-495-5891). Thank you.

Sincerely yours,

James Hanken Director

\* Confirmed speakers: Douglas Futuyma, Axel Meyer, Mary Jane West-Eberhard, Walter Bock, Andrew Knoll, Ira Rubinoff, Kerry Shaw, Frank Sulloway, and Lynn Margulis.

James Hanken <hanken@oeb.harvard.edu>

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### Krakow ESEB Aug15-20 2005

CALL FOR SYMPOSIA for the 10th Congress of the European Society for Evolutionary Biology, Krakow, Poland, 2005

According to our tradition the biennial congress of the European Society for Evolutionary Biology will be held in 2005. I am pleased to announce that the tenth ESEB

Congress will be held in Krakow, Poland, from 15-20 August 2005. The Program starts on Tuesday morning with arrivals planned for Monday, 15 August, allowing participants to take advantage of less expensive airfares. The location is in vicinity of Krakow's old city.

The structure of the Congress will be similar to previous meetings, each day starting with a plenary keynote speaker, followed by parallel symposia. The congress will cover the field of evolutionary biology in a wide sense but with emphasis on processes and mechanisms of evolutionary phenomena.

There is room for about 25 regular symposia. Everyone is invited to submit a symposium proposal (deadline July 31, 2004). Successful Symposia will be selected by the Congress Executive. A few open sessions may also be organized.

**TOPICS.** A symposium should cover a well defined topic in the field of evolutionary biology. It can deal with; population biology, genetics, palaeontology, behavioural ecology, sexual selection or any other field that aims at understanding processes and mechanisms of evolution. We are looking for areas in which there is exciting current activity or novel synthesis, or young fields that are likely to grow in the near future.

**SET-UP.** Symposia will be strictly modular with three invited speakers and 10 contributed papers (full day symposia) or 5 contributed papers (half day symposia). Time for an invited speaker will be 30 minutes, and 20 minutes for a contributed paper. No exceptions will be allowed.

**BUDGET.** The budget for a symposium organizer will be limited. ESEB will waive the registration fees for the 3 invited speakers. However, ESEB is unable to cover all costs (travel, accommodation etc.) of invited speakers, implying that you should seek solutions for remaining financial problems yourself.

**TIME SCHEDULE** By July 31, 2004: Submission of symposium proposals. All submissions should be made by website <http://www.eko.uj.edu.pl/eseb/> and enquiries to [eseb2005@eko.uj.edu.pl](mailto:eseb2005@eko.uj.edu.pl) with "symposium" written as a subject.

September 15, 2004: Decisions on proposals.

December, 2004: 2nd mailing, call for contributed papers

15-20 August, 2005: 10th ESEB Congress

**CONTACTS** For general congress enquiries: Jan Kozłowski, [eseb2005@eko.uj.edu.pl](mailto:eseb2005@eko.uj.edu.pl) For enquiries on symposia and submission of symposium proposals: the same address with "symposium" written as a subject. For organizational matters: Maciej Pilch,

[cbin@adm.uj.edu.pl](mailto:cbin@adm.uj.edu.pl) with ESEB Congress written as a subject.

Congress Executive 2005: Jan Kozłowski (chair), Mariusz Cichon, Ryszard Korona, Adam Lomnicki, Jacek Radwan (all from the Institute of Environmental Sciences, Jagiellonian University) and Marek Konarzewski (Institute of Biology, University of Białystok). ESEB 2005 Congress website is accessible via the ESEB website <http://www.eseb.org/>. It is possible to register for further information on the website.

#### SUBMITTING A SYMPOSIUM PROPOSAL.

**SYMPOSIUM ORGANISERS.** There should be one organiser for each symposium, and one co-organiser who will stand in for the former if required.

**PROPOSALS CONTENTS** The proposal should not exceed one A4 page and should contain:

1. Organisers name and address (mail, telephone, fax and email), a four-line description of your research interest, and the references of two recent publications.
2. Co-organisers name and address (mail, telephone, fax and email), a four-line description of your research interest, and the references of two recent publications. Please distinguish clearly between the organiser and the co-organiser.
3. A short (6 line) description of the symposium topic.
4. Suggestions for 3 invited speakers with their addresses and expertise. At this stage there is no need to have a commitment from these speakers, but it is suggested to negotiate with invited speakers before sending out the submission.

**SUBMISSION** Deadline for submission is JULY 31, 2004 Proposals should be submitted through [www.eko.uj.edu.pl/eseb/](http://www.eko.uj.edu.pl/eseb/). **PROCEDURE** You will receive a confirmation of your submission. All proposals will be assessed and the final selection made in September 2004. Criteria for acceptance will be:

1. The topic itself should be such that a symposium at ESEB 2005 is justified, i.e., it falls within the Society's remit. Beyond this, we are looking for areas in which there is exciting current activity or novel synthesis, or young fields that are likely to grow in the near future.
2. When two proposals have a similar topic, we will either choose one or bring organizers into contact with each other.

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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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## Marseille EvolBiol Sep22-24 3

The next evolutionary biology meeting at Marseille will take place this Year from September 22 to September 24. The early registration dead line is the first of May

The program will be similar to the one proposed the former years the following topics will be discuss: systematic, biodiversity, comparative genomics and post-genomics (at all the taxonomic levels), gene duplication and evolution, functional phylogenies, amphioxus genomics and biology, concepts of evolution, environment and evolution. You can submit and register on line on the meeting web site <http://www.up.univ-mrs.fr/evol/congres/> Information concerning housing.. are available on the same web site

At the best Pierre

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

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## NCStateU BruceWeir Jun5

A symposium on “Statistical and Population Genetics” in honor of Bruce Weir’s sixtieth birthday will be held on June 5, 2004 on North Carolina State University campus in conjunction with the Summer Institute in Statistical Genetics. The symposium is contributed by Bruce’s colleagues, collaborators, and former students to celebrate Bruce’s enduring and continuing contributions to statistical and population genetics.

The speakers will include: Michael Clegg, Cathy Laurie, Brandon Gaut, Rebecca Doerge, John Storey, Dmitri Zaykin, Jun Zhu, Spencer Muse, Paul Lewis, Zhao-Bang Zeng, John Buckleton and Bill Hill.

Information for registration of the symposium is at [http://statgen.ncsu.edu/brcwebsite/seminars\\_symposium.php](http://statgen.ncsu.edu/brcwebsite/seminars_symposium.php) Sincerely yours,

Zhao-Bang Zeng

Dr. Zhao-Bang Zeng Professor Departments of Statistics and Genetics & Bioinformatics Research Center

North Carolina State University 1521 Partners II Building, 840 Main Campus Drive Raleigh, NC 27695-7566, USA Tel: 919 515-1942; FAX: 919 515-7315 (Attn: Zeng) Email: [zeng@stat.ncsu.edu](mailto:zeng@stat.ncsu.edu); Home page: <http://statgen.ncsu.edu/zeng/>

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## RhodeIsland MicrobialEukaryotes June3

Symposium: Genome Evolution in Microbial Eukaryotes June 3rd, Smithfield Rhode Island

To elucidate principles of eukaryotic genome evolution, we must increase studies of microbial eukaryotes. The bulk of eukaryotic diversity is microbial yet our current knowledge of eukaryotic genome evolution comes largely from studies of plants, animals and fungi. Our intention in this one-day symposium is to highlight recent achievements in understanding the diversity of eukaryotic genomes, and to expose relevant researchers to advances in techniques for both data acquisition and data analysis.

More information about the symposium: [http://www.biology.uiowa.edu/workshop/SOP\\_symposium.html](http://www.biology.uiowa.edu/workshop/SOP_symposium.html)

Travel funds are available for undergraduates, graduate students and postdocs. Deadline for requests is May 1. These funds will offset costs of those currently working on molecular evolution/genomics of microbial eukaryotes, and those switching into the field. Students and postdocs are encouraged to bring a poster of their work.

Travel funds application: [http://www.science.smith.edu/departments/Biology/lkatz/SOPgenome\\_fundsrequest.html](http://www.science.smith.edu/departments/Biology/lkatz/SOPgenome_fundsrequest.html) The symposium will take place at this year’s Society of Protozoologists meetings.

More information on the SOP meetings: [http://www.uga.edu/protozoa/meetings/sop\\_meeting.html](http://www.uga.edu/protozoa/meetings/sop_meeting.html)

– Laura A. Katz Department of Biological Sciences Smith College Northampton, MA 01063 Phone: 413-585-3825 Fax: 413-585-3786 <http://www.science.smith.edu/departments/Biology/lkatz/> “Laura A. Katz” <[LKatz@smith.edu](mailto:LKatz@smith.edu)>



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## RoscoffFrance HostParasite Sep4-8

Jacques Monod Conference: "Evolutionary ecology of host-parasite relationships"

Roscoff (Brittany), France - September 4-8, 2004

The last quarter of the 20th century witnessed an increase in the interest of evolutionary biologists in understanding and controlling infectious diseases. There is growing awareness that neither "hosts" nor "parasites" are static entities, that their populations are composed of a variety of interacting and competing genotypes, and that this genetic variation is not only important for natural populations, but also for agriculture and human medicine. Understanding host and parasite evolution and coevolution is particularly important at a time when new diseases affecting humans or animals are emerging around the world, while old, well-understood diseases like tuberculosis are acquiring broad resistance to traditional drugs.

The goal of this conference is to stress innovative researches in the field of evolutionary ecology and epidemiology of infectious diseases. Debates will focus on the different ways parasites exploit their hosts; on the epidemiology and population genetics of parasitic infections; on the evolution of virulence, resistance and host immunity. In all cases, we will try to bridge the gap between theory and empirical works.

The total number of participants is limited to about 100 and all participants are expected to attend for the whole duration of the conference. Selection is made on the basis of the affinity of potential participants with the topics of the conference. Scientists and PhD Students interested in the meeting should send:

\* their curriculum vitae \* the list of their main publications for the 3 last years \* the abstract of their presentation

to the Thierry Rigaud (chairman) of the conference before the deadline.

Registration fee, including board and lodging 360 Euros for PhD Students 500 Euros for other participants

Deadline for application: 15 May 2004.

Information about the symposium: [http://www.cnrs.fr/SDV/Actions/cjmrigaud\\_e.html](http://www.cnrs.fr/SDV/Actions/cjmrigaud_e.html) Chairman: RIGAUD Thierry Université de Bourgogne C.N.R.S. UMR 5561 - BioGeosciences Equipe Ecologie

Evolution 6, boulevard Gabriel F - 21000 Dijon E-mail: thierry.rigaud@u-bourgogne.fr

Vice-Chairman: EBERT Dieter Université de Fribourg Département de Biologie Unite d'Ecologie et Evolution 10 chemin du Musée CH - 1700 Fribourg, Suisse E-mail: dieter.ebert@unifr.ch

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## StonyBrookU George C Williams Apr24 2

Members of EvolDir-

This previously announced symposium is now free to all, thanks to sponsorship by the Stony Brook President's Office, Provost's Office, and the Deans of the College of Arts and Sciences and of the Graduate School. (Those of you who have already paid will have your fees refunded.) We invite you all to join us for an exciting day of talks!

SYMPOSIUM IN HONOR OF GEORGE C. WILLIAMS

A symposium will be held on April 24, 2004 on the Stony Brook University campus to celebrate George Williams' contributions to Ecology and Evolution - the department and the disciplines. George came to Stony Brook in 1960 even before it existed as such, and his accomplishments were instrumental in building our department. He was elected to the U.S. National Academy of Sciences in 1993 and shared the Crafoord Prize of the Royal Swedish Academy of Sciences with Ernst Mayr, and John Maynard Smith in 1999 for his contributions to evolutionary biology.

Registration for the symposium begins at 8:30 am on April 24 and the talks will run from 9:15 am until 5:00 pm.

George has assembled a group of distinguished speakers for the symposium:

MARY JANE WEST-EBERHARD - What George Williams said about sex but didn't really believe. DAVID HAIG - Reflections on pregnancy and Darwinian medicine. RANDOLPH NESSE - Maladaptation and natural selection. BOBBI LOW - Women's lives in evolutionary perspective. HELENA CRONIN - Adaptation. GEORGE BARLOW How to decide that a species is sex-role reversed? MARTIN DALY and MARGO WILSON - Facultative modulation of risk-taking and future discounting in Homo sapi-

ens. STEVEN FERRARO - Red-letter days. MART GROSS - Sex ratio theory.

For more information, including directions, check out the symposium website: <http://life.bio.sunysb.edu/~ee/williams/> Hope to see many of you!

Daniel Stoebel Department of Ecology and Evolution Stony Brook University Stony Brook, New York 11794-5245

Lab Phone: 631/632-8718  
 mailto:dstoebel@life.bio.sunysb.edu <http://life.bio.sunysb.edu/~dstoebel/>

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### 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 pmArrival and Check-in 6:00 pmDinner 7:30 pm - 9:30 pmMotors 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 amBreakfast 8:30 amGroup Photo 9:00 am - 12:30 pmSpatial 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 pmLunch 6:00 pmDinner 7:30 pm - 9:30 pmInnovations in Theoretical Immunology Discussion Leader: Ramit Mehr (Bar-Ilan University) Can Kesmir (Utrecht University) Nigel Burroughs (University of Warwick) 9:30 pmPoster Session

TUESDAY 7:30 am - 8:30 amBreakfast 9:00 am - 12:30 pmNeurobiology of Breathing, Whiskering and Electrollocation 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 Reintz (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>

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### UAlaskaFairbanks SSB 2005

Call for Proposals for 2005 SSB Symposia. - The Society for Systematic Biologists invites proposals for symposia at the 2005 SSB meetings to be held at the University of Alaska, Fairbanks. The meetings will be held jointly with the American Society of Naturalists and the Society for the Study of Evolution. Each proposal should include (1) a descriptive title, (2) one or two paragraphs explaining the purpose of the symposium and its relevance to systematics, (3) a list of presentations including proposed speakers, their institutions or affiliations, and their presentation titles, (4) an indication of whether the speakers have been invited and whether they have agreed to participate, and (5) the proposed length of each talk. Symposia are restricted to half-day sessions. The society is particularly interested in symposia whose topics do not overlap with those



from previous meetings, that introduce new ideas or synthesize important concepts, or those that are particularly good examples of the analysis of empirical data. Proposals that unite systematics with other fields are also desirable. We encourage participation from young investigators and others typically under-represented in symposia. Limited partial funding is available. The target date for receipt of proposals is May 1, 2004. Proposals will be discussed and two will be selected at the SSB Council meeting during the 2004 annual meeting in Ft. Collins, Colorado. Soon after, organizers will be notified of the status of their proposals. Proposals should be sent by email to the Program Director, Kevin P. Johnson, at: [kjohnson@inhs.uiuc.edu](mailto:kjohnson@inhs.uiuc.edu) (Kevin P. Johnson, Illinois Natural History Survey, 607 East Peabody Drive, Champaign, Illinois 61820).

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Kevin P. Johnson Associate Research Scientist Illinois Natural History Survey 607 East Peabody Drive Champaign, IL 61820-6970 Phone: (217) 244-9267 Fax: (217) 333-4949 e-mail: [kjohnson@inhs.uiuc.edu](mailto:kjohnson@inhs.uiuc.edu) e-mail: [kjohnson@inhs.uiuc.edu](mailto:kjohnson@inhs.uiuc.edu)

## Valencia MEEGID Jul19-23

05/04/04

The 7th International Meeting “Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases” (MEEGID VII) will be held in Valencia (<http://www.valencia-on-line.com/>), Spain, 19th-23rd July 2004. As for the 6 first MEEGID meetings, it will be co-organized by the Centers for Disease Control and Prevention (CDC; <http://www.cdc.gov/>) in Atlanta and the Institut de Recherche pour le Développement (IRD; <http://www.ird.fr/>) in France.

MEEGID VII will be hosted by the 9th European Multicolloquium of Parasitology (EMOP IX; <http://www.uv.es/emop9/>). Many sessions will be organized in common by the 2 meetings. EMOP IX is expected to attract 2000-4000 participants. Communications done in the framework of MEEGID VII will therefore have much impact. EMOP IX is organized by Professor Santiago Mas Coma, professor of parasitology at the university of Valencia, receiving editor of *Infection, Genetics and Evolution* (Elsevier) for Spain, and co-organizer of MEEGID VII ([S.Mas.Coma@uv.es](mailto:S.Mas.Coma@uv.es))

Preliminary programme is communicated below. Many

slots are still available. Proposals are therefore still accepted and welcome for: (1) Posters; (2) Oral communications; (3) Organizations of roundtables/symposia (2 hours, 4-6 speakers); (4) Express debates (1 hour, only one speaker with a communication of 15-20 mn followed by free discussion); (4) Plenary lectures (45 mn). Proposals dealing with roundtables/symposia, express debates and plenary lectures should be submitted as soon as possible.

MEEGID is not restricted to evolution only. The scopes proposed can deal with genetics, genomics, proteomics, population biology, mathematical modelling, bioinformatics, molecular epidemiology, molecular diagnosis and morphometrical identification. They can consider the host, the pathogen or the vector. Papers considering host + pathogen or pathogen + vector (co-evolution) are particularly encouraged. All pathogens are within the scope of MEEGID: viruses, parasitic protozoa, helminths, fungal organisms, prion. All infectious models can be considered, including those of veterinary or agronomical relevance. As for the former MEEGID congresses, special consideration will be given to communications of high relevance for developing countries.

The papers communicated for MEEGID VII will be published in a special issue of *Infection, Genetics and Evolution*, as already done for MEEGID VI (Paris, July 2002). *Infection, Genetics and Evolution* is now covered by Medline and Index Medicus, since the 1st issue of the journal.

Awards will be attributed to the best communication, the best communication by a student and the best communication by a scientist from the Southern World on a problem specifically relevant to these areas.

Limited funds will be made available to travel students and scientists from developing countries.

See you in Valencia!

Michel Tibayrenc, MD, PhD Editor -in-chief *Infection, Genetics and Evolution* (Elsevier) <http://www.elsevier.nl/locate/meegid> Director Unit of Research 165 “Genetics and Evolution of Infectious Diseases” UMR CNRS/IRD 2724 IRD, BP 64501 34394 Montpellier cedex 5, France Tel. 33 4 67 41 61 97 (secretary) 33 4 67 41 62 07 (direct) Fax 33 4 67 41 62 99 Email [Michel.Tibayrenc@mpl.ird.fr](mailto:Michel.Tibayrenc@mpl.ird.fr) Website <http://cepm.mpl.ird.fr> Website MEEGID VII: <http://www.uv.es/emop9/MEEGID>

MEEGID VII Valencia, Spain 19th-23rd July 2004

Preliminary programme

Plenary lectures

Thierry de Meeus (IRD, Montpellier, France)

Clonal reproduction and linkage disequilibrium in diploids: simulation studies

Steve Frank (UC Irvine, California)

Immunology and evolution of infectious diseases

Robin Bush (UC Irvine, California)

Influenza evolution

Shyam Sundar, Institute of Medical Sciences, Benares Hindu University,

Leishmaniasis in India

Jean-Loup Lemesre (IRD, Montpellier, France)

Leishmania vaccine

Jane Carlton (The Institute for Genomic Research [TIGR], Rockville, Maryland)

Parasite genome sequencing programmes

Michael Stanhope (GlaxoSmithKline, Collegeville, Pennsylvania)

SARS molecular evolution and epidemiology

Marc Ouelette (Burroughs Wellcome Fund Scholar, Quebec, Canada) (response pending)

The impact of megatechnologies on infectious disease research

Altaf Lal (Human Health Services, U.S. Embassy, New Delhi, India)

why do we need molecular epidemiologists for strong public health response

Symposia (4 hours, 4 to 6 communications)

Chair: Andrew Thompson, Murdoch University, Australia

Cryptosporidium molecular epidemiology and evolution

Chairs: Jean-Pierre Hugot, Museum National d'Histoire Naturelle,

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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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## GradStudentPositions

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### EastAnglia FishSpeciation

NERC funded PhD studentship (available to UK residents only)

Speciation in marine fishes: a population genetic assessment of hamlets.

The main aim of this project is to investigate the mech-

anisms of speciation in hamlets, the most famous example of a marine radiation, using population genetic analyses. Nine to 12 species (colour morphs) of these small, carnivorous fish are distributed across the Caribbean. Many morphs co-occur on reefs and all are identical except in colour pattern. Hamlet morphs will be sampled at 10 localities across the Caribbean and individuals will be screened with a battery of AFLP primer combinations to generate multi-locus genotypes for individual fish. These AFLP profiles will be used to investigate the phylogenetic and phylogeographic relationships among

and within colour morphs and to investigate gene flow between morphs in sympatry.

