
E v o l D i r

March 1, 2005

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

Forward

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

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

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



Forward	1
Conferences	2
GradStudentPositions	11
Jobs	22
Other	37
PostDocs	60
WorkshopsCourses	71
Instructions	75
Afterward	75

Conferences

Auckland SMBE05 Jun19-23 WalterFitchPrize 2	Potsdam PlantPopBiol May4-8 6
Bordeaux PhDEvolBiol Sep5-9 2	SUNY Stonybrook SSB 2006 6
Budapest EvolEthol Aug20-27 3	SouthernIllinoisU MEEC Mar11-13 2 7
Harvard Mind Brain Behavior May 12-13 3	UAmsterdam MarinePopStructure Apr14 7
JagiellonianU EmergingGenomeData Aug15-20 4	UGeorgia SEEC Mar11-13 2 8
KrakowPoland ESEB AbstractsRegistration 4	UMinnesota Genetics Apr9 8
Marseille 9thEvolBiol 4	UToronto EGLME Apr30 9
Marseille EvolBiol Sep21-23 2 5	Valencia MEEGID July 10
MaryCartwrightLecture London Feb25 5	
Paris MathEvol Jun17-21 2 6	

Auckland SMBE05 Jun19-23 WalterFitchPrize

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

Abstracts to be considered for the Fitch Prize should be submitted to the SMBE05 Web Site (<<http://www.jevon.org/mbe/index.php>><http://www.mbe05.com>) by 15th March. The Society has appointed a Convenor for the Panel who select 8-10 abstract for oral presentation at the conference. All those selected receive some support from the Society towards travel.

Because of the location, it is apparent that some students are unable to confirm that they have arranged travel costs by 15th March. In such cases, students should still submit their abstracts by 15th March and then have until 1st May to confirm their registration, and be eligible for 'early bird' registration costs (US\$200).

Eligibility: PhD students and postdocs who have graduated from July 2004 onwards

For additional information, contact Susan Wright <<mailto:S.M.Wright@massey.ac.nz>>S.M.Wright@massey.ac.nz but all applications must be made through the Web site.

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

<http://AWCMEE.massey.ac.nz>

s.m.wright@massey.ac.nz s.m.wright@massey.ac.nz

Bordeaux PhDEvolBiol Sep5-9

11th Meeting of PhD Students in Evolutionary Biology

The 11th Meeting of PHD Students in Evolutionary Biology will take place in Bordeaux, France, from Monday September 5th to Friday September 9th. This meeting gives the opportunity to 100 PhD students working in European laboratories to present and discuss their work and to participate in lively discussions on hot topics of evolutionary biology today. Each participant is encouraged to give a short talk, which will be followed by a discussion with the audience. Eight sessions are scheduled: - Population genetics - Phylogenetics / phylogeography / Macro-evolution - Coevolution - Experimental and microbial evolution - Life history traits - Behavioral ecology - Conservation ecology - Evo-Devo / Evolutionary genomics One expert will rule each session and organize a round table on a particular theme.

For information, the website of the previous meeting can be found here: <http://students.bath.ac.uk/-bspght/index.html> An online registration procedure will be opened around March (to be announced later on this list).

The organizing committee:

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

Julien.Dutheil@univ-montp2.fr Julien.Dutheil@univ-
montp2.fr

Budapest EvoEthol Aug20-27

Dear Colleague,

We are pleased to announce that the 29th International Ethological Conference (IEC) will be held in Budapest (Hungary). The conference will take place in the new building of Eötvös University on the Danube riverbank near Budapest city centre between August 20-27 2005.

The IEC has a long tradition of attracting ethologists, comparative psychologist, neuroethologists, cognitive scientists and behavioural ecologists from all over the world. The IEC is organised every second year and the last conference was in Brazil 2003. Given the continuously growing interest in behavioural research we expect good number of people to attend our conference. Note that Budapest sits in convenient distances from Vienna and Prague, and it is one of the most beautiful cities in Central Europe.

We would be pleased if your research will be represented at our conference. Please visit our website at <http://www.behav.org/IEC> The deadline for abstract submission is 1st April 2005

Sincerely yours,

Organising Committee jointly with the Hungarian Ethological Society

–

Dr Tamas Szekely Department of Biology and

Biochemistry University of Bath, Bath BA2 7AY, UK 01225 383676 (phone) 01225 386779 (fax) T.Szekely@bath.ac.uk (email) <http://www.bath.ac.uk/Departments/BiolBioch/tamas.html> <http://www.bath.ac.uk/bio-sci/biodiversity-lab/-framework.html> WORKSHOP ON SEXUAL SIZE DIMORPHISM - AUGUST 2005 <http://www.bath.ac.uk/bio-sci/szekely/workshop/-SSD%20Workshop2%20webmod.htm> Tamas Szekely <bssts@bath.ac.uk>

Harvard Mind Brain Behavior May 12-13

CALL FOR SUBMISSIONS

1st Annual Harvard Mind, Brain and Behavior Graduate Student Conference The Nature of Thought Thursday, May 12 to Friday, May 13, 2005

The Nature of Thought, in four sessions:

I. Language & Thought Invited Speaker: Steven Pinker, Johnstone Family Professor of Psychology, Harvard University.

II. The Brain & Thought Invited Speaker: Earl Miller, Picower Professor of Neuroscience, MIT.

III. Computers & Thought Invited Speaker: Stuart Shieber, Welch Professor of Computer Science, Harvard University.

IV. Evolution & Thought Invited Speaker: Peter Godfrey-Smith, Visiting Professor of Philosophy, Harvard University.

Graduate students from the Mind, Brain and Behavior Initiative at Harvard are pleased to announce an interdisciplinary conference on the Nature of Thought. The conference is for graduate students, and intended to increase dialogue among graduate students from a variety of disciplines, including (but not necessarily limited to) neuroscience, psychology, computer science, neurobiology, linguistics, organismic and evolutionary biology, biological anthropology, history of science and philosophy.

We are soliciting graduate student contributions to this conference. For each of our four sessions, there will be two graduate student presentations of no more than 30 minutes each (followed by approximately 20 minutes of discussion each). We will construe the boundaries of each topic broadly, and welcome contributions from

any field that aims to understand the nature of thought. Presentations should be aimed at a non-specialist audience. To be considered for a presentation, please email an abstract of no more than 500 words, purged of any identifying information, to mbb@eecs.harvard.edu. Please also include a separate cover sheet with your name, institutional affiliation, email address, telephone number, the title of your presentation, and the title of the session at which you would like to present (e.g. Computers & Thought). You may send the abstract and cover sheet as a plain text or pdf file. Unfortunately, we do not have funds to pay for the transportation costs of speakers; but we will house speakers with local graduate students upon request. The deadline for submissions is March 1, 2005. Authors will be notified by March 21, 2005 of the status of their submissions.