This NERC funded project is supervised by Drs Brent Emerson ([b.emerson@uea.ac.uk](mailto:b.emerson@uea.ac.uk)) and Isabelle Côté ([i.cote@uea.ac.uk](mailto:i.cote@uea.ac.uk)) at the Centre for Ecology, Evolution and Conservation, School of Biological Sciences, University of East Anglia. The start date is 1 October 2004, and applications will be accepted until the position is filled. For further information, contact Brent Emerson.

General information and formal application forms are available from the Science Graduate Studies Office: [www.uea.ac.uk/bio/studentships/welcome.html](http://www.uea.ac.uk/bio/studentships/welcome.html). Tel (+44) 1603 593002 e-mail: [scipg@uea.ac.uk](mailto:scipg@uea.ac.uk).

– Brent Emerson Lecturer in Evolutionary Biology Centre for Ecology, Evolution and Conservation School of Biological Sciences e-mail: [b.emerson@uea.ac.uk](mailto:b.emerson@uea.ac.uk) University of East Anglia ph: (44) 01603 592237 Norwich NR4 7TJ fax: (44) 01603 592250 ENGLAND mob: (44) 0795 121 8827

Brent Emerson <[b.emerson@uea.ac.uk](mailto:b.emerson@uea.ac.uk)>

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## UBern 2 BehavEcol

Dear Colleague,

Please pass this announcement on to all potentially interested candidates. We have two PhD-positions available in Behavioural Ecology at the University of Bern. The job description is attached also as a Word-file for advertisement on your notice board. If you have any questions, please contact me per e-mail ([michael.taborsky@esh.unibe.ch](mailto:michael.taborsky@esh.unibe.ch)).

Sorry for cross-posting

————— TWO PhD- POSITIONS in BEHAVIOURAL ECOLOGY are available at the Department of Behavioural Ecology of the Zoological Institute, University of Bern, Switzerland. One project will focus on the mechanisms underlying cooperative behaviour in a highly social Lake Tanganyika cichlid. In particular we are interested in the influence of ecology and social relationships on the propensity to cooperate. This study will involve experimental manipulation of habitat, social conditions and behaviour, both in the lab and field. The second project will focus on the ecology and evolution of sperm competition and alternative reproductive tactics when fertilization is external. A Lake Tanganyika cichlid breeding in empty snail shells will be

used as the model system. The breeding substrate will be manipulated to measure responses at the levels of behaviour and population. We are particularly interested in the influence of ecology and female behaviour on the coexistence of alternative life history morphs within a species. Again, lab and field work will complement each other.

Candidates should have a masters degree (or Diplom) in Biology and research experience in animal behaviour, a firm, theoretical background in behavioural or evolutionary ecology, and a strong commitment to basic science. Practical skills in the work with fish, both under water and in the lab will be very helpful. The person appointed will be collaborating with the other members of the group, which will include approximately 4 advanced research staff, 5 PhD-students and a varying number of masters students.

Besides research, PhD students are expected to assist in undergraduate teaching and supervision, with a training load not exceeding 10 percent of working time. Salaries will follow the scheme of the province of Bern and the Swiss National Research Foundation (approx. 32,000.- to 38,000.- CHF/year).

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of any published or in-press papers if applicable, and 2 letters of recommendation, should be received by April 15, 2004 to assure full consideration. The position will start at the earliest possible date and will be for three years. Candidates should indicate in a cover letter when they could take up the position.

Please send material to the secretaries office, c/o Susanne Maurer, Dept. Behavioural Ecology, University of Bern, Baltzerstr. 6, CH-3012 Bern, Switzerland; or as an e-mail attachment to [susanne.maurer@esh.unibe.ch](mailto:susanne.maurer@esh.unibe.ch). For inquiries please contact [michael.taborsky@esh.unibe.ch](mailto:michael.taborsky@esh.unibe.ch).

————— Prof. Michael Taborsky University of Bern Dept. Behavioural Ecology, Institute of Zoology, Wohlenschtr. 50a, CH-3032 Hinterkappelen/Bern Switzerland

Phone: +41-(0)31 631 9156 Secret: +41-(0)31 631 9111 Fax: +41-(0)31 631 9141 e-mail: [Michael.Taborsky@esh.unibe.ch](mailto:Michael.Taborsky@esh.unibe.ch) <http://zoology.unibe.ch/behav/>

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## UCanterbury EvolCommunications

Ph.D. Scholarship in Animal Communication at the University of Canterbury

We are seeking a Ph.D. student to study mechanisms of social communication in archaic New Zealand frogs (genus *Leiopelma*). These frogs are “living fossils” that have remained virtually unchanged over the past 200 million years and never evolved bioacoustic signalling systems. *Leiopelma* are extremely long-lived, do not stray far from small home ranges, and repeatedly interact with the same individuals. These conditions foster the formation of complex social networks, which might be structured through chemical signalling. The project takes an integrative approach and makes use of microsatellite analyses to investigate genetic relatedness, chemical methods to characterise the signals, and field studies to examine how communication occurs in natural populations. For further background, see *Behavioral Ecology* 15 (1): 88-93 (2004).

The scholarship is supported for three years by the Marsden Fund (Royal Society of New Zealand) and includes a \$19,000/year tax-free stipend, full international tuition/fees, and generous support for research expenses.

The University of Canterbury has a strong programme in behaviour, ecology, and evolution, as well as excellent facilities in chemistry and molecular genetics. The programme is directed by Bruce Waldman (School of Biological Sciences) and John Blunt (Department of Chemistry).

The deadline for applications is 15 June 2004. For further information, please contact us. To apply, send your Curriculum Vitae, a letter detailing your experience and career goals, and contact details for three referees to:

Dr Bruce Waldman School of Biological Sciences University of Canterbury Private Bag 4800 Christchurch New Zealand

Voice: +64 3 364 2066 FAX: +64 3 364 2590 Web: [www.biol.canterbury.ac.nz](http://www.biol.canterbury.ac.nz) Email: Bruce.Waldman@canterbury.ac.nz

Bruce Waldman <bruce.waldman@canterbury.ac.nz>

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## UCanterbury EvolGenomics

Ph.D. Scholarships Available in Evolutionary Genomics at the University of Canterbury, Christchurch, New Zealand.

We are currently seeking students with interests in genomics, evolution and bioinformatics to conduct research on microsatellite evolution. Positions are available immediately for a period of 3 years.

**Project Description** Microsatellites are abundant, highly variable, repeated DNA sequences that are regarded as the most versatile genetic markers yet discovered. They are the cornerstone of the current biological revolution and are used in gene mapping, DNA forensic work, and as population markers. Conclusions drawn from such studies in many cases depend critically on assumptions about how microsatellites evolve. Current models of microsatellite evolution are overly simplistic and almost certainly incorrect, leading to widespread data misinterpretation. To avoid continued misinterpretation, it is vital that we understand fully how microsatellites evolve. This project will investigate the processes governing microsatellite evolution by comparing microsatellite sequences derived from the human, mouse, rat and other genome projects using a combination of bioinformatics and comparative molecular genetics.

**The Ideal Candidate** The ideal candidate will possess experience in both molecular genetics and bioinformatics. They will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research program that will span molecular genetics, bioinformatics and biomathematics. They will be a competent laboratory worker, with experience of all routine molecular genetic techniques, particularly microsatellite genotyping and sequencing, and should be computer literate with familiarity with database management and statistical analyses. Minimum qualifications: B.Sc. (Hons), M.Sc. in Genetics, Molecular Biology or equivalent.

**Remuneration** Students will receive an annual stipend of NZ\$19,000 plus local fees for 3 years. Please note that students from countries other than New Zealand, Germany, France, and Australia will normally be required to pay international fees currently NZ\$23,000 per annum which will not be covered by the stipend. Additional scholarships for international fees are avail-

able, but only to the very best international graduates. Interested applicants are encouraged to make informal enquires to Dr. Neil Gemmell, in the first instance. To apply, please send your Curriculum Vitae, a copy of your academic transcript and the names of three referees with a covering letter to:

Dr. Neil J Gemmell Senior Lecturer in Molecular Genetics School of Biological Sciences, University of Canterbury Private Bag 4800, Christchurch, New Zealand Phone: +64 3 364 2009 Fax: +64 3 364 2590 e-mail: [neil.gemmell@canterbury.ac.nz](mailto:neil.gemmell@canterbury.ac.nz)  
<http://www.biol.canterbury.ac.nz>  
[neil.gemmell@canterbury.ac.nz](mailto:neil.gemmell@canterbury.ac.nz)

biosci/MEE.html Genome Analysis Suite <http://www.hull.ac.uk/GAS/>

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

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 Cichlids

PhD position University of Hull, UK

#### GENOMIC APPROACHES TO THE STUDY OF CICHLID ADAPTIVE RADIATIONS

A NERC-funded 3-year PhD studentship is available to work in the Molecular and Evolutionary Ecology sector of the Department of Biological Sciences at Hull University, UK. The project will examine the adaptive radiations of cichlid fish in African Great Lakes by investigating the rate and nature of genome change. The successful applicant will gather multilocus nuclear sequence data and employ both bioinformatics and molecular phylogenetic approaches to the study of cichlid speciation. Although all training will be provided the ideal applicant would have an interest in, or experience of, some of the following- phylogenetics, molecular evolution, bioinformatics, molecular ecology or speciation studies.

The MEE sector at Hull is a large and multinational group with excellent molecular genetic resources and a newly funded bioinformatics laboratory. There are extensive tropical fish aquaria and a range of collaborators experienced in cichlid biology, speciation studies and molecular genetics.

Because of the nature of the award funding is restricted to UK students. Applicants should email a CV and cover letter to Dr David Lunt ([d.h.lunt@hull.ac.uk](mailto:d.h.lunt@hull.ac.uk)) by April 30th 2004.

Department of Biological Sciences <http://www.hull.ac.uk/biosci/> Molecular and Evolutionary Ecology sector <http://www.hull.ac.uk/>

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### ULausanne Colour polymorphism

Two PhD as well as one postdoctorate positions are available to study THE EVOLUTION AND MAINTENANCE OF GENETIC COLOUR POLYMORPHISM at the Department of Ecology and Evolution at the University of Lausanne (Switzerland).

One of the PhD position involves the teaching of practical (mostly in French) to undergraduate students.

Deadline for application: May 15th 2004

Please send a CV, a summary of experience, research interests and contact details (mainly email address and phone number) of two referees to Alexandre Roulin, Department of Ecology and Evolution, University of Lausanne, Biology Building, CH-1015 Lausanne, Switzerland. [Alexandre.Roulin@ie-zea.unil.ch](mailto:Alexandre.Roulin@ie-zea.unil.ch)

Further information: <http://www.unil.ch/jdee/-page7006-en.html>

Prof. Alexandre Roulin Department Ecology & Evolution Biology Building University of Lausanne CH-1015 Lausanne Switzerland

Fax: 0041 21 692 41 65 Email: [Alexandre.Roulin@ie-zea.unil.ch](mailto:Alexandre.Roulin@ie-zea.unil.ch)

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### ULausanne LandSnails

University of Lausanne (Switzerland), Department of Ecology and Evolution

As part of an ongoing project, a PhD student position is available for studying population biology of the land



snail *Trichia sericea* and its closely related species. Including investigations on population ecology, life history traits, and fine scale genetic structuration, the main aim of this study would be to understand which factors induce and maintain local morphological and genetic differentiation. The candidate is expected to be independent and at ease with field work (driving licence necessary) as well as with lab work in molecular biology. As the candidate will be requested to contribute to practical teaching in our department, a reasonable level of french is required.

Please send application by E-Mail with CV, contact details and addresses of two referees to

Prof. J. Hausser Department of Ecology and Evolution Biology Building University of Lausanne CH-1015 Lausanne-Dorigny E-Mail: [jacques.hausser@iezea.unil.ch](mailto:jacques.hausser@iezea.unil.ch) tel: ++ 41 21 692 41 62 fax: ++ 41 21 692 41 65

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## ULondon PopulationDynamics

PhD studentship: Mathematical modelling of the population dynamics of a predator with multiple prey

Supervisor: Vincent AA Jansen School of Biological Sciences, Royal Holloway - University of London.

The modelling of predator and prey dynamics is a well-studied problem in ecology, yet the majority of the research has focused on the interaction between a single prey and one predator. The interaction between one predator and multiple prey is less well studied, despite the fact that in general there are more prey species than predator species. This project aims to develop a mechanistic model for the population dynamics of a predator feeding on multiple prey species.

The modelling of the interaction between a predator and prey hinges on the descriptions of the functional and numerical responses. For the interaction between a predator and a single prey the standard description is that of a Holling type II functional response. For the interaction between a predator and more than one prey a Holling type III functional response is often used, however this description is not based on a mechanistic underpinning. This project aims to model the interaction between a predator and multiple prey species on a mechanistic basis and explore the resulting population dynamics and the evolution of the interaction. There are a number of fundamental questions that can be ad-

ressed in the context of this research: how different do prey need to be in order to coexist? How many prey species can coexist if predated upon by a single predator? What are the spatio-temporal dynamics? What are the evolutionary consequences? The results of this theoretical project can potentially be applied to biological control or conservation issues.

This project will involve model formulation and mathematical analysis, supplemented with computer simulations. It will suit a biologist with an affinity for mathematical modelling, or graduates from a discipline with a substantial mathematical content (e.g mathematics, physics or computer science) with an affinity for biology. If you fulfil these requirements but would like to do a PhD in mathematical biology on a subject of your own choice, please contact the supervisor. The studentship is a Thomas Holloway studentship (see <http://www.rhul.ac.uk/Studying/-Graduate-School/pgfunding2.html>) and covers fees and subsistence for UK or EU residents. To apply please follow the instructions on <http://www.rhul.ac.uk/-studying/Admissions/pgapplication.html>. Please also provide two letters of reference which should be sent directly to the supervisor. The deadline for applications is 4 June 2004.

Professor Vincent Jansen School of Biological Sciences Royal Holloway - University of London Egham, Surrey TW20 0EX, U.K.

Tel : (..) 44 1784 443179 Fax : (..) 44 1784 470756  
Email: <mailto:vincent.jansen@rhul.ac.uk> Web: <http://web.rhul.ac.uk/Biological-Sciences/jansen>

Vincent Jansen <[Vincent.Jansen@rhul.ac.uk](mailto:Vincent.Jansen@rhul.ac.uk)>

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## USheffield Speciation

BBSRC funded PhD studentship (available to UK residents only)

Genetics of male sterility in a grasshopper hybrid zone

This studentship is available from October 2004 to work with Prof. Roger Butlin on the *Chorthippus parallelus* hybrid zone on the French-Spanish border. It will combine quantitative genetic and gene expression based approaches to hybrid sterility which is observed in F1 males but not in the hybrid zone, apparently because of displacement of clines for incompatible alleles.

The studentship will be held in the Department of An-

imal and Plant Sciences, The University of Sheffield. r.k.butlin@leeds.ac.uk  
 For further information, contact Roger Butlin:

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### California StatGenetics

STATISTICAL GENETICS ANALYST Perlegen Sciences 2021 Stierlin Court Mountain View, CA 94043 <http://www.perlegen.com/> At Perlegen Sciences, we conduct genetics research and develop products that impact and improve people's lives. Established in March 2001, we are a well-funded, pre-IPO company aggressively developing our core competencies in research, genome scanning, bioinformatics, and other key areas of our business. We invite you to consider our team as we apply this technology to bring focus to biological research and to accelerate the discovery of drugs and diagnostics.

We currently have an opportunity for you to join a team of highly motivated and independent data analysts responsible for the analysis of whole genome scan data, exploratory analysis of novel genomic datasets, process improvement initiatives, production data quality control and other analysis projects. We'll rely on you to analyze and interpret data from individual and pooled genotyping, design and implement novel algorithms for analysis and data knowledge representation. The ability to work effectively in cross-functional collaborative

project teams, develop and apply novel data analysis algorithms and provide written and oral feedback will be keys to your success.

To qualify, you should have an MS/PhD in Genetics or Biological Sciences with a strong statistical background or an MS/PhD in Statistics or equivalent with a strong genetics or biology background or equivalent training and working experience. Additional requirements include 2-5 years of relevant work experience, familiarity with statistical genetics, strong data management and programming skills and demonstrated success in technical proficiency, scientific creativity, collaboration with others and independent thought. Familiarity with data mining techniques would be a plus.

Job ID MDB01

E-mail application to: [careers@perlegen.com](mailto:careers@perlegen.com)

Telephone: 650-625-4500 Fax: 650-625-4510

Dennis Ballinger <[Dennis\\_Ballinger@perlegen.com](mailto:Dennis_Ballinger@perlegen.com)>

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### Chile MolecularSystematics

Professor in Molecular Systematics Depto. Zoologia.

Universidad de Concepcion. Chile Degree A12 (US\$ 1350 free monthly)

Young PhD with publications in Molecular Systematics and Phylogeny with animals.

Some teaching experience Send CV, recommendation letter and a letter describing general interest in research areas.

Send all antecedents via E mail (pvictori@udec.cl) or to the adress detailed below. Deadline: May 3 2004

Thank you very much Sincerely

Dr. Pedro F. Victoriano Depto. Zoolog?a Fac. de Cs. Nats. y Oceanogr?ficas Universidad de Concepci?n Casilla 160-C Concepci?n. Chile.

Pedro Victoriano <pvictori@udec.cl>

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### Hannover MolecularEvol

Job Title: Assistant Professorship Employer: School of Veterinary Medicine Hannover

Job Description Assistant Professorship in the Institute of Animal Ecology and Cell Biology / Department of Ecology and Evolution

Applications are invited for an Assistant Professorship (six years, non-tenure track) in molecular evolution and development. Salary is at the German university W1 level. Start up funds are available.

The successful candidate will be expected to establish an internationally recognized, externally funded research program that integrates well with the primary research strengths (molecular ecology and evolution) of the department.

The School of Veterinary Medicine Hannover is an Equal Opportunities Employer

Applications, including CV, list of publications, statements of research and teaching interests, and the names and contact information for three professional references should be sent to

The President of the School of Veterinary Medicine Hannover, P.O. Box 71 11 80, D-30545 Hannover, Germany

by 30th April 2004, or by email to: Bernd.Schierwater@ecolevol.de

Angie Faust <Angie.Faust@tiho-hannover.de>

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### HighlandsBiolStation FieldAssist PlantEvol

SUMMER FIELD ASSISTANT POSITION: Plant pollinator-interactions

LOCATION: Based out of Highlands Biological Station, Highlands NC and Athens, GA; throughout GA, NC, SC, FL.

DATES AND DURATION: End of June through August (approximately 10 weeks). Start and end dates are flexible.

JOB DESCRIPTION: Assistant in plant ecology & evolution study investigating plant-pollinator interactions and demography in a native herbaceous annual of the Eastern United States. Work involves assistance locating populations and performing demographic censuses, pollinator observation watches, and pollination experiments in communities such as open woods, pine glades, rocky outcrops, and open fields. We will travel throughout parts of Georgia, North Carolina, South Carolina, and the Florida panhandle. One month will be spent at Highlands Biological Station, located in a summer resort town and situated on a high plateau of the Blue Ridge Mountains.

QUALIFICATIONS: Interest in plant-pollinator interactions or plant demography preferable and enthusiasm a must!!!!. Although the actual work is not strenuous, you must be willing to work long days. Must also be willing and able to live and work out of campsites for a few days at a time as we will be traveling in addition to working out of Highlands Biological Station and Athens, GA. This is an excellent opportunity to gain research experience in ecology!

BENEFITS: Room and board will be provided throughout the 10 week position.

APPLICATION: Send resume with GPA and at least one reference along with a cover letter/statement of interest including potential start/end dates. Applications may be sent via postal mail or email.

CONTACT: Rachel Spigler 2502 Miller Plant Sciences Department of Plant Biology University of Georgia Athens, GA 30601 Email: rspigler@plantbio.uga.edu

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## ImperialCollegeLondon MicrobialEcology

Postdoctoral Research Associate in microbial population biology

NERC Centre for Population Biology Imperial College London, Silwood Park

Summary of Post:

An experimental biologist to work on the population biology of micro-organisms. Our current work in this area includes work on experimental evolution in yeast and spatial processes in bacteria.

One of the research themes of the CPB (<http://www.cpb.bio.ic.ac.uk/>) is microbial ecology which currently includes three projects. (i) Spatial process in bacteria: using *Pseudomonas* bacteria we are currently studying a range of phenomena such as plasmid maintenance and metabolic parasitism in biofilms. (ii) Experimental evolution in yeast: we have been investigating the evolution of sex by genetically manipulating yeast so that they cannot go through meiosis and than comparing adaptation to novel environments. (iii) Community structure of protists: we have been testing theories in community ecology by constructing food webs involving algae, ciliates and other protists. We seek an experimental biologist, ideally with a background in microbial population biology, who will develop a research programme to extend or complement these existing projects. The CPB has extensive molecular microbial facilities (including DNA sequencing and real-time PCR), a major chemostat facility, and increasing equipment for the visualisation of bacteria in biofilms. Our work on bacteria is conducted jointly with a group at CEH Oxford led by Professor Mark Bailey.

Knowledge / Experience: You should have a PhD in microbial ecology or a closely related discipline. Candidate should have expertise in the area of microbial ecology or related area.

Salary and Conditions: The contract is for 3 years. Research and Education scale B, £19068 - £28842. Applicants would normally be expected to have submitted their PhD prior to taking up the appointment. This is an Imperial College scale and is equivalent to the R&A1A scale in other universities. Starting salary depends upon experience, and partly on age, rising within the scale in annual increments dependant on perfor-

mance. Normal university conditions apply, including optional membership of pension schemes.

Applications : Your application should clearly highlight your qualifications, experience, abilities and attitudes that are specifically relevant to this position, giving evidence and examples where possible . General, non-specific applications will not be sufficient.

Please write enclosing your application form (required), CV and the names and addresses of two academic referees, to: Miss Sarah Snellin NERC Centre for Population Biology Imperial College at Silwood Park Ascot, Berkshire SL5 7PY, UK

You can download the application form: <http://www.cpb.bio.ic.ac.uk/job/vector0304.html> Closing date: 30 April 2004 Expected interview dates: week beginning 17th May, please inform us of your availability that week. –

Prof. Ian P. F. Owens Department of Biological Sciences and NERC Centre for Population Biology Imperial College London Silwood Park Ascot, Berkshire SL5 7PY UK

Fax +44 (0)20 759 42339 Tel +44 (0)20 759 42215  
Web [www.bio.ic.ac.uk/research/iowens/](http://www.bio.ic.ac.uk/research/iowens/) Ian Owens  
<i.owens@imperial.ac.uk>

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## ImperialCollegeLondon VectorBiology

Postdoctoral Research Associate in the population biology of insect vectors

NERC Centre for Population Biology Imperial College London, Silwood Park

Summary of Post:

A scientist with a background in biology or the mathematical sciences to work on modelling the population biology and population genetics of insect vectors of human and animal diseases.

The CPB (<http://www.cpb.bio.ic.ac.uk/>) is planning over the next five years to develop a research programme in vector biology and is currently talking with a number of potential partners and funders. This programme will have a major experimental component involving field studies of malaria-transmitting mosquitoes, and laboratory investigations of insects genetically manipulated so that they cannot transmit

pathogens. The present position is for a theoretician to work with our and other experimentalists to develop models of vector population dynamics, and vector-disease interactions, as well as to investigate new ideas in the genetic control of vectors (and other pests).

**Knowledge / Experience:** You should have a PhD in population biology or mathematical sciences or closely related disciplines. Candidate should have expertise in the area of population biology, vector disease interactions, genetic control of vectors and/or mathematical models relating to any of these areas.

**Salary and Conditions:** The contract is for 3 years. Research and Education scale B, £19068 - £28842. Applicants would normally be expected to have submitted their PhD prior to taking up the appointment. This is an Imperial College scale and is equivalent to the R&A1A scale in other universities. Starting salary depends upon experience, and partly on age, rising within the scale in annual increments dependant on performance. Normal university conditions apply, including optional membership of pension schemes.

**Applications :** Your application should clearly highlight your qualifications, experience, abilities and attitudes that are specifically relevant to this position, giving evidence and examples where possible . General, non-specific applications will not be sufficient.

Please write enclosing your application form (required), CV and the names and addresses of two academic referees, to: Miss Sarah Snellin NERC Centre for Population Biology Imperial College at Silwood Park Ascot, Berkshire SL5 7PY, UK

You can download the application form: <http://www.cpb.bio.ic.ac.uk/job/vector0304.html> Closing date: 30 April 2004 Expected interview dates: week beginning 17th May, please inform us of your availability that week. –

Prof. Ian P. F. Owens Department of Biological Sciences and NERC Centre for Population Biology Imperial College London Silwood Park Ascot, Berkshire SL5 7PY UK

Fax +44 (0)20 759 42339 Tel +44 (0)20 759 42215 Web [www.bio.ic.ac.uk/research/iowens/](http://www.bio.ic.ac.uk/research/iowens/) Ian Owens <i.owens@imperial.ac.uk>

The Department of Biology at Southwestern University ([www.southwestern.edu](http://www.southwestern.edu)) invites applicants for a 1-year, full-time, Visiting Assistant Professor position beginning mid-August 2004. Specific area of training is open, although this person is expected to teach an upper-level Evolutionary Biology course with lab and a non-majors Environmental Science course in the Fall. Spring courses are undecided, but will need to include a non-majors course as well.

Ph.D. strongly preferred but competitive ABDs may be considered. Please submit a cover letter, curriculum vita, statement of teaching philosophy, and names of 3 references to: Visiting Assistant Professor Search, Department of Biology, 1001 E. University Avenue, Southwestern University, Georgetown, TX 78626.

**PREFERRED:** Email applications to Dr. Romi Burks ([burksr@southwestern.edu](mailto:burksr@southwestern.edu)) or contact her for more information. Applications will be reviewed as soon as they are received.

**Added Info:** Salary initially set at 38K for nine months + benefits; Schedule MWF Evol Bio 8-8:50; W Lab 2-5; Environmental Science 2:30 - 3:20 Tu/Th with Tu/Th Lab 3-5

Southwestern University is a selective, undergraduate institution committed to a broad-based liberal arts, sciences, and fine arts education. Southwestern currently enrolls approximately 1,250 students and maintains a student to faculty ratio of 10 to 1. The University's endowment ranks among the highest per student of undergraduate institutions in the country. In addition to a number of other national organizations, Southwestern University is a member of two consortia of premier liberal arts colleges, the Associated Colleges of the South and the Annapolis Group. Located in Georgetown, Texas, 28 miles north of downtown Austin, Southwestern is affiliated with The United Methodist Church. Southwestern University is committed to fostering a diverse educational environment and encourages applications from members of groups traditionally under-represented in academia. For information concerning the University, visit our web site at [www.southwestern.edu](http://www.southwestern.edu). Southwestern University is an Equal Opportunity Employer. EOE/M/F

Romi L. Burks, Ph.D. Assistant Professor Department of Biology Southwestern University Georgetown, TX 78626

Office Phone: 512-863-1280 Lab Phone: 512-863-1640 FAX: 512-863-1696 Website: [www.southwestern.edu/~burksr](http://www.southwestern.edu/~burksr) “The mediocre teacher tells. The good teacher explains. The superior teacher demonstrates. The great teacher inspires.” W. A. Ward, English novelist



Hope Hollocher Clare Boothe Luce Associate Professor  
 Department of Biological Sciences Galvin Life Sciences  
 University of Notre Dame Notre Dame, IN 46556 USA  
 tel.: (574) 631-4569 FAX: (574) 631-7413 e-mail:  
 Hope.Hollocher.1@nd.edu

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### StanfordU ResAssist

Description Research technician, 35 hrs/wk, for a newly funded project located at Stanford University's Hopkins Marine Station, in Pacific Grove, California. Under the direction of the Principal Investigator, Stephen Palumbi and project trainee, the technician will assist with research related to genetic characterization of populations of marine vertebrates and invertebrates in the context of ongoing research into marine conservation and management. The primary responsibility of the technician will be to extract DNA and document genetic variation, help collect larval and adult specimens. This primary responsibility will require the use (or development) of many research skills using a variety of molecular genetic tools. In addition, the technician will participate in a variety of research activities including: field monitoring of multiple sites in central California, animal care, and laboratory maintenance. This project is currently funded for one year although there is potential for extension of the technician position to other research projects, and has the possibility of co-authorship of at least one resulting publication. QUALIFICATIONS: The successful applicant will be highly organized, have an attention to detail, be able to work as an independent part of a team, have a basic understanding of and facility with standard computer software programs, and have practical experience with a variety of standard molecular tools (for example, DNA extraction, PCR, gel electrophoresis, DNA sequencing, etc). In addition to these basic requirements, we desire an applicant with an interest in marine ecosystems and their ecological functioning.

Send resume and letter of interest to :

Dr. Stephen Palumbi Hopkins Marine Station Stanford University Pacific Grove, CA 93950 Ph. (831) 655-6210 Fax (831) 655-6215 email: spalumbi@stanford.edu

Stephanie Belliveau <sbelli@stanford.edu>

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### UHawaii LabTech

Molecular Evolutionary Genetics Research Technician Position

We are seeking a qualified applicant for a full-time laboratory manager position to oversee the research programs of a joint evolutionary genetics laboratory at the Hawaii Institute of Marine Biology (<http://www.hawaii.edu/HIMB/>). The official job ad (Research Support PBB, Molecular Research Technician, position number 0077573T) is posted on the University of Hawaii job site at [http://workatuh.hawaii.edu/-zoom\\_job.php?2541](http://workatuh.hawaii.edu/-zoom_job.php?2541) - applicants will be considered after April 14th until the position is filled.

#### 1) IMPORTANCE OF EXERCISED JUDGEMENT

Judgments and decisions exercised may: \* directly impact operations, functions, programs, management, or policies of the program or its organizational segments \* impact the direction, accomplishment of goals, and schedules of projects \* impact the decisions of immediate supervisor and the career paths of other laboratory personnel Therefore qualified applicants must be mature, responsible, reliable and capable of exercising rational judgment at all times.

#### 2) DUTIES AND RESPONSIBILITIES

\* Coordinate and facilitate a wide range of research activities in Drs. Bowen & Toonen's laboratory \* Operate, maintain, adjust, and calibrate basic laboratory equipment \* Follow and act upon complex oral and written instructions \* Establish a organizational system for laboratory inventory and storage \* Track laboratory inventory, order materials and supplies as needed \* Train and oversee other laboratory personnel (interns, undergraduates and graduate students) and assist senior lab members \* Collect animals, sample experimental tanks and isolate tissue samples using fine dissection and homogenization techniques \* Extract and quantify genomic DNA from tissue samples \* Perform a suite of molecular analyses including: Polymerase Chain Reaction (PCR); cloning; automated and manual sequencing; preparation of glycerol stocks; isolation and characterization of novel microsatellite loci; developing, hybridizing and scanning microarrays; \* Analyze DNA sequences generated in the lab or mined from GenBank using a suite of population genetic software including: Arlequin, Sequencher, PAUP\*, Lamarc, etc. \* Imple-

ment appropriate university state and federal fiscal and safety policies \* Other duties as assigned

Expected originality:

\* Offers constructive ideas to increase the efficiency, effectiveness, productivity or scientific merit of research underway in the laboratory \* Explores and develops new or improved methodologies, and refines existing ones \* Checks other fields of study for methodologies and approaches that might have utility in the research program \* Evaluates new technologies for their applicability to the goals of the research programs underway in the laboratory

### 3) CONTROLS OVER POSITION

\* Works will be frequently reviewed by Drs. Bowen & Toonen \* Technician will be expected to work independently in the laboratory without direct supervision, but perform most assignments with instructions regarding the general approach and outcomes of the activity

### 4) SUPERVISION EXERCISED

\* Coordinates, directs, reviews and/or monitors the work of others and their accomplishment of specific tasks in the laboratory \* Reviews the work of others and provides guidance or training to others with regard to above Duties and Responsibilities

### 5) MINIMUM QUALIFICATIONS:

Education and Professional Work Experience

\* Completion of a pertinent baccalaureate educational degree and relevant professional experience \* Competency in technical knowledge, critical thinking skills, communication skills and interpersonal skills outlined below

Expected knowledge, skills & abilities

\* Demonstrated hands-on experience in a biological laboratory setting \* Considerable working knowledge of the principles, practices and techniques of molecular ecological research as demonstrated by a broad understanding of the full range of pertinent standard and evolving concepts, principles and methodologies \* Demonstrated ability to resolve a wide range of complex problems through the use of creative reasoning and effective problem solving, especially troubleshooting and resolving technical problems in the laboratory \* Demonstrated ability to interpret and present information and ideas clearly and accurately in writing, verbally and by the preparation and oral presentation of reports and other materials \* Demonstrated ability to establish and maintain effective working relationships with internal and external organizations, individuals, groups, and team leaders \* Demonstrated ability to op-

erate and maintain personal computers,

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## UIdaho ZebrafishTech

The Robison Lab in the Department of Biological Sciences at the University of Idaho, Moscow is seeking a Scientific Aide to participate in studies of the genetic basis of behavioral, morphological, and physiological changes associated with domestication in fish. The ideal candidate will have experience with zebrafish husbandry (or fish husbandry in general) and molecular techniques such as PCR, and will have good organizational, writing, and communication skills. See the formal vacancy announcement below or go to: <http://www.uidaho.edu/hrs/employment/jobs/-C04-034.pdf> for details on how to apply.

Scientific Aide Department of Biological Sciences, University of Idaho

This position is contingent on continuation of funding. This position is subject to completion of a criminal background check.

Classified position, PG G (\$11.53/hr.â\$15.22/hr. ; \$23,982/yr.â\$31,657/yr.) Closing date for receipt of application materials is 4/15/04 or until suitable applicant has been identified.

APPLICATION MATERIALS REQUIRED: (Please read carefully) Complete and submit a 1) UI application form, 2) answers to the attached supplemental questionnaire, and 3) a resume, prior to 5:00 p.m. on the above closing date. Only specifically requested employment materials for applicants who meet minimum qualifications will be forwarded to the hiring department. Materials submitted that are not requested above will be shredded.

Interested applicants contact Human Resource Services, University of Idaho, P.O. Box 444332, 415 W. Sixth St., Moscow, ID 83844-4332. Phone: 208-885-3609 or TDD 885-3617. Call the Human Resources Jobline at 208-885-3595 or visit our home page at <http://www.uidaho.edu/hrs/> for a list of current openings.

**DUTIES:** The employee will be responsible for the maintenance of a zebra fish colony through supervision of routine feeding and husbandry tasks. The employee will also be responsible for conducting experiments in the molecular lab as directed by the Principal Investigator. Some supervision of irregular help will also be required.

**MINIMUM REQUIRED QUALIFICATIONS:**

**Education/Experience:** B.S. degree in related field as appropriate to the scientific research discipline plus approximately two (2) years of experience in the research discipline or closely related field. Additional graduate level course work may be substituted for up to three years of experience.

**Good Knowledge of:** scientific principles; computer hardware and software programs.

**Demonstrated ability to:** perform a variety of specialized tasks and laboratory techniques specific to the needs of the position; operate, maintain, calibrate, troubleshoot and resolve basic problems with instruments and equipment; keep records and compile written information for reports; follow good safety practices; possess good interpersonal and communication skills; **MAY** train and supervise other workers.

**Physical ability to:** perform assigned duties; may be required to work with toxic, volatile and corrosive chemicals and/or carcinogenic substances; may be required to work in adverse environmental conditions and/or carry or lift heavy materials.

**Must:** Applicants who are selected as final possible candidates must be able to pass a background check and show proof of eligibility to be employed in the United States.

**Desirable Qualifications:** â Bachelorâs Degree in Biology or related field such as = Psychology, Fisheries, and Chemistry â Experience with the care and maintenance of a zebrafish = colony. â Experience with in vitro fertilization and chromosome set = manipulation in fish. â Experience with one or more of the following molecular = techniques: â PCR, Genotyping with microsatellite markers, DNA sequencing, = Gel electrophoresis, DNA extraction â Experience with one or more of the following bioinformatics = techniques: o PCR primer Design, DNA sequence alignment and analysis, Computer programming, Database management

**Date:** 10/22/03 **Classification:** Technical/Paraprofessional To enrich education through diversity the University of Idaho is an equal opportunity/affirmative action employer.

**RESPONSIBILITIES:** The University of Idaho does

not discriminate against an individual with a disability in regard to job application procedures, the hiring or discharge of employees, employee compensation, advancement, job training, and other terms, conditions, and privileges of employment. Based on this commitment, various job duties on the job description have been analyzed to be essential to this position. Employers can continue to require all applicants and employees, including those with disabilities, to be able to perform the essential, non-marginal

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## UMaryland ResTech ReproductiveIsolation

Research Technician Position

Wilkinson Lab, University of Maryland, College Park

Applicants are invited for an NSF-funded research technician to help investigate the role of genomic conflicts in reproductive isolation of stalk-eyed flies. Seeking a motivated individual with strong interest in evolutionary research. BS in Biology or similar major required. Experience with maintaining insect cultures and DNA sequencing an advantage. Starting salary \$30,000 per year, with option for renewal for up to 3 years.

Please send inquiries or applications with CV and names of three referees to Dr Jerry Wilkinson ([wilkinso@umd.edu](mailto:wilkinso@umd.edu), Tel: 301-405-6942, Fax: 301-314-9358), Department of Biology, University of Maryland, College Park, MD 20742

Applications received by May 1, 2004 will be given best consideration. Position is available beginning June 1, 2004.

See <http://www.life.umd.edu/faculty/wilkinson> for recent citations

[gw10@umail.umd.edu](mailto:gw10@umail.umd.edu)

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**UMontreal BioinformaticsTech**

We are seeking a senior Bioinformatician to lead a small team of software developers working on the design and development of specialized sequence analysis and genome annotation tools, and an integrated workbench environment including workflow systems.

Requirements: Ph.D. (or M.Sc) in Computer Science or Bioinformatics with 2+ years experience in software development for sequence analysis, databases and web applications; Strong background in Linux, CORBA, JDBC, Java, JSP, SQL, PHP, MYSQL and PostgreSQL.

The position is available immediately. In the case of equivalent qualification, preference will be given to applicants with Canadian citizenship or permanent residence.

Applications including: CV, publications and project descriptions, as MS Word- compatible attachments

should be sent to: Dr. Gertraud Burger Universite de Montreal Departement de biochimie 2900 Boulevard Edouard-Montpetit Montreal, Quebec Canada H3C 3J7 E-mail: jobs@bch.umontreal.ca Fax : (514) 343-2210

Gertraud Burger <Gertraud.Burger@Umontreal.ca>

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## UNSW Sydney Biology

Associate Professor or Professor of Ecology/Environmental Science (2 positions) FACULTY OF SCIENCE SCHOOL OF BIOLOGICAL, EARTH & ENVIRONMENTAL SCIENCES REF. 2777 Applications are invited for two appointments to the position of Associate Professor or Professor in the School of Biological, Earth and Environmental Sciences (BEES). The positions are full-time continuing. Preference may be given to applicants with interests in the area of vertebrate ecology/conservation, the interaction between plants and their environment or research programs focused on environmental cultural sustainability.

The School of BEES is a new School that was established in January 2002 by amalgamation of the former Schools of Biological Science and Geology, and elements of Geography, notably physical geography and spatial information science. The School has broad teaching and research interests in biology, ecology, marine science, earth and spatial sciences, and environmental science including CSU (Conservation through sustainable use)

programs. The successful applicants will be expected to provide academic leadership in the development and integration of teaching programs and research in environmental science with the new School and across UNSW.

Enquiries may be directed to Associate Professor Peter Steinberg, Head of the School of Biological, Earth and Environmental Sciences, on telephone (61 2) 9385 2067; facsimile (61 2) 9385 3327, or email: p.steinberg@unsw.edu.au An information package is available from the Senior Appointments Officer, Human Resources, UNSW, Sydney 2052, on telephone (61 2) 9385 2887; facsimile (61 2) 9662 2832; or email: j.cabatu@unsw.edu.au Visit UNSW's website at: <http://www.unsw.edu.au> and the School's website at: <http://www.bees.unsw.edu.au> Applications close 7 May 2004.