A website with additional conference information will be available soon and linked to the main Harvard MBB website at <http://mbb.harvard.edu/>. Inquiries should be directed to mbb@eecs.harvard.edu.

mpatten@oeb.harvard.edu mpatten@oeb.harvard.edu

JagiellonianU

EmergingGenomeData Aug15-20

10th congress of the European Society for Evolutionary Biology, Jagiellonian University, Cracow, Poland from 15 to 20 August 2005

We would like to encourage applications for the following symposium:

'Emerging genome data: lessons for ecology and evolution'

Abstract: Recent genome sequences have radically affected our perception of how genes and genomes evolve, but arguably have had less impact on organismal ecology and evolution. One limitation is that understanding evolution requires adequate taxon sampling, yet so far most sequenced genomes have been confined to a few taxonomically isolated model organisms. As emerging genome data encompasses new branches from the tree of life, and begins to include multiple genome sequences from closely related species, the aim of this symposium is to highlight genomic research and its increasing influence in understanding ecology and evolution.

Organisers: Angus Davison, Institute of Genetics, University of Nottingham (angus.davison@nott.ac.uk) and Douda Bensasson Dept of Biological Sciences, Imperial

College (d.bensasson@imperial.ac.uk)

Invited speakers: Mark Blaxter (University of Edinburgh) and Jeffrey Boore DOE Joint Genome Institute

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

Angus Davison

– Dr. Angus Davison

Institute of Genetics The University of Nottingham
Queen's Medical Centre Nottingham NG7 2UH

email angus.davison@nott.ac.uk tel 0115 849 3239 (int. 35239) fax 0115 970 9906

www.nottingham.ac.uk/genetics

zel-

dia.cap.ed.ac.uk/mollusca.html

angus.davison@nottingham.ac.uk

an-

angus.davison@nottingham.ac.uk

KrakowPoland ESEB AbstractsRegistration

On-line registration for ESEB is open now!

Conference web page: <http://www.eko.uj.edu.pl/-eseb/> Deadline for abstract submission and reduced fee is 30th April 2005.

regards ESEB Team

gawelczyk@bieszczady.info

Marseille 9thEvolBiol

The registration dead line for the next "evolutionary biology meeting at Marseille" is April 2nd

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

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

We organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/pierre.pontarotti@up.univ-mrs.fr>

Marseille EvoBiol Sep21-23 2

the next evolutionary biology meeting at Marseille will take place this Year from September 21 to September 23. The registration dead line is April 2nd

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, 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 Best regards Pierre

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

We organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/pierre.pontarotti@up.univ-mrs.fr>

MaryCartwrightLecture London Feb25

The Mary Cartwright Lecture, an annual event run by the London Mathematical Society, will this year for the first time be in the area of statistical genetics. It will take place in London (UK) on the afternoon of Friday February 25. The Notice is on the web at [<http://www.lms.ac.uk/meetings/MC05.html>](http://www.lms.ac.uk/meetings/MC05.html) and is reproduced below.

The Mary Cartwright Lecturer, Professor Elizabeth Thompson, is coming from Seattle specially for the pur-

pose. She plans to announce and describe significant new work. She will be supported by a companion lecture by Professor Steffen Lauritzen. It is clear that this will be a landmark scientific occasion, not to be missed.

All are welcome to the lectures, for which there is no fee or registration.

Organiser (for the LMS): Charles Goldie, University of Sussex. C.M.Goldie@sussex.ac.uk

LONDON MATHEMATICAL SOCIETY

MARY CARTWRIGHT LECTURE

Friday February 25, 2005 University College London (Chemistry Auditorium, Christopher Ingold Building, 20 Gordon Street, London WC1, UK)

3.30 - 4.30 Professor Steffen Lauritzen (Dept. of Statistics, Univ. of Oxford) "A pedigree perspective of local computation"

4.30 - 5.00 Tea

5.00 - 6.00 Mary Cartwright Lecture: Professor Elizabeth Thompson (Depts of Statistics and Biostatistics, Univ. of Washington, Seattle) "Relatedness, genome sharing, and the detection of genes"

The talks by Elizabeth Thompson and Steffen Lauritzen are concerned with the genetic analysis of large pedigrees. A pedigree, defined as a full specification of family relationships between a group of individuals, is naturally represented by a directed graph. Almost every problem associated with pedigree analysis involves a difficult computation, but algorithms for so-called local computation on graphs allow feasible calculations to be done, and this is the topic of the first talk. The second talk focuses on genome sharing arising from pedigree relationships, and on using the dependence in sharing at different loci on a common chromosome to infer linkage of a trait to a set of marker loci. A new way to assess the evidence for linkage from unobserved genome sharing will be discussed.

A reception will be held at De Morgan House at 6.15 pm with a dinner afterwards at Poons Restaurant, 50 Woburn Place, London WC1 at 7.15 pm. The cost will be 25 pounds per person, inclusive of wine. Those wishing to attend should inform The Administrator, Susan M. Oakes, London Mathematical Society, De Morgan House, 57-58 Russell Square, London WC1B 4HS, enclosing a cheque payable to the London Mathematical Society to arrive no later than Monday 21 February.

There are limited funds available to contribute in part to the expenses of members of the Society or research students to attend the Society meeting. Requests for support, including an estimate of expenses, may be

addressed to the Programme Secretary at the Society (<grants@lms.ac.uk>).

“Charles M. Goldie” <C.M.Goldie@sussex.ac.uk>

Paris MathEvol Jun17-21 2

Mathematics of Evolution and Phylogeny Institut Henri Poincaré, Paris, June 17-18 and 20-21, 2005.

This conference follows a similar workshop that was held in June 2003. The subject is evolution, which is considered at different scales: sequences, genes, gene families, organelles, genomes, and species. The focus is on the mathematical and computational tools and concepts, which form an essential basis of evolutionary studies. Recent years have witnessed rapid progress in this area, with models and methods becoming more realistic, powerful, and complex. The goal of the conference is to provide pedagogical presentations of the main subjects in the field, from basic principles to the cutting edge, with time for discussion and debate. There will be presentations by some of the leading experts in the field. Each speaker will survey a broad range of methods, techniques and results. Young scientists will also be selected, to give short talks or present posters.