..... School of BEES The University of New South Wales Kensington, Sydney 2052 NSW, Australia

<http://www.bees.unsw.edu.au/staff/academic/-brooks/brookslab/rob.html> rob.brooks@unsw.edu.au

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## USheffield FieldAssist

FIELD ASSISTANT needed from around May 1 to early July 2004 for a PhD study on behavioural ecology of house sparrows on Lundy Island, Bristol Channel, UK. Preferred experience in field and bird handling, but not essential. More importantly, I am looking for a person with a positive attitude, interpersonal skills and an ability to get up early (very early sometimes). Daily routines involve checking nest boxes, nest box watch and setting video cameras. Travel within UK, camping fee on the island and food will be covered. The island is a beautiful place with great wildlife. Please send a letter of interest, resume, and names, telephone numbers, and E-mail addresses of 2 references to SHINICHI NAKAGAWA by as soon as possible, preferably by email (EM: s.nakagawa@sheffield.ac.uk), Dept. of Animal and Plant Sciences, University of Sheffield, Sheffield, UK, S10 2TN.

- Shinichi Nakagawa Department of Animal & Plant Sciences, University of Sheffield, Sheffield S10 2TN, UK Tel: +44-114-222-0064 Fax: +44-114-222-0002

S Nakagawa <S.Nakagawa@sheffield.ac.uk>

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## UppsalaU EvolGenetics

Applications are invited for a 4-year position as

### ASSISTANT PROFESSOR IN EVOLUTIONARY GENETICS AT UPPSALA UNIVERSITY

Dept of Evolutionary Biology, Evolutionary Biology Centre

The position includes independent research in the area of molecular evolutionary genetics in eukaryotic systems. The approach may be empirical and concern experimental or bioinformatic studies, or theoretical. Teaching within the undergraduate programmes in Biology at Uppsala University and supervision of PhD students are also included. The successful candidate will join a Department working with molecular evolutionary genetics and shall contribute with his/her competence and research to the activities at the Department.

The Department is situated in the recently-built Evolutionary Biology Centre of Uppsala University. The Centre is an exciting arena for multi-disciplinary research in evolutionary biology, housing some 400 scientists and graduate students, with research programs in ecology, systematics, genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

The successful candidate must have a Ph.D. Priority is given to applicants who completed their PhD within the last five years. Uppsala University's general employment regulations also require that teachers possess all skills necessary to carry out their duties proficiently. The ability to teach in Swedish or English is a requirement. The successful candidate is expected to teach in Swedish within two years.

The full announcement including ranking criteria and to where the application shall be submitted is available at <http://www.personalavd.uu.se/ledigaplats/1303forasseng.html> General instructions on how to apply can be found at <http://www.teknat.uu.se/english/instructions.php> For further information please contact Prof Hans Ellegren (Hans.Ellegren@ebc.uu.se).

Closing date is May 10, 2004.

– Professor Hans Ellegren Dept of Evolution, Genomics

and Systematics Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

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

Web address: <http://www.egs.uu.se/evbiol/index.html>

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## WoodsHole SummerCompBiol

SUMMER COMPUTATIONAL BIOLOGY ASSISTANT [SCBA], Seasonal/Temporary, Full-time Josephine Bay Paul Center for Comparative Molecular Biology and Evolution The Marine Biological Laboratory, Woods Hole, MA

Laboratory of Andrew G. McArthur (<http://jbpc.mbl.edu/mcarthur>)

Description: The Marine Biological Laboratory is seeking candidates for a seasonal/temporary scientifically rewarding position in Computational Biology with the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution.

Duties: Providing software design and programming assistance to the on-going development of the GiardiaDB project ([www.mbl.edu/Giardia](http://www.mbl.edu/Giardia)) within the approaches of the Gene Ontology Consortium (<http://www.geneontology.org>) and GMOD Initiative (<http://www.gmod.org>). Primary effort will be in the use of molecular evolutionary techniques for high-throughput phylogenetic annotation of genomes and ESTs, using Beowulf clusters. The successful candidate will additionally participate in projects involving molecular evolution, computation biology and molecular systematics of a variety of organisms and genes.

Conditions: This is a seasonal/temporary position available as early as mid May through the end of August, 2004.

Education/Experience: The successful candidate must be enrolled or recently completed undergraduate training in computer science or bioinformatics. Must be skilled in design, construction and maintenance of on-line relational databases. Specific skills with MySQL, Perl, HTML and phylogenetic methods (ClustalW, Mr-Bayes, PAUP) strongly desired. Specific training in computation biology, bioinformatics or genomics is desirable, but training will be provided is needed. As part of professional development, this positions will provide



thorough training in genomics and bioinformatics.

Please apply to: Marine Biological Laboratory, ATTN: Human Resources, reference code [SCBA], 7 MBL Street, Woods Hole, MA 02543-1015, or email re-

sume@mbl.edu. An Equal Opportunity/Affirmative Action Employer/Non-smoking workplace.

Deadline: Until a suitable candidate is identified.

mcarthur@mbl.edu mcarthur@mbl.edu

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## Other

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### Allee effect

Dear Evoldir,

We are working on the Allee effect, a dynamical process by which populations at small sizes, or low densities, experience a reduction of growth rate and an increased risk of extinction.

We are looking for studies that have looked for such an effect, but that didn't find any. Such "negative" studies are difficult to find because they are typically not published, yet they are of major importance in ecology

and conservation biology.

If you have heard of such "negative" results, could you please ask the scientists concerned to contact me, or provide me with a way to contact them?

Please reply directly to me: franck.courchamp@ese.u-psud.fr Thank you very much in advance

(for those of you interested in finding more on the Allee effect, several reviews are available here: <http://www.ese.u-psud.fr/epc/conservation/pages/-PublisFranck.html>, papers 19, 26 & 30) –

Franck Courchamp Universite Paris-Sud XI Tel (0033/0) 1 69 15 56 85 Batiment 362 Fax (0033/0) 1 69 15 56 96 F-91405 Orsay Cedex FRANCE <http://www.ese.u-psud.fr/epc/conservation/pages/->

Franck.html franck.courchamp@ese.u-psud.fr

staffan.bensch@zoekol.lu.se

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### Atlantic herring samples

I am currently studying the population genetic structure of Atlantic herring in the north sea and adjacent areas and require some additional samples to complete my analysis. I am looking for well preserved Herring samples (*Clupea harengus* and *Clupea pallasii*), preferably fin clips, from the following locations:-

Western Atlantic - South of Newfoundland Iceland  
Greenland Barents Sea North East Baltic Sea Pacific

I would be grateful to hear from anyone who could assist me.

Jennie — Jennie Brigham Email:  
J.Brigham@hull.ac.uk University of Hull

Jennifer E Brigham <J.Brigham@hull.ac.uk>

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### BirdBlood mRNA

We have been discussing the possibility to investigate mRNA expression in blood obtained from birds in a couple of long term studies. The rationale behind using blood is that we think this is the only way of obtaining mRNA without jeopardizing the health of the birds. We wonder whether some of you have information on one or all of these 3 questions:

- 1) How much blood is needed (in microliter) for getting sufficient amount of mRNA (enough for 100 PCRs)? Or rather, what is the yield in terms of nano gram mRNA / micro liter blood?
- 2) What storage buffers are recommended? We are considering to use Qiagen's RNeasy.
- 3) How many different mRNA's might be retrieved from the blood of adult birds during the breeding season?

Staffan Bensch

Associate Professor Molecular Population Biology Lab  
Office +46(46) 222 4292 Dept. of Animal Ecology Lab +46(46) 222 4326 Lund University Fax +46(46) 222 4716 S-223 62 Lund Sweden Home page: [http://fisher.teorekol.lu.se/ekol\\_inst/mol\\_ekol/](http://fisher.teorekol.lu.se/ekol_inst/mol_ekol/)

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### Colonisation via micros

I am investigating population structure in Atlantic salmon from a river in the UK. One of the four main tributaries of this system has undergone a very recent population expansion following the removal of an impassable barrier (weir removed in 1987). The tributary was extensively restocked for 11 years with fish from below the barrier but within the same tributary. I have sampled 10 loci from fairly large sample sizes in all four tributaries. My question is, how would I detect the recent range / population expansion? I observe no significant difference in heterozygosity or allelic richness between tributaries. There is no significant departure from HWE in either tributary. Both Principal Components Analysis and a NJ tree suggest that the recently re-colonised tributary is differentiated from everything else - and they are all quite similar.

Is it possible to test for mismatched distribution using genetic distance (e.g. D, or DCE) in microsatellites, in the same way as using sequence variation? And would this be possible over so short a period of time?

Is there an easier method for investigating population expansion using microsatellites?

Any suggestions greatly appreciated.

Nigel Massen

n.massen@soton.ac.uk

School of Biological Sciences University of Southampton Bassett Crescent East Southampton SO16 7PX

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### ColoradoStateU Evol2004 BookDonations 2

I don't think I actually got the message below to go out to evoldir when I attempted to send it a while back, so here it is again. Sorry. What is really embarrassing is that it is a correction to a previous e-mail. Arrgghhh. It's one of those months! Shanna

Oops! It was pointed out to me that I neglected to say what the money from the auction will be used for.

Sorry for that major oversight. All proceeds will be donated to a graduate travel fund, especially for funding travel to the Evolution meetings in New Zealand in 2007. We are also donating the profits from T-shirt sales (purchased at time of registration or at the conference - but note that only a small # will be available on site) to this same fund. So please be generous in your donations for the auction, and be sure to pick up a T-shirt or 2! Thanks again, Shanna -----

Hi All, As you may know, the Evolution Meetings this year will be held at Colorado State University. As one of the organizers, I would like to ask you for your help. We are planning to have a book auction (and perhaps other items like art or scientist memorabilia - whatever that might mean), so we would appreciate contributions that might be considered valuable by the evolution community. If you have written one or more books and would be willing to contribute autographed copies, we would be very grateful. Additionally, if you have any of the classics available (e.g., books out of print and hard to come by), those would certainly be welcome as well. If you have ideas for other items that you think might fetch some money, feel free to write me about them, and we will consider their suitability. They can be silly or serious items (e.g., perhaps an eraser thrown by Sewall Wright), as we hope this will be a fun event as well as a money-maker. Please contact me directly - my info is below. Best wishes, Shanna Carney

----- Shanna Carney Department of Biology Colorado State University Fort Collins, CO 80523-1878 970-491-1092 Fax: 970-491-0649 secarney@lamar.colostate.edu <http://lamar.colostate.edu/~secarney/> -----

Shanna Carney <secarney@lamar.colostate.edu>

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## DNA sequence analysis answers

Hello everybody,

I recently inquired alternatives for the Sequencher software (GeneCodes Corp.) that we use in the lab. There were a couple of notions that a Sequencher Mac OSX version 4.2 just became available, as well as suggestions for alternative programs. One response mentioned problems with a hardware key (probably for the dongle version?) when running the classic program in OSX. I remember we also encountered such problems. A good alternative may be Codoncode Aligner. Below, I compiled some of the responses that I received since then.

My inquiry: I wonder whether you could name a good and reasonably prized DNA sequence analysis software that you are routinely using in the lab. We are using Gene Codes' Sequencher so far, mostly for proofreading of ABI sequence chromatograms and (small) contig assembly. However, it seems that the Mac version is running only in the classic environment on Mac OS X machines. I find this a bit outdated considering that OS X is already three years old. Also, there seems to be no improvement regarding functionality when comparing our current Sequencher v3 with the latest v4.1.

Reponses:

I recently downloaded the demo of sequencher and was also disappointed that it was still in classic. I asked the company and they assured me that the latest version was OSX, just not the demo.

We just got Sequencher 4.2, which runs natively in OS X. You might want to ask Gene Codes about it. It otherwise appears to be pretty much the same as v4.1. Like you, we've been quite frustrated by the pace of their development.

I use Sequencher. The newest version runs in OS X. There is no huge difference from earlier versions, but a number of incremental improvements. However, I don't know of an adequate cheap substitute. If I did, I would use that instead, because I consider GeneCodes' monopolistic practices to be immoral.

I'm in the process of trying out CodonCode Aligner, I can't go as far as recommending it but it has been recommended to me. If you look at the price tag, though, you'll see that it's much more affordable than Sequencher. <http://www.codoncode.com/>

A free sequence viewer/editing program which is really good is 4Peaks, which is available FREE from <http://www.mekentosj.com/4peaks/> - currently this program does not contig so it might not be ideal for what you want but it is definitely a nice interface to use - give it a try! This website also has a couple of other nice biology programs for OS X. On the topic of Sequencher. We have recently got a G5 and have ordered the OS X upgrade for Sequencher - however in the interim we would like to be able to use Sequencher in the classic environment in 10. Only problem is that the Mac will not recognise the hard key. How did you get around this problem so that you could run your old version of sequencher in classic?

we really like Codoncode Aligner <http://www.codoncode.com/> I highly recommend it, good functionality, very reasonably priced, and the guys seem happy to talk, take suggestions and give support.

people in my lab recommend that, if you are running a Mac with OS X, you try EMBOSS ([www.emboss.org](http://www.emboss.org)). This is an open source clone of GCG; it can be compiled and run under Mac OS X. Further, there are third-party graphical interfaces which function under darwin. (By the way, all of this is free!) I haven't used any of this but know that, after some discussion, it seems to be the favorite for a mac environment here.

My lab and our shared DNA sequencing facility use Sequencher. The latest release is 4.2 on the Mac, which is OSX native. It also has a few small improvements each release. Although Sequencher is expensive, we find it useful due to its menu driven interface and ease of use as well as the availability of essentially identical versions on Macs and PCs.

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

—

Dr. rer. nat. Jens Mayer Human Genetics, Building 60 Medical Faculty University of Saar 66421 Homburg Germany

phone-office: (49) 06841-1626627 phone-lab: (49) 06841-1626189 fax: (49) 06841-1626186 e-mail: jens.mayer@uniklinik-saarland.de

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## DNAsequence analysis more

Hi, I missed this earlier discussion but have this question - does Codoncode Aligner allow you to import files previously set up in Sequencher?

If they have this function or were willing to provide this function, I and I bet others, would love to jump ship from the ABI oligarchy. They really seem to care less about development and they charge an arm and a leg for their stuff.

Georgiana May Dept. EEB U. Minnesota (home of the Golden Gophers women's basketball team!)

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## DNAsequence analysis more2

Hi Georgiana and everyone else,

I have been trying out Aligner for the last few weeks

(they have a month-long trial lisenche) and asked about opening Sequencher projects a couple of weeks ago. Peter Richterich at CodonCode Corp. gave me a quick, clear response - basically he suggested exporting individual sequences or the contig in a standard format from Sequencher. This morning I forwarded your question on to him and asked for more clarification. His two emails are pasted below.

I have found Aligner relatively easy to learn and more useful than Sequencher in a few ways. Especially cool is its ability to automatically detect possible point mutations in assemblies using of Phred and Phrap base quality values.

Here are Peter's two emails:

1. Hi Sky,

> Can Aligner open Sequencher files? I have a bunch that I would love to > import and re-analyze/ evaluate with Aligner.

Aligner cannot currently open Sequencher projects directly. What you can do is export the sequences in a project, either as SCF files or as a CAF assembly, and then import the chromatogram files into Aligner.

After importing chromatograms this way, make sure to first base call the imported files from Aligner, so that you have quality values. Many Aligner functions work better with quality values, or require them, and Sequencher does not write them into SCF files.

Best regards,

Peter

. Hi Sky,

Thank you for your email. I think I will refrain from posting directly to the news group at this time, since it might look too much like a sales pitch. But let me expand on my previous answer on importing Sequencher projects:

The request to directly read Sequencher projects has come up several times, so we will definitely look into it. Since Sequencher uses a proprietary format, we cannot predict how long this will take - it depends on how easy it is to figure out the format. The more promising approach, which we may well implement first, is to support importing of CAF-formatted assemblies. The CAF format is public and well described, and Sequencher can export CAF assemblies.

This said, I still think that exporting SCF files from Sequencher and importing the files into Aligner is often the best solution, for the following reason: Sequencher does not support modern algorithms that use local alignments and sequence quality scores to build

the “consensus” sequence, but Aligner does. The recommended approach in Aligner is to import SCF (or ABI) files, and then re-call the bases with Phred directly from Aligner to get reliable quality scores that can be used in assembly. For example, in areas with two-fold coverage, Sequencher will call an ambiguity base for the consensus at every discrepancy. In contrast, CodonCode Aligner will use the quality scores to automatically pick the higher quality base for the consensus sequence. This can reduce the amount of editing and finishing dramatically, and give you a lower error rate in the finished sequence. I attached two screen shots as an example.

Please feel free to post any of this email or the previous email to the newsgroup you mentioned if you think it is relevant.

Best regards,

Peter – Peter Richterich, Ph.D. CodonCode Corporation 58 Beech Street Dedham, MA 02026 pr@codoncode.com (781) 686-1131 phone (781) 407-0807 fax

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### Drosophila heatshockgenes

Dear members of Evoldir,

As part of an investigation of naturally-occurring transposition into heat-shock genes, we are interested in screening *Drosophila melanogaster* populations recently collected from the wild. We hope to examine a world-wide sample of populations collected from diverse environments. If you have a recently (2000 or later) collected population of reasonable size that you'd be willing to share, please get in touch. Some regions are already represented in our collection, but we would be particularly interested in populations from the following regions:

USA north of Arizona and west of the the Mississippi River  
Canada Europe outside of France Asia outside of India  
Pacific Oceania

We are looking forward to hear from you. Thanks in advance for your help

Best regards,

Jean-Claude Walser

Dr. Jean-Claude Walser Department of Organismal Biology & Anatomy The University of Chicago Chicago IL 60637 USA

Telephone: (773) 834-0467 Fax: (773) 702-0037 Email: jcwals@uchicago.edu –

Jean-Claude Walser <jcwals@midway.uchicago.edu>

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### EU Genomics Biodiversity

Dear All,

The draft third call for proposals under the European Union Framework 6 programme includes a priority area on 'Genomics for terrestrial biodiversity and ecosystem research' - see the extract below. If anyone knows of a consortium that is already being built to address this funding opportunity, I would be very pleased to hear from them. Otherwise, I am prepared to gather names of EU and 'third country' scientists interested in the programme and initiate discussion on a possible bid. Please send name, email and a few key words to indicate your area of interest.

Best wishes

Roger Butlin

R.k.butlin@leeds.ac.uk

III.1.2 Genomics for terrestrial biodiversity and ecosystem research Development of genomic and molecular approaches to enable the understanding of terrestrial biodiversity and as far as feasible ecosystems structures, dynamics and processes in a changing environment, to improve society' s capacity to conserve and manage biodiversity and genetic resources. The selected taxa should have important conservation or functional attributes. The work should comprise a multidisciplinary approach aimed at improving understanding population genetic structures, dynamics and ecosystem processes, the identification of species and evolutionary relationships between taxa. This novel knowledge should also be made available for education, ecosystem monitoring, and the development of biodiversity conservation strategies. The participation of third countries partners is encouraged. (Topic for up-to-one Integrated Project)

R.K.Butlin@leeds.ac.uk



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## Fish specimens Mexico

I am assembling a list of non-Mexican professional biologists who are doing research with native Mexican fishes and need to collect specimens for genetic, morphological or behavioral studies. It is becoming increasingly difficult to obtain collecting permits from appropriate agencies of the Mexican government, and many people have become quite discouraged. In quite a few cases, collecting permits have not been granted or have taken impractically long periods of time. My ultimate goal is to be able to coordinate permit applications, perhaps through a central, organized "clearing house," or perhaps through a Mexican professional society. If we can document the number of people doing this research, and the fact that much of it is funded by NSF and other federal granting agencies, we may be able to elicit help from the US government or even get the issue negotiated at the ambassadorial level.

Consequently, if you are doing work with native Mexican fishes, I would very much like to hear from you with as much informatyion as you care to supply: the species you work with, the funding of your work, the number of collecting trips you have made, whether you are collaborating with a Mexican colleague, the nature of your permit, how you got it, whether you had to pay a fee, etc. Please do not supply any information you do not want to be made public eventually, and let me know if you do not wish to be identified by name in any data cimpilation. I do already know some of this information, but I would like to be able to work with as much data as possible.

Please do participate. At the very least, we can share our pain and frustration, and we might even accomplish something. – \*\*\*\*\* Bruce J. Turner Dept. Biology Virginia Polytechnic Institute and State University Blacksburg, VA 24061-0406 (540)-231-7444 (V) (540)-231-9307 (F) fishgen@vt.edu <http://www.biol.vt.edu/faculty/turner/>

\*\*\*\*\*

BJ Turner <fishgen@vt.edu>

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## Genescan files

Dear all,

I wonder if anyone knows about any PC software (free, if possible) that can import Genescan and Genotyper files generated from an ABI377. I remember there used to be one a couple of years ago, but I can't remember its name and if it is still available. Any help is very much appreciated. Cheers. Ricardo

Dr. Ricardo Pereyra CICESE-Oceanologia Km 107 Carr. Tijuana-Ensenada Código Postal 22860 Apdo. Postal 2732 Ensenada-Baja California, Mexico. Tel: +52 (646) 175-05-00 ext. 24290 <http://www.cicese.mx> e-mail: rpereyra@cicese.mx

Ricardo Pereyra <rpereyra@cicese.mx>

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## Genescan files answers

Dear all

Thanks a lot to all of you who replied to my question. Many of you were also interested about the suggestions I could get. Here they are.

My original question was:

I wonder if anyone knows about any PC software (free, if possible) that can import Genescan and Genotyper files generated from an ABI377.

Below you will find all the suggestions:

Hi Ricardo–

Genographer allows you to score fragment bands from ABI machines. Its available free at [hordeum.oscs.montana.edu/genographer](http://hordeum.oscs.montana.edu/genographer) I hope that helps!

Stuart

I'm pretty sure that ABI has a conversion software program for Mac to PC. When they switched their sequencers to a PC format, they created a conversion method so that folks midway through a project could consolidate all their data on one platform. Their tech support should know about it. Judith

Dear Ricardo

Genographer can use directly genescan files and it's for free!

here is the link: <http://hordeum.oscs.montana.edu/-genographer/> Good luck and cheers Vicky

Hi Richard,

the one program I know of is called GeneScanView and you can get it from the University of Padua, Italy. However, this software does only import one lane at a time, so you can't do cross-comparisons very well. It's good enough for a "quick glance", though. I for my part ended up using Genotyper back at the lab that analyzed my samples.

You can get GeneScanView at: <http://bmr.cribi.unipd.it>. The site's in Italian, but you can easily find the download link for the software.

Best wishes, -Christian

If it is for AFLP, maybe it is Genographer. It is a free PC software you can download at <http://hordeum.oscs.montana.edu/genographer/>

The installation is not obvious (you have to use a shortcut to open the application with Java).

The free version is a little bit unstable (lost of buttons and sometimes problems with the redraw option) but it is a very useful software to encode AFLP.

All the best Florence

Hi Ricardo,

There is a good program called STRand that you can download for free from UC-Davis: <http://www.vgl.ucdavis.edu/STRand/> Neil

Cheers,

Ricardo

Dr. Ricardo Pereyra CICESE-Oceanologia Km 107 Carr. Tijuana-Ensenada Código Postal 22860 Apdo. Postal 2732 Ensenada-Baja California, Mexico. Tel: +52 (646) 175-05-00 ext. 24290 <http://www.cicese.mx> e-mail: rpereyra@cicese.mx

Ricardo Pereyra <rpereyra@cicese.mx>

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## Geometridae moths loci

Dear All,

I am a PhD student at the University of Sheffield, modeling a metapopulation of the Winter moth inhabiting Orkney, Scotland. As part of this study, I hope to use microsatellite markers to gain an idea of relatedness and dispersal between population patches on the different islands. I was wondering if anybody has developed microsatellite loci for Winter moth (*Operophtera brumata*) or (probably more likely) from any species belonging to the Family:Geometridae (Larentiinae).

Please send replies to bop03eoj@shef.ac.uk.

Many thanks for any help.

Ed Jones

EDWARD JONES <bop03eoj@sheffield.ac.uk>

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## Glasgow TaxNameServer

The "Glasgow Taxonomy Name Server" (<http://darwin.zoology.gla.ac.uk/~rpage/MyToL/www/>) is an experimental web site for finding taxonomic names and classifications. At present it is populated with names from ITIS and GenBank, with additional names from Mammal Species of the World.

Users can type in a name (e.g., "Primates") and can browse the resulting classification. The site features a range of tools for displaying classifications, such as a hyperbolic tree viewer, as well as providing classifications in a range of formats for downloading (such as XML, and dot and GML graph formats).

As well as finding names in the database, the server can look for approximate matches (rather like Google's "did you mean" feature). For example, typing in "Dugong dugong" returns no hits, but the server will ask whether you meant "Dugong dugong."

The site is experimental, and heavily biased towards animals. It is mainly a test bed for research on how to query, display, and compare classifications. There is also some support for web services (enabling remote querying of other databases).

I would welcome any feedback, comments, or suggestions.

Regards

Rod Page

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

Tel: +44 141 330 4778 Fax: +44 141 330 2792 www:  
<http://taxonomy.zoology.gla.ac.uk/rod/rod.html>

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### Insect preservation

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)

I am considering using a dessicant and hoping that the DNA will remain largely intact.

Any suggestions?

Thanks, Steve

Steven J. Rauth Dept. of Bioagricultural Sciences and Pest Management Plant Sciences Building Colorado State University Fort Collins, CO. 80523 lab: (970)491-5984 Email: [srauth@holly.colostate.edu](mailto:srauth@holly.colostate.edu)

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### Isozyme linkage program

Does anyone have a computer program for calculating recombination values between pairs of isozyme loci both of which show codominant inheritance? Or does anyone know who might? Thank you.

Richard H. Whalen Professor of Biology Genetics South Dakota State University Brookings, SD 57007

e-mail: [Richard.Whalen@sdstate.edu](mailto:Richard.Whalen@sdstate.edu) phone: 605-688-4553

“WHALEN, RICHARD”  
 <[Richard.Whalen@SDSTATE.EDU](mailto:Richard.Whalen@SDSTATE.EDU)>

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### John Maynard Smith

Dear Evolutionists,

With the greatest possible sadness, I am writing to tell you that we have just lost one of the greatest minds ever

to consider the subject of biological evolution. John Maynard Smith passed away yesterday at home, while sitting in his chair.

John had just finished his latest book (on animal communication, with David Harper) and has recently been working on various theoretical and empirical problems, particularly in bacterial population genetics. He had also started work on a new edition of his book on the Major Transitions in Evolution (with Eors Szathmary). He was thinking, working, and helping his colleagues until the very end.

He was not totally comfortable in the last months of his life (mostly due to breathing difficulties) but he was not suffering very badly either.

Professor Maynard Smith is survived by his wife, Sheila, and his three children, Anthony, Carol and Julian.

Yours, Joel

Joel R. Peck Reader in Evolutionary Biology

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

Phone: (01273) 678843 Phone: (from outside the UK) 441273678843

Email: [j.r.peck@sussex.ac.uk](mailto:j.r.peck@sussex.ac.uk)

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### John Maynard Smith 2

Sadly Prof John Maynard Smith has died, on 19th April. An obituary is at

<http://www.guardian.co.uk/obituaries/story/0,3604,1200211,00.html> J.W.Grahame@leeds.ac.uk

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### Lepidopteran phylogeny answers

Dear all, Because a number of people have shown interest in the answers to my query of March 17 2004 about Lepidopteran divergence times, I have made a summary list of the e-mails I received. Unfortunately, there seems to be more interest than answers as far as Lep phylogenies with time calibration are concerned. I thank all those who sent me information. Sincerely, Patricia Beldade ....

ANTONIA MONTEIRO: In relation to your (and Tony's) question about divergence dates, here is what I have found out from the Kristensen (1999) book and also from the web: Oldest fossil Hymenoptera - 225 MY Oldest fossil Diptera - 228 MY Oldest fossil Lepidoptera - 200 MY Since Hymenoptera is thought to have split before the Diptera - Lepidoptera split (see Tree of Life), the split between Diptera and Lepidoptera is at least 228 MY old. Now within the Lepidoptera: There are "only" around 600-700 fossils known, 500 of which preserved in resin (which helps in the correct identification). Oldest fossils of Noctuoidea (from Kristensen's morphological phylogeny this superfamily originated at the same time as the Bombycoidea (where Bombyx belongs), which does not contain any known fossils) - 55MY Oldest fossil of Geometroidea (a lineage that split after the Noctuoidea) - 65MY Oldest fossil of a hesperid butterfly (superfamilies Hesperioidea + Papilionoidea, which originated after the Noctuoidea and Bombycoidea) - 65 MY Oldest fossil of Pyraloidea (a lineage that split before the Noctuoidea) - 65MY So, putting it all together, Bicyclus and Bombyx are at least 65 million years apart... Recommended reading for a "corrosive" view on phylogenetic clocks: Graur, D. and W. Martin. 2004. Reading the entrails of chickens: molecular timescales of evolution and the illusion of precision" Trends in Genet. 20: 80-86. ....

FREERK MOLLEMAN: I am sure you know the paper by Gaunt and Miles 2002 in Mol. Bio. Evol 19 (5) 748-761 and Niklas Wahlbergs website with the most up to date classification of butterflies. ....

KARLENE RAMSDELL: There may be something for the brachyceran flies, Wiegmann, B. M., Yeates, D. K., Thorne, J. L. and Kishino, H. 2003. Time flies, a new molecular time-scale for brachyceran fly evolution without a clock. Syst. Biol. 52: 745-756. ....

MARTIN FEDER: Contact Ward Watt at Stanford ....

ADRIANA BRISCOE I am not aware of any organized reference for lepidopteran divergence times, however, there is a nice book which proposes a large-scale phylogeny for some of the moth and butterfly groups that you are interested in. The book is: Handbuch der Zoologie, Lepidoptera, Moths and Butterflies, Volume 1: Evolution, Systematic and Biogeography edited by Niels P. Kristensen (de Gruyter, 1999). ....

MATHIEU JORON Beltrán M et al. Phylogenetic discordance at the species boundary: comparative gene genealogies among rapidly radiating Heliconius butterflies. Molecular Biology and Evolution 19, 2176-2190 (2002). Brower AVZ. Parallel race formation and the evolution of mimicry in Heliconius butterflies: a phylo-

genetic hypothesis from mitochondrial DNA sequences. Evolution 50, 195-221 (1996). Brower AVZ. Phylogeny of Heliconius butterflies inferred from mitochondrial DNA sequences (Lepidoptera: Nymphalidae). Molecular Phylogenetics and Evolution 3, 159-174 (1994). Brower AVZ & Egan MG. Cladistic analysis of Heliconius butterflies and relatives (Nymphalidae: Heliconiiti): a revised phylogenetic position for Eueides based on sequences from mtDNA and a nuclear gene. Proceedings of the Royal Society of London Series B Biological Sciences 264, 969-977 (1997).

.....

A number of people recommended getting in contact with Andrew Brower at Oregon State University ... which I have yet to do.

.... Patricia Beldade University of California at Irvine Ecology and Evolutionary Biology 321 Steinhaus Hall Irvine, CA 92697-2525 USA Tel:(949) 824 5994 Fax:(949) 824 2141 [hjmuller.bio.uci.edu/~pbeldade/pages/home.htm](http://hjmuller.bio.uci.edu/~pbeldade/pages/home.htm)

...

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## Matrilines answers

Dear Evoldir members,

A couple of weeks ago I posted following query:

"Does anyone know a software able to calculate number of matriline, when microsatellite data of progeny only are available? I work on Hymenoptera, so data are haplo-diploid (females are diploid and males are haploid) and I assume single mating."

I've received a few useful advices, which I'm very grateful for!

Also, I've learnt that others would be interested in this topic too, so here below are summarized the answers I've got:

Dear Monika,

In answer to your query on EvolDir, check out MateSoft, which was

specifically written by my colleague Jes Soe Pedersen and

collaborators with haplodiploid systems in mind:

<http://www.zi.ku.dk/popecol/personal/JSPedersen/-MateSoft.htm> Yours

David Nash

–

Dear Monica

unfortunately I do not have directly a software for you, but your query inspires me to send you as a private reply a pdf file of an old paper in which, given a known number of potential mothers, we used microsatellites to infer the relative shares of maternity among workers (I also add a TREE review on the topic). I hope that it may be of some interest to you. As for your problem I would start by Queller & Goodnight Evolution paper.

Best of luck with your work

Giorgina

Queller, D.C. and Goodnight, K.F. 1989. Estimation of genetic relatedness using allozyme data. *Evolution* 43:258-275.

Goodnight, K.F. and Queller, D.C. 1999. Computer software for performing likelihood tests of pedigree relationship using genetic markers. *Molecular Ecology* 8:1231-1234

Dear Monika,

The program COLONY does what you seek, using ML. It was first described and used in:

Chapman RE, Wang J, Bourke AFG (2003) Genetic analysis of spatial foraging patterns and resource sharing in bumble bee pollinators. *Molecular Ecology* 12, 2801-2808.

Robert

Kinship, mac freeware, enables you to determine such sib-groups.

Then you can use coverage-based methods such as those of Chao or the

ML equivalent of Pollock to estimate how many matrilineal lines there are

that you didn't see [if you want to go that far].

These approaches grew out of social Hymenoptera studies, and will

work better there than for organisms with both sexes diploid.

Yours sincerely, Ross Crozier

Many thanks!!!!!!!!!!!!

Monika

\_\_\_\_\_

Monika Zavodna, PhD student

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Centre for Terrestrial Ecology

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<http://www.nioo.knaw.nl/CTE/index.htm>

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## Micro silverstaining

Other: Dear EvolDir members

I am trying to do microsatellite by silver staining method, but at the moment I have some problems:

I have good bands on agarose gel, but when I load them on polyacrilami de gel and visualize by Silver staining I have not good results (smear, no bands). I tried different dilution.

Thanks in advance for the help.

Daniele

Daniele Porretta Dip. Gen. Mol. Biol. University of Rome La Sapienza Via dei Sardi 70 00185 Roma tel/fax: 0039 06 49917820 e-mail: daniele.porretta@uniroma1.it

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## Micros species

Dear all,

I am trying to show that two ant species are hybridizing. Specimens that are separable into two species by morphology share the same haplotype. Additionally we have microsatellite data of the same three loci of these two species that share some alleles but seem to be clearly separated otherwise (a number of private alleles and differences in allele frequencies).

My question is: Am I allowed to use F-statistics to show that the individuals are separated even though it seems to be very clear that this cannot be a population in



HWE?

Or does anybody know a programme that may be used to assign individuals to either species via a maximum likelihood approach (i.e. that gives me a result like the specimens can be classified as belonging to two separate species with XY probability)?

Thank you for your help!

Heike Feldhaar

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

e-mail: feldhaar@biozentrum.uni-wuerzburg.de phone: 0049- (0)931- 8884315 fax: 0049- (0)931-8884309  
\*\*\*\*\*

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## Micros species answers

Dear all,

thank you very much for the helpful responses to my query -your answers have saved me a lot of time! I will try several computer programmes. The answers boil down to a recommendation of the programmes Structure by J. Pritchard, NewHybrid by Anderson or GENETIX or GeneClass (links below)

Below you will find some the answers I have received with links to the recommended programmes:

Hallo

was Du beschreibst ist natuerlich ein idealer Fall, fuer einen "assignment test". Dafuer gibt es viele verschiedene ausgezeichnete Freeware Programme (Google). Assignment tests werden klassischerweise benutzt, um Individuen Populationen zuzuordnen. Eine Anwendung, bei der Individuen Arten zugeordnet werden ist aber natuerlich im Prinzip dasselbe. Eines ist GENETIX, dazu als Anwendungsbsp. hier ein link; [http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list\\_uids=12873219&dopt=Abstract%22](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=12873219&dopt=Abstract%22)

Good luck

Patrick

...make an assignment test with one of the Freeware programmes you will find on Google....one programme is GENETIX with a sample of how it works under the

link above... (Heikes translation...)

>>>>>>

Use Anderson's NewHybrids software.

<http://ib.berkeley.edu/labs/slatkin/eriq/software/software.htm> Stuart

>>>>>>

I'd try Jonathan Pritchard's structure program. There's a link on his website <http://pritch.bsd.uchicago.edu/>. It's for identifying populations within a species, but I think you could use it to establish the number of groups that you have and to assign individuals to groups by genetics. You can then compare the assignments to the groups you get by morphology. I'm not sure of the minimum number of loci.

Kristie

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Kristie A. Mather Thomson Laboratory 3060 VLSB Department of Integrative Biology University of California Berkeley CA 94720

>>>>>>

Dear Heike,

I have a similar issue with two recently diverged plant species that share nearly all polymorphisms but are extremely different morphologically. If there has been a limited amount of new mutation in the respective lineages, then Fst is a legitimate measure of divergence, and  $-\ln(1-Fst)$  should increase more or less linearly over time. HWE is not a requirement for Fst estimates - in fact Fst and other F statistics basically partition the deviations from HWE and would be zero if all the data represented a single population under HWE.

The most useful tool for assigning individuals to ancestral populations or estimating their admixture is Jonathan Pritchard's STRUCTURE program which uses a Bayesian approach to infer each individual's ancestry from marker data. However, you would want data from far more than three microsatellite loci to do this. Even if the loci are highly polymorphic, a more comprehensive sampling of the genome would be important, especially if hybridization is suspected.

>>>>>

Hi Heike Feldhaar,

You can use STRUCTURE software (Pritchard et al., 2000). It is a Bayesian clustering procedure implemented, designed to identify the K (unknown) populations of origin of the sampled individuals and assign the individuals simultaneously to the populations. The

most likely value of K is assessed by comparing the likelihood of the data for different values of K. However, I am very interesting in any reply that you received,

Kindly

Dr. Miguel Angel González Pérez Departamento de Biología Campus Universitario de Tafira Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain

>>>>

Dear Dr. Feldhaar

I wonder if this is what you want (assignment calculator) <http://www2.biology.ualberta.ca/~jbrzusto/Doh.php> some of these other programs may prove useful as well <http://www2.biology.ualberta.ca/~jbrzusto/> Best wishes, Diana

>>>>> Hallo Heike, ich habe deine Frage in evolDir gelesen. Hast du schon einmal "GeneClass" ausprobiert um assignment tests zu machen? Normalerweise wird das zur populationsdifferenzierung gebraucht, aber ich wuesste nicht, warum man es nicht fuer dein Problem verwenden koennte. man kann die Software unter <http://www.montpellier.inra.fr/URLB/index.html> runterladen. Bitte lasse mich wissen, ob das funktioniert, bzw. was dir andere Leute raten. Viele Gruesse von Susanne.

– Susanne Hauswaldt Doctoral Candidate Department of Biology University of South Carolina Columbia, SC 29208 phone: (803)777-4606 fax: (803)777-4002

— / —

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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## Moller petition

Dear Colleagues,

As some of you are aware, recently there have been accusations of unethical conduct directed at one of our colleagues, Anders Pape Moller. As someone who has collaborated with Dr. Moller for the past five years or so, I wish to assure you that I personally have never had any cause for concern in my dealings with him. I have worked with Anders in the field, in the lab, and have written several papers with him. My observations sug-

gest that his immense productivity has been the product of his extreme dedication to science, especially the natural history of birds, incredible organizational skills (his undergraduate training was in library science), an immense generosity towards students and colleagues, a compulsive need to share his observations through peer reviewed publications, and more than a little natural talent. For those of you not familiar with his work, Moller has written >400 peer reviewed papers since 1982, and these have garnered over 4000 citations from other scientists in the field.

Although it is very difficult to objectively evaluate such cases, it has become increasingly clear that the recent case against Moller has been in large part motivated by a grudge on the part of a former colleague at the University of Copenhagen. This colleague apparently lost his job as a consequence of concerns raised by Moller during his tenure at this institution. It has been suggested that one reason for Moller's accuser's dismissal was a premeditation for unfounded charges of unethical behavior. In addition, it is apparent that the Danish committee that ruled against Moller, and the director of Danish bird banding centre, were not in any way impartial towards the case as they included former students and supporters of Moller's accuser. It is astounding that such committees would include members who so clearly had conflicts of interest with the subject of the investigation. The outcomes of this witch-hunt include significant personal and financial distress and the revocation of Moller's Danish bird banding permit. One consequence of the latter outcome will be the termination of a 34 year, long term study of barn swallows in northern Denmark. I am certain that no matter what your personal feelings might be towards Anders Moller, we can all agree that basic long term datasets are in very short supply and are fundamental for the investigation of basic ecological and conservation principles.

As a consequence of the perceived lack of impartiality in the proceedings to date, we have assembled a petition directed at the Danish Minister of Science, Technology, and Innovation, Members of the Danish Natural Science Research Council, the Head of the Copenhagen Ringing Centre and the Head of the Zoological Museum, Copenhagen, asking them to reconsider their decision to revoke Moller's banding permit, and to conduct an impartial inquiry into the proceedings that led to the current controversy. The petition can be found at: <http://www.ipetitions.com/campaigns/Moller/>. I urge you to sign this petition if you are concerned about fair and impartial treatment of such cases.