Web site of the conference and online registration:

<http://www.lirmm.fr/MEP05/> LIRMM, 161 rue Ada, 34392 - Montpellier - FRANCE Tel. (33 or 0 from France) 4 67 41 85 47 Fax. (33 or 0 from France) 4 67 41 85 00 <http://www.lirmm.fr/~gascuel> gascuel@lirmm.fr gascuel@lirmm.fr

Potsdam PlantPopBiol May4-8

Dear colleagues,

the call for abstracts is now open for

“Progress in Plant Population Biology”,

the 18th Annual Conference of the Section Plant Population Biology of the Ecological Society of Germany, Switzerland and Austria.

The conference will take place from 4/5 May - 8 May 2005 at the Institute of Biochemistry and Biology and

Botanical Garden of the University of Potsdam. For scope, invited speakers, and important dates, see below. For complete information, and for abstract submission and registration, see the conference homepage at

<<http://www.bio.uni-potsdam.de/akpopbio/-conf2005/>><http://www.bio.uni-potsdam.de/akpopbio/conf2005/> We are looking forward to welcoming you in Potsdam,

Markus Fischer, Thilo Heinken, Mark van Kleunen, Dorit Raudnitschka

Scope of “Progress in Plant Population Biology”

The last years have seen rapid advances in a number of fields relevant for plant population biology. These include molecular ecology, conservation genetics, genomics, mating systems, GIS, mathematical modeling, plant interactions with pollinators, herbivores, pathogens, or seed dispersal vectors, comparative methods, and biological data bases. Several invited talks will outline new plant population biological insights made possible by such new advances. The meeting invites contributions within the general context of plant population biology.

Invited speakers (confirmed)

Jaroslav Burczyk, University of Bydgoszcz, Poland Plant fitness: the neglected paternal side

Outi Savolainen, University of Oulu, Finland Population genomics of plant adaptation

Merel Soons, University of Utrecht, Netherlands GIS meets plant population biology: linking regional habitat dynamics to regional species dynamics

Florian Jeltsch, University of Potsdam, Germany Plant population modelling quo vadis?

Important dates

28 February 2005: Deadline for submission of abstracts for talks and posters 31 March 2005: Deadline for registration of participation

4/5 May - 8 May 2005: Conference

Markus Fischer <fischer@rz.uni-potsdam.de>

SUNY Stonybrook SSB 2006

Call for 2006 Symposia

The Society for Systematic Biologists invites proposals for symposia at the 2006 SSB meeting to be held at the State University of New York, Stony Brook. The meeting will be held jointly with the American Society of Naturalists and the Society for the Study of Evolution. Proposals 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 funding is available. The target date for receipt of proposals is May 15, 2005. Proposals will be discussed and two will be selected at the SSB Council meeting during the 2005 annual meeting in Fairbanks, Alaska. Soon after, organizers will be notified of the status of their proposals. Proposals should be sent by email to the Program Chairperson, George D. Weiblen, gweiblen@umn.edu (Department of Plant Biology, University of Minnesota, 1445 Gortner Avenue, Saint Paul, Minnesota 55108).

George Weiblen Assistant Professor, Department of Plant Biology Curator of Flowering Plants, Bell Museum of Natural History University of Minnesota 250 Biological Sciences 1445 Gortner Avenue Saint Paul, MN 55108 USA

Office: 612-624-3461 Lab: 612-625-8749 Fax: 612-625-1738 Email: gweiblen@umn.edu Web: <http://geo.cbs.umn.edu>

SouthernIllinoisU MEEC Mar11-13

2

MEEC 2005 Deadline Extension

Early Registration and Abstract Deadline: February 11th, 2005

25th Annual Midwest Ecology and Evolution Conference

Southern Illinois University-Carbondale

March 11th-13th, 2005

The graduate students in the Departments of Plant Biology and Zoology at Southern Illinois University-Carbondale would like to invite graduate students and post-doctoral associates from the Midwestern United States to submit abstracts for oral and poster presentations at the 25th Annual Midwest Ecology and Evolution Conference (MEEC).

MEEC is a migratory conference hosted by universities in the Midwest eco-region that is organized by graduate students. This conference provides an informal venue for undergraduate, graduate, and post-doctoral students interested in ecology to present their research to an audience of their peers, fostering an environment of collaboration and communication between future scientists.

This year, MEEC will be hosted by Southern Illinois University in Carbondale, Illinois, and held at the Carbondale Civic Center from March 11-13, 2005. The conference will feature a keynote address by Dr. Robert E. Ricklefs, Curators' Professor of Biology at the Department of Biology, University of Missouri at St. Louis, and a plenary presentation by Dr. Jerry O. Wolff, Program Director for the National Science Foundation.

In addition to contributed sessions on topics in ecology and evolution, invited and contributed papers will be considered for two special symposia: (1) Paleocology, and (2) Conservation and Climate Change. Manuscripts submitted from presentations will be considered for publication in a special issue of the American Midland Naturalist.

Deadline for submission of abstracts and early registration is February 11th, 2005. Early registration fee is \$40.

For more information, go to <http://mypage.siu.edu/meec2005> or email meec2005@siu.edu.

Please forward this solicitation accordingly. Thank you.

bbensc01@siu.edu

UAmsterdam MarinePopStructure Apr14

First announcement of the one-day symposium 'Structure@Sea' on thursday, 14th of April 2005, University

of Amsterdam.

Marine-dwelling organisms are usually imagined to be part of huge populations, characterized by almost unlimited interchange. This is especially true for free-living critters in the plankton that travel wherever the water current takes them. Allopatric divergence and speciation are therefore not expected to play a major role at the spatial scales at which they typically act in other habitats. Nonetheless, species diversity and levels of population genetic structuring are often unexpectedly high. This symposium reviews the observed patterns for pelagic as well as benthic organisms and discusses recent theories on the possible causes for these.

This symposium is organized on the occasion of the PhD defense of Katja Peijnenburg and will consist of eight presentations by a diverse group of internationally renowned as well as up-and-coming scientists, and will include a poster session.

The event is free of charge and open to all. Participants are encouraged to bring posters.

Confirmed speakers are: Nancy Knowlton (University of California, USA) Colomban de Vargas (Rutgers University, New Brunswick, USA) Jeanine Olsen (University of Groningen, Netherlands) Katja Peijnenburg (University of Amsterdam, Netherlands) Galice Hoarau (University of Groningen, Netherlands)

For registration and further questions, please send an e-mail to luttikhuizen@science.uva.nl.