Those of you wishing to contact Danish authorities on your own may do so at the addresses given below.

Tim Mousseau

Dr. Timothy A. Mousseau Professor of Biological Sciences University of South Carolina Columbia, SC 29208 USA tel: 803-777-8047 fax: 803-777-4002 mailto:mousseau@sc.edu

Carsten Rahbek Head of the Copenhagen Ringing Centre Universitetsparken 15 DK 2100 KØDenmark crahbek@zmuc.ku.dk

Niels Peder Kristensen Professor and Director of Zoological Museum Universitetsparken 15 DK 2100 KØDenmark. npkristensen@zmuc.ku.dk

Helge Sander Minister for Science, Technology and Innovation Bredgade 43 DK-1260 Copenhagen K vtu@vtu.dk

Tim Mousseau <mousseau@sc.edu>

---

## Moller petition 2

Dear Colleagues,

At the urging of my friend and colleague, Richard Palmer (and a few other folks), I wish to clarify my position concerning the Moller "situation". I am very much aware of the concerns about Moller's potentially unethical behavior (such as those that Rich Palmer has presented). My comments concerning Moller's conduct only apply to the personal interactions I have had with him over the past 5 years or so, and thus do not apply to his professional conduct in general.

My motivations for becoming involved, and organizing a petition to revisit the Moller case (<http://www.ipetitions.com/campaigns/Moller/>), are to support a fair and impartial evaluation of the circumstances surrounding the current case. It is impossible to wade through the plethora of hearsay and innuendo that have been circulating, and I will leave it to those much more qualified than I to pass judgment based on the objective data presented.

Sincerely,

Tim Mousseau

Dr. Timothy A. Mousseau Professor of Biological Sciences University of South Carolina Columbia, SC 29208 USA tel: 803-777-8047 fax: 803-777-4002 mailto:mousseau@sc.edu

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## Oncopeltus specimens

Dear EvolDir readers,

I am looking for information on the obtaining photographs, live individuals, of museum specimen loans of the following species of milkweed bugs of the genus *Oncopeltus* (Heteroptera, Lygaeidae).

*O. longirostris* (Stål 1874) *O. femoralis* (Stål 1874) *O. sandarachatus* (Say 1832) *O. semilimbatus* (Stål 1874) *O. spectabilis* (Van Duzee 1909) *O. zonatus* (Erichson 1848) *O. miles* (Blanchard 1852) *O. cayensis* (Torre-Bueno 1944) *O. guttaloides* (Slater 1964a) *O. sanguinolentus* (Van Duzee 1914) *O. varicolor* (Fabricius 1794) *O. luctuosus* (Stål 1867) *O. pictus* (Van Duzee 1907) *O. bergianus* (Kirkaldy 1909)

My apologies if the answer is obvious – I'm not an entomologist. Our lab is trying to assess the diversity of several traits of interest from the standpoint of comparative developmental genetics. Therefore, I would greatly appreciate any help you can offer.

Many thanks to the EvolDir community.

-Dave Angelini

----- David R. Angelini Indiana University Department of Biology Jordan Hall 142, Box 99 1001 East Third Street Bloomington, IN 47405-3700 USA 812 855-7674 [lab] dangelin@bio.indiana.edu

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## PopGenet Teaching Software

Last year I asked "Can people recommend population genetics software to use in teaching population genetics? In particular, knowing about programs that include options for single and two-locus selection, genetic drift, gene flow, mutation, and inbreeding, or some of these categories, would be useful. If you have used it in class and found it successful, I would like to know that as well."

I received a number of responses and below is given a list of some of the software packages (and the developer) most commonly used in demonstrating the effects

of population genetics factors to students (with their web sites).

Software Package (developer) Website

Populus (Don Alstad) <http://www.cbs.umn.edu/~populus/>

PopG (Joseph Felsenstein) <ftp://evolution.gs.washington.edu/pub/popgen/popg.html>

AlleleA1 (Jon Herron) <http://faculty.washington.edu/~herronjc/SoftwareFolder/software.html> <<http://faculty.washington.edu/~herronjc/SoftwareFolder/software.html>> . EvoTutor (Alan Lemmon) <http://www.evotutor.org/Software.html> PopGen (Jouni Aspi) <http://cc.oulu.fi/~jaspi/popgen/popgen.htm> <<http://cc.oulu.fi/~jaspi/popgen/popgen.htm>> WinPop (Paulo Nuin) <http://life.biology.mcmaster.ca/~winpop3.zip> Virtually all of these packages cover the basic effects of selection, genetic drift, gene flow, and mutation. Populus appears to be the most widely used from the responses I received and this package also covers a number of more advanced topics, such as two-locus selection and selection in different environments. Some people suggested that for more advanced understanding of these factors, it is often useful for students to use spread sheets or programming to generate the effects of particular factors for themselves.

Phil Hedrick (philip.Hedrick@asu.edu)

---

## Pseudogene phylogeny

Dear members,

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?

Thank you,

Deb Triant

Deborah Triant Department of Forestry and Natural Resources Purdue University West Lafayette, IN 47907-2033 (765) 496-6686 [dtriant@fnr.purdue.edu](mailto:dtriant@fnr.purdue.edu)

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## Running micros

Hi Everyone,

I have a large number of microsatellites I need to run. I only have a 377 here with 36 wells, so I am looking for alternatives. I was wondering if anyone has found a good place to send them in 96-well plates? I can do the PCRs here, I just need the reads. If you have the information, please indicate cost, whether or not the size standard is included, and if there is an extra charge for multiplexed samples.

Thanks so much for your help! Amy – Amy Baco-Taylor, PhD Biology Department MS#33, 2-14 Redfield Wood's Hole Oceanographic Institution Wood's Hole, MA 02543

Phone: (508) 289-2331 FAX: (508) 457-2134

[abaco@whoi.edu](mailto:abaco@whoi.edu)

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## Running micros answers

Thanks everyone for your help and suggestions! Below is the original message and the responses:

>Hi Everyone, > >I have a large number of microsatellites I need to run. I only have >a 377 here with 36 wells, so I am looking for alternatives. I was >wondering if anyone has found a good place to send them in 96-well >plates? I can do the PCRs here, I just need the reads. If you have >the information, please indicate cost, whether or not the size >standard is included, and if there is an extra charge for multiplexed >samples. > >Thanks so much for your help! >Amy

Natalia Belfiore <[nmb@berkeley.edu](mailto:nmb@berkeley.edu)>

I recommend buying some 96 toothed membrane combs for the 377 gels. Get a tray with 96 wells that's made

to dip the combs into. You'll have to use the flat short plate (the one without the divet in it) to make your gels. But these membrane combs work INCREDIBLY well and in spite of what they say on the package, can be used up to 7 times each if you're careful with them.

I am not sure where to buy them. Try "The gel company" in San Francisco. You are likely to get others tell you this reply, possibly with more detail. But if you need me to ask folks in my lab where they got the combs, I can do it. We use the ABI 3730 now.

Good luck,

ps. You can also multiplex the runs, even if the PCR themselves are not multiplexed. Get your labeled primers in different colors so that if there's any overlap in size, the different loci are in different colors. The more you separate them spatially, the better, though. You can usually put 4-6 loci on a single gel, though, if you plan carefully. So that's 4 loci X 96 samples per gel. Vastly increase your throughput.

-- Hy,

You might try genoscreen in France <http://genoscreen.chez.tiscali.fr/> Cheers,

Claire

– Claire BILLOT

--- Hello Amy, check out the paper Toonen, R. J. and Hughes, S. 2001. Increased throughput for fragment analysis on an ABI Prism 377 automated sequencer using a membrane comb and STRand software. *Biotechniques* 31: 1320-1324.

Their technique will let you load 100 lanes on a 377. You'll have to order paper combs (I use Catalog # CAJ96) from the gelcompany.com, which cost \$7.50 each. But I think it's definitely worth it (and easier to optimize loci when you're running them yourself). Good luck! Christiana

Christiane Biermann Adjunct Assistant Professor Department of Biology Portland State University Portland, OR 97207-0751, USA Tel. 360-317-6336 [biermann@pdx.edu](mailto:biermann@pdx.edu) <http://faculty.washington.edu/biermann/>

-----  
Hello Amy, I am sure you would prefer the place to be in your own country! But if you are happy to send your samples abroad then there is a service at the University of Dundee in Scotland where you can send your samples in 96-well plates.

<http://www.dnaseq.co.uk/home.html> The only price I can see on the website is for DNA sequencing. If you

only need them to run the samples I am sure it will be much cheaper but you will have to contact them directly to ask about this. Hope this helps, Kind Regards, Lucy

-----  
Hi Amy,

We might be able to help you out with your USA runs. We have an ABI3100 that is not running at full capacity. How many 96 well plates would you anticipate and over what time period would you be able to deliver them? Assuming you run a fair number of plates, we'd probably be able to charge you \$2 per sample.

One thing you might want to consider is that the migration of alleles may be slightly different on a capillary sequencer than on the slab gel - at least that's what we were told by the ABI folks. If you're going to use data from both, you'd probably want to run a set of individuals on both instruments so that you can calibrate allele sizes, if necessary.

Let me know if you're interested.

Mike

----- Michael Sorenson Assistant Professor Department of Biology Boston University 5 Cummington St. Boston, MA 02215

-----  
Dear Amy,

I saw your question on the evoldir, and I think you might want to look into Nevada Genomics (<http://www.ag.unr.edu/genomics/>). I think they charge less than \$200 to run a 96-well plate, which is a decent deal. I have never used them for genotyping, but we send all of our sequencing to them and they do a great job.

Best wishes, Adam

Adam G. Jones Assistant Professor School of Biology Georgia Institute of Technology 310 Ferst Drive Atlanta, GA 30332 Phone: (404) 385-4435 Fax: (404) 385-4440 Lab website: <http://www.biology.gatech.edu/professors/labsites/joneslab/index.html> -----

— / —

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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## Species specific SSRs

Dear EvolDir,

How likely is it to detect divergence in SSR flanking sequence between species within a subgenus, and has anyone had any success designing species specific SSR primers?

Cheers.

John McMullan <mailto:jjm13@le.ac.uk> Department of Biology University of Leicester UK

“McMullan, J.J.” <jjm13@leicester.ac.uk>

---

## Squamate sex markers

Hi Evolution folks, I would like to determine the sex of juvenile and embryonic Anolis lizards using a PCR based method. This is commonly done in mammals using genes linked to the y-chromosome (such as SRY). I believe that it has also been done in birds. Does anyone know of genes found specifically on the y-chromosome of any squamates (anoles are in fact XX:XY). Likely candidates include spermiogenesis factors and related genes but I cannot find any description of these in the literature or Genbank.

Any assistance and/or guidance would be appreciated.

Thanks a lot. Thom Sanger

tsanger@biology2.wustl.edu Washington University in St. Louis

---

## Terrapin colour vision

Dear all, Has anyone any knowledge of the colour perception of the terrapin. We have been conducting learning trials using coloured containers and are curious to know which colours are discriminable in these species. Alternatively, some sources of literature would help - we have exhausted the possibilities of finding it in previous research! Many thanks, Roger

Roger Davies Department of Biology University College Chester Parkgate Road CHESTER CH1 4BJ  
rdavies@chester.ac.uk roger-davies@lineone.net

Roger Davies <rdavies@chester.ac.uk>

---

## Thanks Mike Whitlock

The many Pacific Northwest evolutionary biologists who attended this weekend's EVO-WIBO conference want everyone to know how much we appreciate all Mike Whitlock's work towards making it happen.

There'll be another one in two years!

Rosie Redfield <redfield@interchange.ubc.ca>

---

## Weevil samples

Dear members of EvolDir, My name is Marcela Rodriguez, PhD student at Department of Ecology, Genetics and Evolution, University of Buenos Aires (Argentina), under the supervision of Dra. Viviana Confaloneri (University of Buenos Aires) and Dra. Analía Lanteri (University of La Plata). The aim of my project is to study the phenomenon of geographic parthenogenesis in weevils of the Naupactini Tribe (*Asynonychus cervinus*, *Naupactus leucoloma* and *Naupactus xanthographus*). I am writing hoping that you may be able to help me to obtain samples. If this would not be possible, could you provide me with any contacts that may be able to help me? Any help you could provide me with would be greatly appreciated. Thanks in advance for your help

Best regards,

Marcela

Lic. Marcela Silvina Rodriguez Laboratorio de Genética Departamento de Ecología, Genética y Evolución Intendente Güiraldes y Costanera Pabellón II - Ciudad Universitaria (1428) Capital Federal Buenos Aires República Argentina

---

## mtDNA extraction answers

Reposted at the request of Douda Benasson

Subject: Other: mtDNA extractions/kits-answers  
Date: Mon, 9 Jun 2003 02:19:51 -0400 (EDT)

I recently posted a query regarding isolation of 'pure' mtDNA from tissue, blood, etc., for use in PCR-based methods. I am grateful for all your responses- a big thank you. It is a pleasure to correspond with members of this group. The topic generated a lot of interest, and I have included a summary of the responses below. I apologise for any cross-postings. Thank you! Gabriela Ibaruchi

Department of Biology, Queen's University Kingston,  
Ontario, Canada

=====

Responses follow:

I used to use an old sucrose gradient or "pad" method (swinging bucket ultracentrifuge required) that produced very clean mtDNA preps for bird tissues (blood was not really doable). It required relatively fresh tissues, or ones put into a sucrose/mannitol buffer, then frozen. The mitochondria were isolated and could be run through 2-3 times to really clean it up, followed by DNA isolation.

Robert C. Fleischer

-----

We used the Wizard miniprep kits (Promega). Other such kits (I believe Qiagen also makes them) work well too. Cesium chloride is a huge pain to work with; although this way is more expensive, it is not nearly so cumbersome or toxic. MF Smith (UC Berkeley) was picking up a nuclear duplication of her mitochondrial gene, and she published a paper on that. I believe that paper included a more detailed description of her strategy (which is what we used) for excluding nuclear DNA, so that she could retrieve her true mtDNA gene copies without the nuclear copy.

Tina Hambuch (protocol by Peg Smith)

-----

WAKO Chemicals has a kit that uses a modified dif-

ferential centrifugation procedure to obtain "enriched" mtDNA. What you get is not as pure as by using CsCl, but it is a lot faster. I have had rare cases of "presumed" pseudogenes when working with WAKO extractions, though.

Francesco Nardi

-----

Reference below includes a quick simple method. You need a Beckman TL-100 ultracentrifuge.

S. M. Carr and O. M. Griffith (1987). Rapid isolation of animal mitochondrial DNA in a small fixed-angle rotor at ultrahigh speed. "Biochemical Genetics," 25:385-390.

Any of the kit-based methods will let in nuclear contamination, the above method gives good separation of mt and nuc bands. We're using it to purify reference individuals for mtDNA clones. Never thought I'd be doing CsCl gradient stuff again.

Steve Carr -----

I think you will have a best chance to amplify the mtDNA in two long PCR fragments. You could use primers in very conservative regions like 12S and 16S and obtain your mtDNA.

Gustavo Ybazeta

-----

I noticed that numt are more common in blood tissues. I had that problem with some of my blood samples (from yellow warblers) but it never happened with my quill samples. If you can't find a protocol that guarantees that the samples are free of nuclear DNA, I would suggest you use quills and extract the DNA with the SIGMA or QIAGEN extraction kits. When I did not have any quill duplicates of my blood samples, I used a different set of primers that amplified a larger fragment that contained the sequence I was interested in.

Marylene Boulet

-----

I have used a sucrose gradient centrifugation in the past to isolate whole mitochondria, from which you can obtain a "mtDNA enriched" extract. This is often done as a preliminary step before a CsCl protocol, but you can stop after the sucrose gradient and have a reasonably good mtDNA prep. The following references about numts may be helpful - there are some other approaches besides purifying mtDNA.

Sorenson, M.D. & T.W. Quinn. 1998. Numts: A challenge for avian systematics and population biology. *The Auk* 115: 214-221.

Sorenson, M.D. & R.C. Fleischer. 1996. Multiple independent transpositions of mitochondrial DNA control region sequences to the nucleus. *Proceedings of the National Academy of Science USA* 93:15239-15243.

Michael Sorenson

-----

Back before PCR was well-established, a number of fish genetics labs used a technique developed by Bob Chapman and Denny Powers to carry out mitochondrially-enriched extractions. It involved gently homogenizing several grams of liver tissue in a TEKS buffer (TE with KCl and sucrose), going through a series of low- and high-speed centrifugations to remove nuclei and pel-

let mitochondria, then lysing mitochondrial membranes with a nonionic detergent (NonIDet). The resultant DNA wasn't pure mitochondrial DNA, but it was highly enriched for mtDNA. Blood should work very well, and potentially much better.

The reference for this method is:

Chapman RW, Powers DA (1984) A method for the rapid isolation of

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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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## PostDocs

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### AllanWilsonCentre EvolRates

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Postdoctoral Fellow - Rates of Evolution A143-04L The Allan Wilson Centre for Molecular Ecology & Evolution, Assistant Vice-Chancellor (Research) -----

You will contribute to research funded by the New Zealand government Centres of Research Excellence initiative, in the project titled "Rates and Modes of Evolution".

Location Albany Term of Contract Fixed Term of 1 Years Closing Date 30 April Position Overview The

Allan Wilson Centre for Molecular Ecology and Evolution, hosted by Massey University, seeks to appoint a postdoctoral fellow with strong analytical techniques, at their Albany campus, Auckland. You will undertake work in a programme titled "Rates and Modes of Evolution", researching rates of evolution in mitochondrial and nuclear gene sequences of Adelie penguins from the Antarctic.

For more details of the project contact David Lambert, Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Private Bag 102 904, Auckland, New Zealand. Email: [D.M.Lambert@massey.ac.nz](mailto:D.M.Lambert@massey.ac.nz).

Job Description Purpose Statement This fellowship will see a PhD graduate participate in evolutionary research

in the Centres of Research-funded Allan Wilson Centre for Molecular Ecology and Evolution. Responsible To Through Professor David Lambert to the Directors of the Allan Wilson Centre. Key Accountability Areas You will be required to: - research rates of evolution in mitochondrial and nuclear gene sequences of Adelie penguins from the Antarctic. - Develop a range of methods for the estimation of evolution using serially preserved DNA sequences obtained from Adele penguins. - undertake other duties as specified by the leader of the research programme - maintain accurate and tidy records of laboratory work - participate fully in the academic activities of the Centre and the Institute of Molecular BioSciences - provide quarterly research reports to the project leader summarising research progress and planned future research - diligently and faithfully serve the Centre and the University and use your best endeavours to promote and protect the interests of the Centre and the University - maintain confidentiality both during and after the appointment as a Fellow Person Specification Qualifications A PhD in analytical biology and/or molecular evolution. Experience Attributes and Skills - Computational and mathematical skills - experimental creativity - ability to write scientific papers - initiative and enthusiasm - commitment to quality improvement, upskilling and personal development - ability to organise and maintain quality records - integrity and confidentiality - time-management skills - ability to work as part of a team

Comments to [RWS.Webmaster@massey.ac.nz](mailto:RWS.Webmaster@massey.ac.nz) Massey University, New Zealand Copyright © 2000-2003 Massey University

— Prof David Lambert Phone: +64-9-443 9700 Allan Wilson Centre for extension 41110 Molecular Ecology and Evolution Fax: +64-9-441 8142 Institute of Molecular Email: [D.M.Lambert@massey.ac.nz](mailto:D.M.Lambert@massey.ac.nz) BioSciences Te Kura Putaiao Koiara-a-Ngota [HTTP://www.massey.ac.nz/~dmlamber/](http://www.massey.ac.nz/~dmlamber/) Massey University Private Bag 102 904 North Shore Mail Centre Auckland New Zealand

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## AllanWilsonCentre EvolRates 2

Reference Number: A143-04L Position Title: Postdoctoral Fellow - Rates of Evolution Department: The Allan Wilson Centre for Molecular Ecology & Evolution Location: Albany Closing Date: 30/04/2004

View the details of this job by following this link:

<http://jobsv.massey.ac.nz/positiondetail.asp?P=-3D2640>

[D.M.Lambert@massey.ac.nz](mailto:D.M.Lambert@massey.ac.nz)

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## DukeU MolEvolCompGenomics

Post-doctoral Fellowship in Molecular Evolution and Comparative Genomics

The Duke Center for Evolutionary and Ecological Genomics is pleased to announce the continuation of its Post-doctoral Fellowships in Molecular Evolution and Comparative Genomics. This Fellowship provides an annual salary of \$30,000 plus benefits and \$11,000 in research funds per year for a two year period. The program allows the Fellow to pursue independent research in the laboratory of a sponsoring faculty member of the Department of Biology or the Center for Evolutionary and Ecological Genomics.