The organisers, Pieternella Luttikhuizen, Katja Peijnenburg, Steph Menken, and Jef Huisman University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, the Netherlands.

Katja Peijnenburg Institute for Biodiversity and Ecosystem Dynamics Faculty of Science, University of Amsterdam P.O. 94062 1090 GB Amsterdam The Netherlands

tel. +31 20 5257761 fax. +31 20 5257878
email: peijnenburg@science.uva.nl website: <http://staff.science.uva.nl/~peijnenb/> "Katja T.C.A. Peijnenburg" <peijnenburg@science.uva.nl>

UGeorgia SEEC Mar11-13 2

LAST CALL FOR ABSTRACTS

SEEC 2005 SOUTHEASTERN ECOLOGY AND

EVOLUTION CONFERENCE THE UNIVERSITY OF GEORGIA ATHENS, GEORGIA 11-13 MARCH 2005 www.uga.edu/seec REGISTRATION DEADLINE: 4 FEBRUARY 2005

We invite all graduate, undergraduate, and post-doctoral researchers studying in the environmental and life sciences to submit abstracts for either oral or poster presentations at the 2nd annual Southeastern Ecology and Evolution Conference (SEEC) to be held March 11-13, 2005, at the The University of Georgia in Athens, Georgia. Talks will be delivered by Drs. Whit Gibbons, John Avise and Gary Barrett.

SEEC is a professional meeting intended for students in the environmental and life sciences to present their research to their colleagues in a comfortable, fun, and low stress environment. Such events are designed to encourage new friendships within our field and to share newly developed research ideas for feedback. While we expect most SEEC participants to be from the Southeast, we encourage and welcome all interested individuals to submit abstracts and/or attend.

To encourage attendance, registration is only \$15 and covers meeting attendance, two continental breakfasts, snacks, coffee, a t-shirt, and \$100 cash awards for the best oral and poster presentations. The registration and abstract submission deadline is February 4, 2005, and may be completed at the following web site:

www.uga.edu/seec We look forward to seeing you at The University of Georgia in Athens for the 2nd Annual Southeastern Ecology and Evolution Conference this March!

For more information, go to www.uga.edu/seec or email Tom Luhring at tluhring@uga.edu

Thomas Luhring <tluhring@uga.edu>

UMinnesota Genetics Apr9

Announcing the University of Minnesota Center for Community Genetics 2005 Symposium

Saturday April 9th, 2005 in Minneapolis, Minnesota

Community Genetics and Phylogenetics Past and ongoing evolutionary and ecological processes interact to shape the biodiversity within ecological communities as well as the genetic diversity of their component species. Recognition of these interactions has prompted efforts toward a synthesis of community ecology and evolution-

ary genetics. This symposium explores the dynamic interplay between ecology and genetics in the ongoing evolution of species interactions while recognizing the importance of history. Of special focus are the joint roles of population processes and phylogenetic relationships in community assembly and the role of community in the divergence of species populations.

Presentations and panel discussions by seven internationally renowned ecologists and evolutionary biologists will be followed by a poster session and a banquet at the University of Minnesota Campus Club.

The event is free and open to the public.

Attendees are asked to register and to contribute posters. Limited funds are available for travel expenses of graduate students and post-docs who present posters.

Symposium Program

Friday April 8th 3:00 - 5:00 pm Hamm Memorial Lecture Dr. Janis Antonovics, University of Virginia "Plant models and infectious diseases"

335 Borlaug Hall, Upper Buford Circle St. Paul Campus, University of Minnesota

Saturday April 9th Campus Club, 4th floor Coffman Memorial Union, Washington Avenue Minneapolis Campus, University of Minnesota

Morning Session: Population-level processes and diversification

9:00 - 9:50 am Dr. Bob Holt, University of Florida "TBA" 9:50 - 10:40 am Dr. Michael Travisano, University of Houston "TBA" 10:40 - 11:30 am Dr. Lacey Knowles, University of Michigan "Disentangling the effects of dynamic climate change on species diversification" 10:30 - 12:00 am Panel Discussion

12:00 - 2:00 pm Lunch in Stadium Village

Afternoon session: The interplay of phylogenetic history and community structure

2:00 - 2:50 pm Dr. Scott Hodges, University of California at Santa Barbara "The genetic basis of floral adaptations in columbines" 2:50 - 3:40 pm Dr. Rosmary Gillespie, University of California, Berkeley "Evolutionary déjà vu: spiders on the remote islands of the Pacific" 3:40 - 4:30 pm Dr. Mark McPeck, Dartmouth University "The genetic and ecological legacies of the Pleistocene in modern communities" 4:30 - 5:00 pm Panel Discussion

Evening session: 6:30 - 7:30 Posters and Mixer 7:30 - 9:00 Dinner

Registration Please send Dr. Peter Tiffin (ptiffin@umn.edu) your name, affiliation, mailing address,

and e-mail address. If you are contributing a poster, please provide a title. If you would like to be considered for funding toward your travel expenses please provide a short statement justifying the request. The cost of the symposium dinner is \$25 per person. Indicate whether or not you will attend the dinner, and whether you have a dietary preference.

UToronto EGLME Apr30

Eastern Great Lakes Molecular Evolution Meeting

CALL FOR PAPERS

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

The 2005 Eastern Great Lakes Molecular Evolution Meeting will be held on Saturday, April 30, 2005, at the Koffler Institute for Pharmacy Management at the University of Toronto, in Toronto, Ont. Registration, coffee, and poster setup will begin at 8:30 A.M., with the talks will end around 5 PM, and will be followed by a reception/poster session. We are pleased that the following speakers have agreed to give a talk a:

Andy Clark (Cornell) Jeff Lawrence (Pittsburgh) Paul Hebert (Guelph) Brian Golding (McMaster) Carlos Bustamante (Cornell)

Further information, registration and abstract submission can be found at <http://bbc.botany.utoronto.ca/-EGLMEM/> In addition to the invited speakers, there will be a selection of shorter contributed talks. Contributed talks will be selected from submitted abstracts, and will be of 12 - 15 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. Abstracts must be submitted by March 30, 2005. Individuals submitting requests to give talks will be informed by April 11, 2005, 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.