We invite innovative proposals from scientists of any nationality to carry out independent research at Duke University for a two year appointment beginning in the Fall of 2004. We are particularly interested in proposals that address mechanisms of molecular evolution, comparative genomics, and the evolution of development. Although proposals focused on exclusively on building phylogenies will not be considered, the application of phylogenetic approaches to analyzing the evolution of genes and genomes is certainly appropriate.

Please send curriculum vitae, a three-page research proposal, a one-page summary of past research, and two letters of recommendation to: Molecular Evolution Search Committee, c/o Greg Wray, Department of Biology, Box 90338, Duke University, Durham, NC 27708-0338, USA. Applications received by 1 June 2004 will be guaranteed full consideration. Duke University is an Equal Opportunity/Affirmative Action Employer.

For more information about the Biology Department at Duke, visit [www.biology.duke.edu](http://www.biology.duke.edu)

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## NewportOR SalmonGenetics

POSITION ADVERTISEMENT Coastal Oregon Marine Experiment Station Post-Doctoral Research Associate

The Coastal Oregon Marine Experiment Station at the Hatfield Marine Science Center in Newport, OR is seeking applicants for a full-time position as a Post-Doctoral Research Associate for the Marine Fisheries Genetics Laboratory (<http://www.oregonstate.edu/dept/comes/genetics/>). Three years funding is available for coho salmon research in pedigree assignment for hatchery/wild and other fitness comparisons. Project involves data from a long-term study with multiple collaborators and addresses various aspects of the coho salmon life history. The duties and responsibilities of this position are to determine maximum statistical power gained from alternate microsatellite loci and apply these to achieve family allocation for samples from the experiment and to analyze, interpret and publish findings in peer review literature.

OSU is one of only ten American universities to hold the Land Grant, Sea Grant, and Space Grant designation and is a Carnegie Doctoral/Research-Extensive university. OSU is located in Corvallis, a community of 50,000 people situated in the Willamette Valley between Portland and Eugene. Ocean beaches, lakes, rivers, forests, high desert, and the rugged Cascade and Coast Ranges are all within a 100-mile drive of Corvallis. The Coastal Oregon Marine Experiment Station is located at the Hatfield Marine Science Center in Newport, which is 55 miles west of Corvallis. Approximately 15,600 undergraduate and 3,400 graduate students are enrolled at OSU, including 2,600 U.S. students of color and 1,100 international students. The university has an institution-wide commitment to diversity and multiculturalism, and provides a welcoming atmosphere with unique professional opportunities for leaders who are women and people of color. All are encouraged to apply.

Salary: \$34,000-\$36,000 annually, commensurate with qualifications and experience.

Required qualifications: 1) a PhD in genetics, ecology, evolution or related field with emphasis in statistics, 2) molecular genetics experience in polymerase chain reaction, microsatellite characterization, 3) population genetics analysis, 4) bioinformatics, 5) demonstrated publication record in peer review journals, 6) demonstrated effective research in a multi-user molecular genetics lab and 7) effective presentation with professional demeanor. Preferred qualifications include a demonstrable commitment to promoting and enhancing diversity.

To apply: please email the following materials to Eunice.Jenson@oregonstate.edu by May 8, 2004 to ensure

full consideration:

A cover letter that includes your experience, qualifications and research and career interests,

A curriculum vitae that includes names, addresses and telephone numbers of at least three references.

Oregon State University is an AA/EO Employer and has a policy of being responsive to the needs of dual-career couples

Michael A. Banks Assistant Professor, Marine Fisheries Genetics Coastal Oregon Marine Experiment Station Hatfield Marine Science Center, Oregon State University 2030 SE Marine Science drive Phone:(541) 867 0420 Newport OR 97365-5229 Fax:(541) 867 0138 <http://marineresearch.oregonstate.edu/genetics/index.htm>

Michael.Banks@oregonstate.edu

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## Paris Human Populations

Inference of demographic history of human populations by means of multi-locus analyses of genetic polymorphisms

Offer description: For those many human populations which origin or history is unknown, the inference of demographic history is achievable by means of population genetics methods. Such indirect approaches rely on the proper modelling of complex phenomena, like demography, mutation and recombination processes. However, most of the methods developed so far do not account for the distribution of polymorphism at several loci: instead, one generally assumes that genetic polymorphism is identically and independently distributed across loci. Yet, the distribution of genetic variation may bring more information than the average variation across loci. Hence, multi-locus approaches may be valuable to estimate past demographic transitions (e.g., changes in the mode and strength of dispersal, changes in population size or social structure). Owing to recent theoretical developments, it is now possible to derive coalescent models that account for the association of genes at distinct loci. Therefore, this project aims at developing new methods to infer demographic history of human populations, from multi-locus data. These methods will then be applied to the data from nomadic populations in Central Asia, which are studied by the research team. The goal is to test different demographic scenarios: Did Eastern and Western populations meet recently and then became sedentary, or do they share



a more ancient history with successive colonisations?

Candidate profile:

The successful should have a PhD or equivalent in population genetics, as well as a strong background in mathematical modelling. In particular, a good expertise in coalescent theory will be essential for this project.

Duration: 1 year Salary : 2150 (brut) per month

Laboratory: UMR 5145 Éco-Anthropologie Equipe « génétique des populations humaines » Musée de l'Homme 17 pl du Trocadéro 75116 Paris - France

DEADLINE : 10th MAY 2004

Contact: Evelyne Heyer 33 (0) 1 44 05 72 52  
 heyer@mnhn.fr [http://www.sg.cnrs.fr/drhchercheurs/post\\_doc\\_2004/](http://www.sg.cnrs.fr/drhchercheurs/post_doc_2004/) Post-doc number SDV 29

Evelyne Heyer <heyer@mnhn.fr>

work in a predominantly French-speaking environment (proficiency in French is not an obligation).

Compensation and conditions: Contract period : one year (renewable). Salary range: NSERC (Visiting Fellowships in Canadian Government Laboratories). Workplace: Natural Resources Canada, Canadian Forest Service-Quebec (Quebec City). Application Deadline: May 15, 2004.

Please send a resume, a description of research experience, and the names of three references to: Dr Nathalie Isabel Natural Resources Canada, Canadian Forest Service-Quebec 1055, rue du P.E.P.S. Sainte-Foy (QC) Canada, G1V 4C7 Email: nisabel@cfl.forestry.ca

labogenetique@hotmail.com

–

Nathalie ESPUNO <espuno@cefe.cnrs-mop.fr>

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## QuebecCity MolEcology

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## QuebecCity MolecularEcology

—Message d'origine— De :  
 evoldir@evol.biology.mcmaster.ca  
 [mailto:evoldir@evol.biology.mcmaster.ca] Envoyé  
 : vendredi 16 avril 2004 07:13 À : Maryse GAUTIER  
 Objet : Postdoc fellowship in Molecular Ecology  
 (Quebec City)

Description: Monitoring of gene flow between exotic species and surrounding natural populations of both genera *Larix* and *Populus*. Development of diagnostic species-specific markers from DNA sequences. Follow-up of the experimental designs on the field and into greenhouses. Evaluation, mapping and modelling of the degree of hybridization (spatial autocorrelation method and regression model based on biophysical characteristics). Supervision of students and technical staff in related areas. Redaction and presentation of scientific papers and reports in referee journals and scientific conferences.

Qualifications: Doctoral degree (Ph. D.) in population genetics, molecular ecology, plant biology, molecular biology or related areas. Experience required in molecular biology. Experience in DNA sequence analysis and genotyping. Background in statistics and modelling. Very good verbal and written communication skills. Demonstrated aptitudes for teamwork. Ability to work independently and to supervise. Ability to

Description: Monitoring of gene flow between exotic species and surrounding natural populations of both genera *Larix* and *Populus*. Development of diagnostic species-specific markers from DNA sequences. Follow-up of the experimental designs on the field and into greenhouses. Evaluation, mapping and modelling of the degree of hybridization (spatial autocorrelation method and regression model based on biophysical characteristics). Supervision of students and technical staff in related areas. Redaction and presentation of scientific papers and reports in referee journals and scientific conferences.

Qualifications: Doctoral degree (Ph. D.) in population genetics, molecular ecology, plant biology, molecular biology or related areas. Experience required in molecular biology. Experience in DNA sequence analysis and genotyping. Background in statistics and modelling. Very good verbal and written communication skills. Demonstrated aptitudes for teamwork. Ability to work independently and to supervise. Ability to work in a predominantly French-speaking environment (proficiency in French is not an obligation).

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line: May 15, 2004.

Please send a resume, a description of research experience, and the names of three references to: Dr Nathalie Isabel Natural Resources Canada, Canadian Forest Service-Quebec 1055, rue du P.E.P.S. Sainte-Foy (QC) Canada, G1V 4C7 Email: nisabel@cfl.forestry.ca labogenetique@hotmail.com

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### Rothamsted PopGenomics

A post-Doctoral position is available to work on population genomics of host adaptation in *Aphidius ervi*, a parasitic wasp attacking various species of aphids. The project will test for selection-driven differentiation within the *A. ervi* complex, and identify genomic regions and candidate genes involved in host adaptation using population genomic and molecular approaches combined with selection experiments.

This position will require an independent and motivated individual with a published record in molecular biology and/or population genetics. Some programming or statistical modelling skills are desirable, previous experience with aphids and parasitoids is desirable but not essential.

Funding is available for three years with a salary range normally between £21,700 and £25,200 per annum.

Closing date: 28 May 2004.

Apply by application form only, available with further particulars from the web <http://www.rothamsted.bbsrc.ac.uk/corporate/vacancies/-tvacancies.html> or from the HR Group, Rothamsted Research, Harpenden, Herts, AL5 2JQ. Please call +44 1582 763133 Ext 2778 and quote vacancy reference 761.

Rothamsted Research is an equal opportunities employer.

Enquiries about the project should be directed to Dr. Igor Emelianov at [igor.emelianov@bbsrc.ac.uk](mailto:igor.emelianov@bbsrc.ac.uk).

“igor emelianov (RRes-Roth)”  
<[igor.emelianov@bbsrc.ac.uk](mailto:igor.emelianov@bbsrc.ac.uk)>

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### UBritishColumbia MolEvol

Postdoctoral Research Associate in molecular and genomic evolution

A postdoctoral research position is available in the lab of Dr. Keith Adams at the University of British Columbia, starting late fall or winter 2004/2005. Research will focus on the evolution, expression, and silencing of genes duplicated by polyploidy in cotton, as part of an NSERC funded research program. See my web page at <http://www.ubcbotanicalgarden.org/research/adamslab.php> for more information. Inquiries about the research area are welcome ([kladams@iastate.edu](mailto:kladams@iastate.edu)).

Candidates should have a strong research background in evolutionary biology and experience with molecular techniques. Applicants should send a curriculum vita, a description of research interests, and names and contact information for 3 references by email to Keith Adams ([kladams@iastate.edu](mailto:kladams@iastate.edu)).

Keith Adams Assistant Professor Botanical Garden and Centre for Plant Research University of British Columbia phone: 515-294-7098 fax: 515-294-1337

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### UCIrvine Butterflies

The Department of Ecology and Evolutionary Biology in the School of Biological Sciences at the University of California, Irvine seeks one Postdoctoral Scholar to join an NSF-funded international research team focusing on the physiological, genetic and developmental basis of eye pattern variation in butterflies. Butterflies have undergone a rapid and extensive radiation in eye patterns (See Briscoe et al. 2003, JCN 458: 334-349). The eye pattern variations are adaptations that reflect the diversity of butterfly host plant usage and wing color evolution. The successful candidate will have opportunities to engage in physiological (electroretinogram recordings) and genomic technologies (candidate gene approaches and mRNA and protein in situ expression data) to study the developmental and genetic basis of this extraordinary evolutionary radiation. For example, the successful candidate will have an opportunity

to pursue this using a combination of lab and computational work to develop an EST library of eye primordia and also to participate in the Bioinformatics Training Program at UCI.

The project start date is June 15, 2004.

Postdoctoral positions start at a salary of \$31,044 per annum, plus benefits. The successful candidate must have research experience in molecular biology (e.g. PCR, cloning, sequencing), neuroanatomical, and/or physiological techniques (electroretinograms, microspectrophotometry). Excellent oral and verbal communication skills are also required.

To apply, send a letter of application, curriculum vitae, two reprints/preprints and the names and e-mail and postal addresses of three references by May 15, 2004 to the address listed below.

Applications due by: 05/15/04

Contact information:

Dr. Adriana D. Briscoe Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 e-mail: abriscoe@uci.edu web site: <http://ecoevo.bio.uci.edu/Faculty/Briscoe/Briscoe.html>

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

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## UEdinburgh EvolGenomics

Postdoctoral Research Fellow in Evolutionary Genomics

University of Edinburgh, School of Biological Sciences

Salary: UK pounds 18,265 - 27,339 pa

Duration: to 31st July 2006

To apply: See <https://www.jobs.ed.ac.uk/jobs/-index.cfm?action=jobdet&jobid=3001606>

A postdoctoral post is available in a Wellcome Trust Functional Genomics Development Initiative project in the laboratories of Dr. Peter Keightley and Prof. Brian Charlesworth to study molecular evolutionary processes in *Drosophila*. The start date is negotiable.

How many mutations occur in the genome each gen-

eration? What are the molecular properties of these mutations? What fraction of them are deleterious, and do most deleterious mutations occur in coding or non-coding DNA? These issues are important for several key questions in evolutionary biology, such as the evolution of sexual reproduction and recombination, the maintenance of variation, and the pattern of variation in the genome. However, evaluating the role of deleterious mutations requires knowledge of parameters that are extremely difficult to measure, and the role of deleterious mutations is currently unresolved. Our project is to develop an integrated approach that compares the genomes of related species, and directly estimates genome-wide mutation rates that will enable us to tackle these questions. Our plan of research is as follows.

- We shall develop approaches to estimate the level of functional constraints on noncoding DNA sequences by comparing rates of evolution in noncoding DNA with rates of evolution in adjacent genes.

- We shall apply these methods to new sequence data on the related *Drosophila* species generated in our own laboratory - *D. pseudoobscura* and *D. miranda* - along with publicly available data from genome sequence projects of *D. simulans*, *D. yakuba* and *D. melanogaster*.

- We shall develop a new approach for obtaining direct estimates of the nucleotide mutation rate, based on Denaturing High Pressure Liquid Chromatography (DHPLC) technology for detecting rare sequence differences. We shall estimate the genome-wide mutation rate in inbred lines of *Drosophila* that have undergone c.200 generations of random mutation accumulation.

Main tasks

- Develop methods and computer programs for estimating the level of functional constraints in noncoding DNA.

- Apply the methods to analyse genome sequence data on homologous regions of *Drosophila* species.

- Work with a laboratory-based postdoctoral scientist as a part of a team to estimate the per nucleotide mutation rate in *Drosophila* by DHPLC (optional).

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Dr Peter Keightley University of Edinburgh School of Biological Sciences Ashworth Laboratories West Mains Road Edinburgh EH9 3JT UK

<http://homepages.ed.ac.uk/eang33/>

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## UManchester 2 GeneticsShape

Two postdoctoral positions are available in the lab of Chris Klingenberg, School of Biological Sciences, University of Manchester. One is part of a project for fine mapping QTLs affecting the craniofacial shape in mice, and the other one is part of a project investigating the genetics of wing shape in *Drosophila*. Both projects will combine genetic approaches with current methods of geometric morphometrics.

When applying, please make sure to indicate clearly for which of the two positions you are applying. It is also possible to be considered for both positions.

The following ads will appear in this week's issue of Nature:

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<http://www.man.ac.uk/news/vacancies/-research.html#385>

THE UNIVERSITY OF MANCHESTER  
SCHOOL OF BIOLOGICAL SCIENCES

Postdoctoral Research Associate Genetics of mouse craniofacial shape We are looking to appoint a Post doctoral Research Associate as part of a project funded by a Wellcome Trust project grant for three years. You will investigate the genetic basis of shape variation in the mouse skull and mandible. Shape will be characterised in three dimensions by current methods of geometric morphometrics. Extensive analyses of QTL effects are planned, and the data on the mouse and human genome will be used systematically to interpret the findings. You should have a strong interest in genetics and quantitative analysis and will possess a PhD degree in a relevant biological discipline. Quantitative and computing skills are essential as is the ability to work both independently and collaboratively as part of a research team. You will have good interpersonal and communication skills and preferably experience in quantitative genetics, genomics, morphometrics or multivariate statistics and data mining. The starting salary will be £26,270 per annum. The appointment is for a period of one year in the first instance and, upon successful completion of this probationary period, is available for a further two years. Informal enquiries can be addressed to Dr Chris Klingenberg, Tel: 0161 275 3899, E-mail: [cpk@man.ac.uk](mailto:cpk@man.ac.uk).

The closing date for applications is the 30 April 2004. Application forms and further particulars are available at <http://www.man.ac.uk/news/vacancies> or from the Office of the Director of Personnel, The University of Manchester, Oxford Road, Manchester, M13 9PL. Tel: ++44 (0) 161 275 2028; fax ++44 (0) 161 275 2471; Minicom (for the hearing impaired): ++44 (0) 161 275 7889; email: [personnel@man.ac.uk](mailto:personnel@man.ac.uk)

As an Equal Opportunities employer, The University of Manchester welcomes applications from suitably qualified people from all sections of the community regardless of race, religion, gender or disability.

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<http://www.man.ac.uk/news/vacancies/-research.html#386>

THE UNIVERSITY OF MANCHESTER  
SCHOOL OF BIOLOGICAL SCIENCES

Postdoctoral Research Associate: Genetics of *Drosophila* wing shape This 3-year post (BBSRC funded), will investigate the developmental and genetic basis of wing shape variation in *Drosophila melanogaster*. The project will use the *DrosDel* deficiency stock collection to carry out a large-scale screen for chromosome regions with defects on wing shape and its variability, and their evolutionary role will be assessed with fly lines from populations of different geographical origins. Wing shape will be quantified with state of the art methods of geometric morphometrics. You should have a strong interest in *Drosophila* genetics and quantitative analysis and possess a PhD degree in a relevant biological discipline. Quantitative and computing skills are essential as is the ability to work both independently and collaboratively as part of a research team. You will have good interpersonal and communication skills and preferably experience in *Drosophila* genetics, quantitative genetics, morphometrics or multivariate statistics. The starting salary will be £20,311 per annum. The appointment is for a period of one year in the first instance and, upon successful completion of this probationary period, is available for a further two years. Informal enquiries can be addressed to Dr Chris Klingenberg, Tel: 0161 275 3899, E-mail: [cpk@man.ac.uk](mailto:cpk@man.ac.uk).

The closing date for applications is the 30 April 2004. Application forms and further particulars are available at <http://www.man.ac.uk/news/vacancies> or from the Office of the Director of Personnel, The University of Manchester, Oxford Road, Manchester, M13 9PL. Tel: ++44 (0) 161 275 2028; fax ++44 (0) 161 275 2471; Minicom (for the hearing impaired): ++44 (0) 161 275 7889; email: [personnel@man.ac.uk](mailto:personnel@man.ac.uk)



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>

## UMichigan EvolGenetics

POSTDOCTORAL POSITION IN EVOLUTIONARY GENETICS at the University of Michigan with Lacey Knowles

I am looking for a person with a strong background in phylogenetics and/or population genetics. Research opportunities include the collection and analysis of DNA sequence, AFLP, and SNP variation to test different models of speciation.

Support is available for two years. Applications or inquiries should be emailed to Lacey Knowles ([knowlesl@umich.edu](mailto:knowlesl@umich.edu)). Send a full CV that includes educational background, publications and a statement of research interests. The position can start in the summer or fall 2004.

– L. Lacey Knowles Assistant Professor and Curator of Insects Department of Ecology and Evolutionary Biology 1109 Geddes Ave. Museum of Zoology University of Michigan Ann Arbor, MI 48109-1079 (734)763-5603

## UReading PlantEvol

The University of Reading School of Plant Sciences

Post-doc. Salary Scale, £18,893 to £28,279 p.a.