Please feel free to duplicate and distribute copies of this notice and the registration form 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 distributed by email no later than April 22nd to all those who preregister. It will also be posted at: <http://bbc.botany.utoronto.ca/EGLMEM/registrants.html>

Information about traveling to Toronto, maps of the Toronto campus, and descriptions of research and educational activities at the University of Toronto can be found on the University of Toronto Home Page and related pages: <http://www.utoronto.ca/toronto.htm> <http://www.osm.utoronto.ca/map/> <http://www.utoronto.ca/> If you have any questions, please contact: David Irwin Department of Laboratory Medicine and Pathobiology e-mail: david.irwin@utoronto.ca phone: 416-978-0519 Fax: 416-978-4108

Belinda Chang Department of Zoology e-mail: changb@zoo.utoronto.ca phone: 416-978-3507 FAX: 416-978-8532

David Guttman Department of Plant and Microbial Biology e-mail: david.guttman@utoronto.ca phone: 416-978-6865 FAX: 416-978-5878

Allan Baker Royal Ontario Museum e-mail: alanb@rom.on.ca phone: 416-586-5520 FAX: 416-585-5553

Valencia MEEGID July

19/02/05

Dear Colleague,

please find below some important news about the three tightly-linked undertakings (journal/congress/society) above-mentioned.

(1) The journal *Infection, Genetics and Evolution* (Elsevier; <http://www.elsevier.com/locate/meegid>) launched in 2001 (19th issue presently being compiled), aims to be the forum for developing a holistic and integrated approach to the epidemiology of transmissible diseases. This approach considers together the host, the pathogen and the vector (for vector-borne diseases), with the tools of genetics, evolutionary biology, genomics, post-genomics and bioinformatics. *Infection, Genetics and Evolution* welcomes papers on infectious models of medical, veterinary and agronomical relevance. All pathogens are considered: helminths, parasitic protozoa, fungal organisms, bacteria, viruses, prion. Since many traits can be com-

mon between them, with the goal of establishing general laws, comparisons between different kinds of pathogens are encouraged, which makes possible to establish general laws. Similarly, integrated studies including host, pathogen and vector are encouraged. *Infection, Genetics and Evolution* aims to favor cross-fertilization and mutual inspiration between parasitologists, mycologists, bacteriologists, virologists, entomologists, human geneticists, molecular epidemiologists and evolutionists. *Infection, Genetics and Evolution* has been quoted 3.5/4.0 ("very good") by the National Library in Washington DC. It is now covered by medline, pubmed and scholar.google starting from the first issue. Just waiting for your manuscripts!

(2) the MEEGID congresses: coorganized by the Institut de Recherche pour le Développement (IRD; the French governmental agency for research in developing countries), the Centre National de la Recherche Scientifique (CNRS; the French governmental agency for basic research) and the Centers for Disease Control (CDC) in Atlanta. The MEEGID congresses rely on the same concept and have the same scope than *Infection, Genetics and Evolution*, which publishes abstracts and selected papers from them (and from other congresses with related topics) in special issues. MEEGID VII has been held in Valencia, Spain, July 2004 (<http://www.uv.es/emop9/MEEGID>). MEEGID VIII is scheduled May 2006 at the CDC in Atlanta. A "mini-MEEGID", specialized on major parasitoses (malaria, toxoplasmosis, sleeping sickness, Chagas disease and leishmanioses) is scheduled in Montpellier, France, September 2005, with special training sessions on molecular epidemiology and evolutionary biology for students and postdoctoral fellows. Scientists and students from developing countries will benefit from reduced rates.

(3) The MEEGID society aims to support the activities of *Infection, Genetics and Evolution* and of the MEEGID congresses. Members benefit from free access to the journal (the paper version) and from reduced registration fees to the MEEGID congresses. In 2005, new activities are scheduled, including regular warning messages for hot papers and important events, discussion forums on email and delivery of PDF articles. Time to register!

Please circulate this message.

For additional information, contact me at the address below:

With all best regards,

Michel Tibayrenc, MD, PhD Editor-in-chief *Infection, Genetics and Evolution* (Elsevier) <http://www.elsevier.com/locate/meegid> Director Unit of Re-

search 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 (sec-

retary) 33 4 67 41 62 07 (direct) Fax 33 4 67 41 62 99 Email Michel.Tibayrenc@mpl.ird.fr Website <http://gemi.mpl.ird.fr> Michel.Tibayrenc@mpl.ird.fr

GradStudentPositions

AmericanU EvolBiol 2	11	UCologne Evo Devo	16
AmericanU FluctuatingAsymmetry	12	UGroningen 2 EvolGenetics	17
AmericanU HumanMateChoice	12	UHawaiiManoa InsectConservation	18
GeorgiaTech EvolBiol	12	ULouisianaMonroe SystMalacology	18
IdahoStateU ComputationalEvolBiol	13	UManchester PhylogenomicsWorkflow	19
MarieCurieNetwork EvolAnimalForm	13	UNevadaReno ComputationalEvolBiol	19
MaxPlanck ComputationalBiol	14	UNewOrleans ConservationBiol	20
MichiganStateU CyanobacterialControl	14	UNewcastle BarnacleVariation	20
NHMLondon Phylogeography	15	UdeNeuchatel PlantSurvival	20
NetherlandsInstEcol Birds	15	UppsalaU ComplexTriats	21
UCollegeLondon ReproductiveIsolation	16		

AmericanU EvolBiol 2

The Department of Biology at American University would like to offer you an exciting opportunity to visit and learn more about our graduate programs in Biology and Environmental Sciences. We have recently instituted new funding for both additional stipends and research supplies. Qualified graduate students can now over \$20,000 a year to support their graduate education.

We are holding a Graduate Student Open House on Monday, February 21, 2005 for you to visit and learn about potential research projects and graduate funding opportunities. This day-long event is designed to familiarize you with our campus resources and give you a better idea about the themes and goals of our Master’s programs. At these events, there will be many opportunities to talk with both faculty and graduate students.

The day will start at 9 AM with a welcome and introduction to the Department, followed by a tour of our

facilities and the campus, then a luncheon with faculty in the department. In the afternoon we will have some short research talks from our faculty and graduate students. At the end of the day, the graduate students will take you out for an informal pizza social.

Please reply to Dr. Nancy Zeller, letting us know if you plan to attend the February 21st open house by Friday, February 18, 2005. We will also try to find you accommodations with the graduate students or faculty for the nights of the 15th or the 16th. Contact Nancy Zeller at nzeller@american.edu or 202-885-2191. Let Dr. Zeller know if you would like to arrange accommodations and if you would like a copy of the agenda.

Applicants interested in funding are strongly encouraged to attend the Open House, as the departmental review of applications begins in late February. Also note that attendees are awarded waivers for their application fees. I also encourage you to inquire about reimbursement for your travel costs to the event! We hope you will be able to visit and learn more about our graduate programs. If you have any questions, please feel free to contact Nancy Zeller at 202-885-2191. We look forward to meeting you.

Nancy Zeller, Ph.D. nzeller@american.edu Department

of Biology American University Washington, DC 20016
 ScienceAmbassador@american.edu

AmericanU FluctuatingAsymmetry

Funded Graduate Positions

Recently, conservation biologists have been investigating the usefulness of a relatively new tool, fluctuating asymmetry (FA), for assessing the impact of environmental and genetic stresses on populations. One of the main advantages of FA is its increased sensitivity relative to other bioindicators. If effective, this tool could allow biologists to monitor populations and make recommendations before a severe problem arises, often without the high cost of other solutions. I have a number of funded FA projects available for graduate students interested in obtaining their MS degree at American University. Study subjects include marine mammal and endangered species. The projects combine FA data with other measures of population health to determine, on a species-by-species basis, whether FA can be used to identify stressed populations before detrimental population decline occurs.

Funded positions include tuition, stipend and, if desired, hourly wages for work as a TA. Basics research support is also provided. If interested please contact Cathy Schaeff, schaeff@american.edu. Additional information about the MS program (http://www.american.edu/cas/bio/programs_media/ms.html) and the department (<http://www.american.edu/cas/bio/deptprofile.html>) is available online.

Cathy Schaeff Department Chair American University
 Washington, DC 20016

ScienceAmbassador@american.edu

AmericanU HumanMateChoice

AMERICAN UNIVERISTY would like to announce a number of funded graduate student positions available for projects investigating human mate choice. Straights and gays differ in the sex of their mates and it is unclear how that influences individuals? assessment of mate attractiveness. Our current studies focus on fa-

cial symmetry and sexually dimorphic facial features, both of which influence human perception of individual attractiveness.

Funding for MS graduate students includes tuition remission, stipend and, if desired, hourly wages for work as a TA. Basics research support is also provided. If interested please contact Cathy Schaeff, schaeff@american.edu. Additional information is available online: about the MS program (http://www.american.edu/cas/bio/programs_media/ms.html) and the department of Biology (<http://www.american.edu/cas/bio/deptprofile.html>).

Science Ambassador American University Washington, DC 20016

kd8550a@american.edu

GeorgiaTech EvolBiol

Georgia Institute of Technology - Graduate Studies in Evolutionary Biology.

The School of Biology at the Georgia Institute of Technology seeks graduate students interested in Evolutionary Biology. The department is in the midst of expansion with renewed focus towards evolutionary biology, evolutionary ecology, evolutionary and behavioral genomics, and integrative approaches to biological systems (systems biology). We aim to build strength in these areas of our graduate program via collaborations among School of Biology faculty and with faculty from other top-ranked programs in Science and Engineering. We are especially interested in students who want to explore the interface of ecology, behavior, genetics, development, evolution and engineering. Faculty in Evolutionary Biology include:

Chris Klausmeier: Theoretical and aquatic ecology, <http://www.biology.gatech.edu/professors/klausmeier.html>

Michael Goodisman: Molecular ecology, Behavioral ecology, <http://www.biology.gatech.edu/professors/goodisman.html>

Mark Hay: Evolutionary Ecology, <http://www.biology.gatech.edu/professors/hay.html>

Julia Kubanek: Chemical Ecology, <http://www.biology.gatech.edu/professors/kubanek.html>

John McDonald: Genome Evolution and Cancer, <http://www.biology.gatech.edu/professors/McDonald.htm>

Terry Snell: Environmental Biology, <http://www.biology.gatech.edu/professors/snell.html>

Todd Strelman: Evolution and development of functional systems, <http://www.biology.gatech.edu/professors/strelman.html> Marc Weissburg: Sensory Ecology, <http://www.biology.gatech.edu/professors/weissbrg.html> Jeannette Yen: Sensory Ecology, Oceanography, <http://www.biology.gatech.edu/professors/yen.html> Soojin Yi: Evolutionary genomics, Molecular evolution, <http://www.biology.gatech.edu/professors/yi.html> To learn more about specific opportunities in graduate education at Georgia Tech, interested students should contact individual faculty directly, or should consult <http://www.biology.gatech.edu/programs.html>. J.T. Strelman Assistant Professor School of Biology The Georgia Institute of Technology 310 Ferst Drive Atlanta, GA 30332-0230 404-385-4435 (office) 404-385-4436 (lab) 404-894-0519 (fax department) 404-897-3395 (fax home) E-mail: todd.strelman@biology.gatech.edu <http://www.biology.gatech.edu/professors/strelman.htm> <http://www.biology.gatech.edu/professors/strelman.htm>

IdahoStateU ComputationalEvolBiol

PhD position: Computational Evolutionary Biology

A five-year doctoral position is available to work on the computational analysis of alternative splicing and natural selection with Michael A. Thomas at Idaho State University in Pocatello, ID.

This position is funded by the Pharmaceutical Research Manufacturers Association of America (PhRMA) and the National Institutes of Health (NIH). The salary is approximately \$15,000/yr in addition to benefits, tuition/fees and an research budget of \$2000/yr Starting date should be around mid-2005. The ideal candidate will be independent and motivated, have some programming skills and a background in molecular evolutionary genetics. Information about the research in our lab is described on our web page: <http://egg.isu.edu> Pocatello is nestled in the mountains of southeast Idaho about a two hour drive from Salt Lake City, Jackson Hole, Yellowstone & Grand Teton National Parks, City of Rocks (climbing area), Sun Valley, and other attractive locations. ISU's Biology Department has about 100 graduate students and nearly 40 faculty members. Information about the department and university can be found at: <http://www.isu.edu/departments/bios/> For any questions about this PhD position, email

mthomas@isu.edu

Michael A. Thomas Assistant Professor Department of Biological Sciences Idaho State University Pocatello, ID 83209-8007 ph: (208) 282-2396 fax: (208) 282-4570 url: egg.isu.edu

mthomas@isu.edu

MarieCurieNetwork EvolAnimalForm

9 EARLY STAGE STUDENTSHIPS (PHD OR SHORT-TERM TRAINING) AND 8 EXPERIENCED RESEARCHER FELLOWSHIPS (POSTDOCTORAL) ARE AVAILABLE IN THE MARIE CURIE RESEARCH TRAINING NETWORK "ZOONET":

DEVELOPMENT AND EVOLUTION OF ANIMAL FORM: TRAINING MODERN COMPARATIVE ZOOLOGISTS.