A three-year position funded as part of a Leverhulme Trust Academic Network to support studies of the evolution of the Cape flora of South Africa. The network comprises 20 scientists working in 11 institutions. The research network's aim is to use multiple phylogenies reconstructed for large genera to determine the mode and tempo of evolution in this biome. The successful applicant will have a network coordination role, and undertake biogeographical and temporal interpretation of these multiple phylogenies. You will be an employee of The University of Reading, working with Dr Julie

Hawkins in the School of Plant Sciences. There is also the possibility of working for some time at the Institute of Systematic Botany, University of Zurich with Professor Peter Linder or with other network members in Cape Town. You may be given an allowance to cover secondment and living costs in Zurich and Cape Town.

Informal enquiries to Dr Julie Hawkins ([j.a.Hawkins@reading.ac.uk](mailto:j.a.Hawkins@reading.ac.uk) or 0118 378 6546).

Application forms are available from the Personnel Office, The University of Reading, Whiteknights, PO Box 217, Reading, RG6 6AH. Telephone (0118) 378 6771 (answerphone). E-mail: [Personnel@reading.ac.uk](mailto:Personnel@reading.ac.uk) giving name and full address. Application forms are also available in Word/RTF format from [www.reading.ac.uk/Jobs](http://www.reading.ac.uk/Jobs) Closing date for applications 23 April 2004. It is anticipated interviews will take place on Friday 30 April 2004. Please quote reference number R0414.

Julie Hawkins <[j.a.hawkins@reading.ac.uk](mailto:j.a.hawkins@reading.ac.uk)>

## USDA FargoND PopGenetics

The Plant Science Unit of the USDA Agricultural Research Service in Fargo ND is interested in hiring a post-doctoral research associate to study the population genetics and bio-geography of Canada thistle. We are offering this position as GS11 starting salary (44,136/yr with government benefits). Some additional benefits of the Fargo location are an exceptionally low crime rate, good schools, good health care, and low cost of living (which is compounded by the high government post-doc pay). A cDNA library and SST library are currently being constructed and will be available for use in this project. If you are a US citizen or a citizen from one of the allied countries (see below), and have expertise in population genetics, we would encourage you to send a CV and letter of interest to Dr. Mike Foley at [foley@m.fargo.ars.usda.gov](mailto:foley@m.fargo.ars.usda.gov)

Allied countries Argentina, Australia, Bahamas, Belgium, Bolivia, Brazil, Canada, Chile, Colombia, Costa Rica, Cuba (as a signatory of the Rio Treaty in 1947), Czech Republic, Denmark, Dominican Republic, Ecuador, El Salvador, France, Germany, Greece, Guatemala, Haiti, Honduras, Hungary, Iceland, Italy, Japan, Korea (Republic of), Luxembourg, Mexico, Netherlands, New Zealand, Nicaragua, Norway,



Panama, Paraguay, Peru, Philippines, Poland, Portugal, Spain, Thailand, Trinidad and Tobago, Turkey, United Kingdom, Uruguay, and Venezuela

David Horvath <HORVATHD@fargo.ars.usda.gov>

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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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### LyonMarseille ComparativeGenomics

Comparative genomics of vertebrates: concepts and bioinformatic tools

Organizers: Laurent Duret (UMR CNRS 5558, Université Lyon 1, Lyon), Pierre Pontarotti (Laboratoire de Phylogénomique, Université d'Aix-Marseille, Marseille)

Phase I - Critical assessment May 27-28, 2004 & La Londe Les Maures (Toulon)

Aims This workshop has two main goals. The first one is to give an overview on genome projects and on re-

cent advancements in the understanding of vertebrate genome organization and evolution. The second one is to give an introduction to the concepts (molecular evolution, population genetics) and methods (bioinformatics) of comparative sequence analysis that have been developed to identify functional features within genomes (not only protein-genes but also untranslated RNAs and regulatory elements) or to analyze changes of gene function (expression pattern, interaction networks, etc.).

Audience Researchers, engineers, post-docs and PhD students. Talks will be given in English and French.

Maximum number of participants : 80

Programme Main topics: Vertebrates genome projects. Genome organization and evolution. Gene and genome

duplications. Phylogeny of vertebrates. Evolution of gene function (comparative analysis of gene expression patterns, of interaction networks). Analysis of regulatory regions, of untranslated RNA genes; Homology searches (orthologues, paralogues). Alignment of large genomic sequences. Tools for molecular phylogeny; Analysis of substitutions and polymorphism to detect functional regions (detection of negative or positive selective pressures).

Programme:

Wednesday 26 May

16h-19h Registration

Thursday 27 May

9h 9h10 Introduction 9h10 10h E. Douzery: evolution of vertebrates 10h 10h50 H Roest-Crolius : comparative genomics in vertebrates 10h50 11h20 break 11h20 12h10 T. Hubbard: tools for genome annotation and comparative genomics 12h10 13h40 lunch 13h40 14h30 P. Pontarotti: using amphioxus for the comparative genomics of vertebrates 14h30 15h20 M. Lynch : gene duplication and evolution of gene function 15h20 15h50 break 15h50 16h40 E. Sonnhammer: similarity search; identification of orthologs/paralogs 16h40 17h30 M. Gouy: methods for molecular phylogeny 17h30 18h break 18h 19h open discussion

Friday 28 May

9h 9h50 J. Imbert: analysis of regulatory elements 9h50 10h40 D. Gautheret: finding non-coding RNA genes 10h40 11h10 break 10h10 12h W.H. Li: inter-species comparison of gene expression profiles 12h 13h30 lunch 13h30 14h20 D. Liberles : detecting adaptive evolution in proteins 14h20 15h10 N. Galtier: methods for detecting selection from DNA sequence data 15h10 15h40 break 15h40 16h30 A. Eyre-Walker : detecting adaptive evolution in primates 16h30 17h open discussion

Phase II - Practical course June 21-23, 2004 & Lyon

Programme Bioinformatic tools for comparative sequence analysis: databases (sequences, genomes, polymorphism). Similarity searches (BLAST, PSI-BLAST); multiple alignment. Alignment of large genomic sequences. Multiple comparisons. Phylogeny (orthology, paralogy). Analysis of substitutions (synonymous and non-synonymous) and of polymorphism.

Selection 16 people will be selected among the participants of phase I for a practical course lasting 3 days.

Registration deadline: April 10, 2004 further information

Ateliers de formation Inserm 101, rue de Tolbiac 75654 Paris cedex 13 Tel: 01 44 23 62 03 Fax: 01 44 23 62 93

E-mail: ateliers@tolbiac.inserm.fr

– Pierre Pontarotti EGEE (Evolution Génome Environnement) Université d’Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol> We organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/>

– Pierre Pontarotti EGEE (Evolution Génome Environnement) Université d’Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol> We organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/>

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## Muenster AsexualDiversity Oct6-10

FIRST ANNOUNCEMENT for workshop on “Diversity in asexuals: Patterns and processes” 6.-10. October 2004 Muenster, Germany Organizers: Nico Michiels, Thomas D’Souza, Claus-Peter Stelzer.

TOPIC The workshop covers various aspects of diversity in asexual populations: geographical parthenogenesis, asexual species concepts, phylogenetic constraints, phylogenetic distribution, hybrid zones, niche differentiation, adaptability, genetic diversity, and terminology. Our workshop is one out of four within the Parthenogenesis Network (PARTNER), an initiative funded by the European Science Foundation (ESF). PARTNER is aimed to bring together empiricists and theorists who work in the field of parthenogenesis in botany and zoology (for more information, see <http://www.nioo.knaw.nl/networks/partner>).

ALREADY CONFIRMED SPEAKERS Michael Mogie (University of Bath, UK), Robert Vrijenhoek (Monterey Bay Aquarium Research Institute, USA), Leo Beukeboom (University of Groningen, Netherlands), Anssi Saura (Umea University, Sweden), Peter van Dijk (Netherlands Institute of Ecology), Hugh Loxdale (Rothamsted Research, Harpenden, UK), Isa Schoen (Royal Belgian Institute of Natural Sciences), Lawrence Kirkendall (University of Bergen, Norway).

APPLICATIONS We are happy to invite ca. 20 additional participants. Each invited attendant is expected to contribute a short oral presentation during the workshop (ca. 15 min). Applications should include a short CV and a brief description of the research interests (together max. two pages). Selection among the

applicants will be based on research record and topic. The workshop organization will cover the accommodation costs in the facilities provided by the organization for invited attendants, but cannot cover their travel expenses. Applications, preferably by email, should be submitted before June 15, 2004 to: partner3@uni-muenster.de

or to: Claus-Peter Stelzer Institute for Animal Ecology and Evolution Department of Evolutionary Biology Huefferstr. 1 48149 Muenster, Germany

— Dr. Claus-Peter Stelzer Department of Evolutionary Biology Institute of Animal Ecology and Evolution Universitaet Muenster Huefferstrasse 1 D-48149 Muenster

Email: stelzerc@uni-muenster.de Tel. +49 (0)251 83 21095 Fax. +49 (0)251 83 24668  
[www.uni-muenster.de/Biologie.EvoEco/bio/about/folks/stelzer.htm](http://www.uni-muenster.de/Biologie.EvoEco/bio/about/folks/stelzer.htm) Evol-

Claus-Peter Stelzer <stelzerc@uni-muenster.de>

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### NottinghamU TheoGenetics Aug23-27 2

BBSRC THEORETICAL GENETICS AND EVOLUTION SUMMER SCHOOL Nottingham University 23-27 August 2004

Second Mailing: Closing Date for Applications:- 30th April 2004

The BBSRC will be running a summer school for Postgraduate and Postdoctoral researchers working on quantitative aspects of evolutionary biology, dealing with variation both within and between species. We are looking for applications from young scientists who take an ongoing and broad interest in molecular evolutionary biology, and wish a greater understanding of quantitative and theoretical tools and approaches that will aid their interpretation of evolutionary data. Those chosen for the school will be asked to present a short seminar about their research project, and there will also be plenary talks and practical sessions.

The Summer School will cover the following areas of micro- and macroevolution:

Theme A: Genetic diversity within populations The neutral theory and the coalescent Mutation Human minisatellites Genomic context and molecular evolution Theme B: Genetic variability between popula-

tions. Theme C: Macroevolution and variation between species Alignment of sequences Reconstruction of Phylogenetic Trees, Detecting natural selection from gene genealogies Gene families, Gene duplications in evolution Genome alignment: Theme D: Evolution of development Theme E: Evolution in microorganisms

Lecturers will include: Des Higgins (Cork University), Peter Keightley, Brian Charlesworth and Deborah Charlesworth (Edinburgh University), David Conway (London School of Tropical Hygiene and Medicine), John Armour, John Brookfield, and Paul Sharp (University of Nottingham), Michael Akam (Cambridge University) Gil McVean (Oxford University), Adam Eyre-Walker (Sussex University),

Accommodation expenses for participants at this course (but not travel to Nottingham) will be covered by the BBSRC.

If, interested, please contact me at john.brookfield@nottingham.ac.uk for an application form, which should be returned to me. An application form can also be obtained from the BBSRC website at <http://www.bbsrc.ac.uk/news/-events/23.aug.04.tgess.html>, but please note that the form should be returned to the email address john.brookfield@nottingham.ac.uk, and not that included on the form.

The closing date for applications will be 30th April 2004. The easiest way to apply is to use the application form and send it as an email attachment to:

john.brookfield@nottingham.ac.uk John Brookfield Institute of Genetics University of Nottingham Queens Medical Centre Nottingham NG7 2UH

John Brookfield <John.Brookfield@nottingham.ac.uk>

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### RiodeJaneiro Complexity Nov 3

Apologies to those of you who have received this workshop calling notice via another route or have no interest in the event. Hi All This is the last general email I send out regarding the forthcoming Complexity and Philosophy Workshop to be held in Brazil in November.

Currently many more of you have shown interest (about 100) in the event than we can accommodate (30). We could of course make the event much bigger, but we are keen to keep the numbers low and more intimate than is possible with a larger gathering. We may work towards

putting together a larger conference in the future, but for now we'd like to focus on the workshop.

Getting to Brazil for many of us cannot be a last minute exercise and so rather than keep the proposed submission dates as they are I propose a slight change. Extended abstracts will now be due at the end of May so that a decision can be made regarding submission of a full paper by the end of June, rather than the end of August as previously proposed. It is hoped that this will avoid disappointing prospective attendees long before the event itself, as well as give attendees more time to prepare for the event.

A couple of points I'd like to stress (which come in response to some of the communications we have received so far):

Please bear in mind that this is NOT a management science event. Our aim is to talk about the philosophical implications of complexity theory at a more general abstract level. I'm sure that during the discussions examples of management strategies will be used to exemplify/clarify a particular philosophical idea, but this will not be the focus of the event. I feel the need to state this as we have already received a number of papers of the general sort "Managing Creativity in Organisations" - this is not what is meant by 'philosophical' in the context of this particular event. "The Role of Creativity in Understanding Complex Systems" would certainly be relevant however. So please be sure to pay attention to the workshop themes listed in the calling notice (attached below) before submitting abstracts. My secondpoint may cause a few political problems. The aim of a workshop is to talk, not to spend the majority of listening to presentations. As such it is unlikely that more than 5-6 papers will be 'formally' presented during the event, so that much of the time can be devoted to critical discussion (in either roundtable format or in break sessions). These papers will be chosen from the 30 or so submitted and will likely focus on the themes listed in the calling notice. However, asking our institutions to pay for a trip to go and 'talk' in Brazil may be a difficult sell for some of you. Even if a submitted paper is not presented it will certainly be included in a proceedings, and considered for either book or journal publication - our hope is that this approach will be sufficient for you to meet the requirements of your respective institutions. All papers will be made available before the event so that each participant might familiarise him/herself with some of the perspectives on display. The boundaries of the event will not just be the two-days we have in Brazil - we hope some level of dialogue, or at least preparation, will start longer before that. Encouraging paper submission is of course a way of facilitating this. That's it for now. Please find

full details of the event below. We look forward to receiving your abstracts and very much look forward to working with you all to organise an exciting, and maybe profound, event!

Regards,

Kurt Richardson Workshop Organiser [http://echoconferences.com/philosophy\\_workshop\\_2004.html](http://echoconferences.com/philosophy_workshop_2004.html)  
<http://isce.edu> <http://kurtrichardson.com> Workshop on Complexity and Philosophy

Co-hosted by: Federal university of Rio de Janeiro Institute for the Study of Coherence and Emergence Cathedra for the Study of Complexity (Instituto de Filosofia de La Habana)

Second Calling Notice 18-19 November 2004, Rio de Janeiro Hotel Florida - Rua Ferreira Viana, 81 - Flamengo - RJ

Call for Participants I am writing to you today to remind you about the upcoming two-day Complexity and Philosophy workshop to be held this November (2004) in Rio de Janeiro and hosted by the Institute for the Study of Coherence and Emergence (<http://www.isce.edu>), U.F.R.J. (Federal university of Rio de Janeiro), and the Cathedra for the Study of Complexity (Instituto de Filosofia de La Habana). The aim of this meeting is to explore the philosophical implications of the fledgling 'science' of complex systems.

This workshop complements the 2nd Biennial International Seminar on the Philosophical, Epistemological and

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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>

## RutgersU DIMACS Sep20-21

DIMACS Workshop on Reticulated Evolution

September 20 - 21, 2004 DIMACS Center, CoRE Building, Rutgers University

Organizers:

Mel Janowitz, DIMACS, [melj@dimacs.rutgers.edu](mailto:melj@dimacs.rutgers.edu)  
Randy Linder, University of Texas, [rlinder@mail.utexas.edu](mailto:rlinder@mail.utexas.edu)  
Bernard Moret, University of New Mexico, [moret@cs.unm.edu](mailto:moret@cs.unm.edu)

Presented under the auspices of the Special Focus on Computational Molecular Biology.

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Announcing a workshop and working group on reticulated evolution. The workshop will be held September 20-21, 2004 and the working group on September 22, 2004. Registration details and further information for the workshop may be obtained from the website

<http://dimacs.rutgers.edu/Workshops/Reticulated>

The working group is open by invitation only. Invitations may be obtained by contacting one of the organizers. The organizing committee consists of Mel Janowitz, DIMACS, melj@dimacs.rutgers.edu; Randy Linder, University of Texas, rlinder@mail.utexas.edu; Bernard Moret, University of New Mexico, moret@cs.unm.edu A brief description of the goals of these events follows.

Species evolution has long been modeled as a branching process that can uniquely be represented by a tree topology. In such a topology, each species can only be linked to its closest ancestor, while interspecies relationships such as species hybridization or lateral gene transfer in bacteria are not allowed. With the advent of phylogenetic analysis at the molecular level, there is increasing evidence that such a model is inadequate. This workshop will explore the history and latest status of these new models of "reticulate evolution", and will be coupled with a smaller working group meeting designed to explore promising avenues for future research.

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Registration:

Pre-registration deadline: September 13, 2004

Please see website for additional registration information.

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Information on participation, registration, accommodations, and travel

can be found at:

<http://dimacs.rutgers.edu/Workshops/Reticulated/>

**\*\*PLEASE BE SURE TO PRE-REGISTER EARLY\*\***

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Sy-compmolecbio-local mailing list Sy-compmolecbio-local@dimax.rutgers.edu <http://dimax.rutgers.edu/-mailman/listinfo/sy-compmolecbio-local>

## UMontpellier Speciation May10-13

A short course on the foundations of the theory of speciation will be offered twice by Sergey Gavrilets (University of Tennessee, Knoxville)

Dates May 10 and 13, 2004

Location University of Montpellier, France  
Local organizer Yannis Michalakis (Yannis.Michalakis@mpl.ird.fr)

Dates June 7 and 14, 2004 Location Universite de Paris-Sud, Orsay, France  
Local organizer Frederic Hospital (fred@moulon.inra.fr)

Attendance is free. To register, please contact the local organizers.

Tentative course outline:

1 Fitness landscapes (1 hour) Working example: one-locus, two-allele model of viability selection Fitness landscape as fitness of gene combinations Fitness landscape as the mean fitness of populations The metaphor of fitness landscapes Wright's rugged fitness landscapes Fisher's single-peak fitness landscapes Kimura's flat fitness landscapes Fitness landscapes for mating pairs Fitness landscapes for quantitative traits Fitness landscape as fitness of trait combinations Fitness landscape as the mean fitness of populations Fitness landscapes for mating pairs Nearly neutral networks and holey fitness landscapes Simple models Russian roulette model in two dimensions Russian roulette model on hypercubes Generalized Russian roulette model Neutral networks in RNA landscapes Neutral networks in protein landscapes Other evidence for nearly neutral networks

2 Steps toward speciation on rugged fitness landscapes (1 hour) Stochastic transitions between isolated fitness peaks Fixation of an underdominant mutation Peak shift in a quantitative character Fixation of compensatory mutations in a two-locus haploid population Some consequences of spatial subdivision and density fluctuations Spatial subdivision Stochastic transitions in a growing population Peak shifts by selection

3 Speciation in the Bateson-Dobzhansky-Muller (BDM) model (2 hours) The 2-locus 2-allele BDM model of reproductive isolation Fitness landscapes in the 2-locus 2-allele BDM model The mechanisms of reproductive isolation in the BDM model Population genetics in the 2-locus 2-allele BDM model Haploid population Diploid



population Dynamics of speciation in the 2-locus 2-allele BDM model Allopatric speciation Parapatric speciation Multilocus BDM models The Walsh model Divergent degeneration of duplicated genes Three- and four-locus models Accumulation of genetic incompatibilities Allopatric speciation Parapatric speciation

4 Models of sympatric speciation (2 hours) Maintenance of genetic variation under disruptive natural selection Spatially heterogeneous selection Spatially uniform disruptive selection Frequency-dependent selection in a single population Evolution of nonrandom mating Similarity-based nonrandom mating Matching-based nonrandom mating Interaction of disruptive se-

lection and nonrandom mating The Maynard Smith model The Udovic model The Felsenstein model The Diehl-Bush model

————— Sergey Gavrilets Department of Ecology and Evolutionary Biology Department of Mathematics University of Tennessee Knoxville, TN 37996

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Sergey Gavrilets <[sergey@tiem.utk.edu](mailto:sergey@tiem.utk.edu)>

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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  $\LaTeX$  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  $\LaTeX$  do not try to embed  $\LaTeX$  or  $\TeX$  in your message (or other formats) since my program will strip these from the message.