ZOONET brings together 9 leading European research groups from 5 European countries for a co-ordinated, multidisciplinary study of the evolution of animal diversity and form.

The training network will recruit 9 early stage researchers with 0-4 years experience (minimum B.Sc. or equivalent) and 8 experienced researchers with 4-10 years of experience (postdocs) for long-term studentships/fellowships for 2-3 years. Applications for short-term training visits, between 3-12 months, will also be considered.

The training and research will consist of a diversity of approaches aimed at increasing our understanding of the evolutionary patterns and processes that have resulted in the enormous diversity of animal forms living today. The recruited fellows will benefit from training in relevant aspects of diverse research fields including comparative embryology, molecular systematics, palaeontology, molecular biology and bioinformatics.

ZOONET is funded by the European Unions 6th Framework Programme for four years from 1 Jan 2005. Applicants should not have resided or carried out their main activity in the country of the host institution for more than 12 months in the 3 years immediately prior to the start date.

For details of all available appointments please see www.zoonet.eu.com To apply please send your CV,

a brief letter of intent explaining your motivations and project interests and the contact details of 2 academic referees to the team leader at your preferred host institution.

Team leaders: Max Telford. University College London, UK. m.telford@ucl.ac.uk Michael Akam. Cambridge, UK. akam@mole.bio.cam.ac.uk Detlev Arendt. EMBL, Germany. arendt@embl.de Maria Ina Arnone. Naples, Italy. miarnone@szn.it Michalis Averof. Iraklio Crete, Greece. averof@imbb.forth.gr Graham Budd. Uppsala, Sweden. graham.budd@pal.uu.se Richard Copley. Oxford, UK. copley@well.ox.ac.uk Wim Damen. Cologne, Germany. damen@uni-koeln.de Ernst Wimmer. Goettingen, Germany. ewimmer@gwdg.de

Co-ordinator: Dr Max Telford, Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 20 7679 2554, Fax +44 20 7679 7096 email: m.telford@ucl.ac.uk

– Dr Max Telford Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax: +44 (0)20 7679 7096

<http://www.ucl.ac.uk/biology/new/admin/-staffpages/telford/telford.html> Zoonet website: <http://www.zoonet.eu.com> m.telford@ucl.ac.uk
m.telford@ucl.ac.uk

MaxPlanck ComputationalBiol

Dear colleague,

we are happy to announce the International Max Planck Research School for Computational Biology and Scientific Computing, a joint graduate program of the Free University of Berlin and the Max Planck Institute for Molecular Genetics, Berlin.

Applications are invited for a PhD program in the fields of Computational Biology and Scientific Computing. The PhD program is designed as a 3-year program starting in October.

The closing date for applications is April 1st, 2005.

We were grateful if you could communicate the announcement to your students. A poster can be downloaded from

<http://www.imprs-cbsc.mpg.de/download/-poster2005.pdf> For further details and the application

procedure, please visit

<http://www.imprs-cbsc.mpg.de> Kind regards,
the IMPRS-CBSC team

International Max Planck Research School for Computational Biology and Scientific Computing (IMPRS-CBSC) c/o Hannes Luz Max Planck Institute for Molecular Genetics | Tel: +49 30 8413 - 1154 Computational Molecular Biology | Fax: +49 30 8413 - 1152 Ihnestrasse 73 | Email: luz@molgen.mpg.de D-14195 Berlin, Germany | www.imprs-cbsc.mpg.de Hannes Luz <luz@molgen.mpg.de>

MichiganStateU CyanobacterialControl

Graduate Position- Molecular Biology/Freshwater Ecology/Public Health

We are seeking a graduate student at the MS or PhD level, beginning Fall 2005, to join a multi-disciplinary research team investigating the promotion and suppression of harmful cyanobacterial blooms by exotic filter-feeders (dreissenid mussels), and the consequences of increases in toxic cyanobacteria for public health. The project is a collaboration among faculty and scientists from Michigan State University and the Great Lakes Environmental Research Laboratory (NOAA). We are looking for a student with interests and/or experience in the molecular genetics of phytoplankton in the context of ecological, evolutionary and/or public health questions. Potential student projects include: comparative fitness of cyanobacterial genotypes under varying nutrient and grazing regimes, early-detection of toxic and grazing-resistant cyanobacterial genotypes, evolutionary relationships among coexisting cyanobacterial genotypes.

A minimum of three-years of stipend support, in the form of RA-ships and TA-ships (which include tuition waiver and health insurance), is available given satisfactory progress toward the degree. Additional funding to support the student's research activities will also be provided. The student will have the opportunity to collaborate with scientists at both MSU and GLERL, and access to well-equipped molecular biology facilities at MSU.

Please review requirements for acceptance into the FW program at MSU (<http://www.fw.msu.edu/>-

graduates/index.htm), and email a CV and unofficial copies of transcripts and GRE scores to Dr. Sarnelle (sarnelle@msu.edu), before applying.

Scientists involved in the project include:

Dr. O. Sarnelle (<http://www.fw.msu.edu/people/sarnelle/index.html>) Dr. J. Rose (<http://www.fw.msu.edu/people/RoseJoan/index.htm>) Dr. S. Hamilton (<http://www.kbs.msu.edu/Faculty/Hamilton/Index.htm>) Dr. S. Peacor (<http://www.msu.edu/~peacor/>) Dr. H. Vanderploeg (<http://www.glerl.noaa.gov/about/pers/profiles/vanderploeg.html>) Dr. M. Dionisio Pires

NHMLondon Phylogeography

PhD position:

PhD in PHYLOGEOGRAPHY AND EVOLUTION (London) The evolution of biodiversity in blackflies of the Gulf of Guinea- one of the global hot-spots of endemism.

The position is based in London jointly between the Natural History Museum and Queen Mary University of London.

Funding is available to cover the full cost of EU-based students (including the UK). Students from outside the EU would have to cover the higher University fees.

Details can be obtained from <http://alpha.qmul.ac.uk/~ugbt112/> Richard A Nichols Professor of Evolutionary Genetics Tel: +44 (0)20 7882 3058 Web Page [Heredit Office 10.30-18.30] Map showing our location

Richard Nichols <r.a.nichols@qmul.ac.uk>

NetherlandsInstEcol Birds

The Department of Animal Biology at the Netherlands Institute of Ecology (NIOO-KNAW), Centre for Terrestrial Ecology seeks a PhD student for the interdisciplinary research programme on the genetics, development and function of behavioural syndromes (strategies), or personalities, in a wild territorial songbird: the great tit. These avian personalities have a strong, context dependent influence on life history traits that are

under natural selection.

Function description The PhD student will carry out a project on the functional aspects of personalities in natural populations of a territorial passerine, the great tit (*Parus major*). He/she will extend the long-term data set of measurements of personalities in a natural population and analyze these data on context- and frequency-dependent selection on personality, and its consequences for the population structure. He/she will experimentally manipulate the frequencies of the different personalities in the the same population to test hypotheses for the coexistence of different personalities. The candidate will work in a small team of research scientists, assistants and students involved in the general project on the influence of developmental, mechanistic and functional aspects of personalities on life history traits and population structure.

Function requirements The candidate should possess an appropriate university qualification (BSc or MSc, depending on the country) in (Evolutionary) Biology, Ecology, Behavioural Ecology or Population Genetics, a background in experimental and quantitative approaches and an interest in population genetics or theoretical biology. The candidate should be willing to work flexible hours as required by the project in a team and have good social, verbal and writing skills. A driver's licence is needed to do the fieldwork

Conditions of employment The appointment will be for 4 years starting on the 1st April 2005, and be in accordance with the regulations of the Royal Netherlands Academy of Arts and Sciences. The gross monthly salary will increase gradually from 1.813, – in the first year to 2.283, – in the fourth year.

Information For additional information please contact Dr Pieter Drent (p.drent@nioo.knaw.nl) tel. 031-264791255 or Dr Marcel Visser (m.visser@nioo.knaw.nl) tel. 031-264791253. A short project description can be obtained from P. Drent. Information on the Netherlands Institute of Ecology (NIOO), the Centre for Terrestrial Ecology and the Department of Animal Population Biology can be found at <http://www.nioo.knaw.nl>. Application Applications, quoting the reference number (CTE-PVD-05088) and including a detailed Curriculum Vitae and the names of three scientific referees, should be sent to Prof. Dr J.A. van Veen, Centre Director, Centre for Terrestrial Ecology, NIOO-KNAW, P.O. Box 40, 6666 ZG Heteren, The Netherlands or by e-mail to h.vanveen@nioo.knaw.nl. Closing date 26 February 2005.

The Netherlands Institute of Ecology (NIOO-KNAW) focuses on fundamental, strategic research into indi-

vidual organisms, populations, ecological communities and ecosystems. More than 240 staff are employed at the three centres (including the central management). The Centre for Limnology (CL) in Nieuwersluis focuses on freshwater ecology. The Centre for Estuarine and Coastal Ecology (CEME) in Yerseke deals with ecosystems in brackish and salt water, and the emphasis at the Centre for Terrestrial Ecology (CTE) in Heteren is on land-based ecology. The Netherlands Institute of Ecology is a research institute of the Royal Netherlands Academy of Arts and Sciences (KNAW).

P.Gienapp@nioo.knaw.nl

Greig, D. Louis, E. J., Borts, R. H. and Travisano, M. (2002) Hybrid speciation in experimental populations of yeast. *Science* 298: 1773-1775

–
Duncan Greig

The Galton Laboratory Department of Biology University College London Wolfson House 4 Stephenson Way London NW1 2HE

Office +44 (0)20 7679 5106 Lab +44 (0)20 7679 5113 Fax +44 (0)20 7679 5052

Duncan Greig <d.greig@ucl.ac.uk>

UCollegeLondon ReproductiveIsolation

SUBJECT: PhD studentships at UCL

TEXT: PhD studentships at the Department of Biology, University College London.

The Department expects to receive a number of Research Council studentships starting September 2005. If you are interested in applying for the following project, please send a CV and a brief cover letter by email to Duncan Greig (d.greig@ucl.ac.uk)

Using single chromosome transfers between yeast species to identify the genetic bases of reproductive isolation

Saccharomyces cerevisiae can mate with other *Saccharomyces sensu stricto* species, but the resulting hybrids are sterile, producing inviable gametes. The sterility is caused, in part, by genes from one species that are incompatible with genes from the other (Greig et al 2002). Such recessive hybrid incompatibilities are often called speciation genes. This project will identify chromosomes carrying speciation genes. We will transfer single chromosomes from *Saccharomyces paradoxus* to *Saccharomyces cerevisiae* to determine whether or not each is compatible. The method to be used is modified from Chambers et al (1996). A genomic library will then be screened to identify the incompatible genes. The project will suit those with good laboratory skills and an interest in evolutionary genetics.

References Chambers, S. R., Hunter, N., Louis, E. J. and Borts, R. H. (1996) The mismatch repair system reduces meiotic homeologous recombination and stimulates recombination-dependent chromosome loss. *Molecular and Cellular Biology* 16:6110-6120

UCologne Evo Devo

U COLOGNE.Evo.Devo: 10 PhD Fellowships are available at the University of Cologne, Germany

The International Graduate School in Genetics and Functional Genomics offers a three-year PhD programme. Research covers all aspects of cellular and molecular genetics in plant, animal and microbial systems. Projects with a focus on molecular aspects of evolution and evo-devo are available in the groups of D. Tautz, S. Roth, T. Wiehe. M. Melkonian and W. Werr.

The programme starts with a six-month rotation and course period, followed by a Ph.D. project in one of the participating groups. Seminars and training courses complement the research work. Comprehensive support is provided throughout the duration of the project. The programme language is English, and no tuitions apply.

10 competitive three-year fellowships (initially 1000 EUR, then 1250 EUR per month) are available. In addition, up to 10 students with self-provided funding may be selected.

Applications for fall 2005 must be submitted until March 11, 2005.

For information on the application process and the admission requirements, please visit our website: www.uni-koeln.de/bio-graduateschool <<http://www.uni-koeln.de/bio-graduateschool>> .

Thanks a lot and best regards,

Sebastian –

Dr. Sebastian Granderath Programme Coordinator In-

ternational Graduate School in Genetics and Functional Genomics University of Cologne Zùlpicher StraÙe 47 D-50674 Kùln, GERMANY

phone: +49(0)221-470-7727 fax: +49(0)221- 470-1632
 sebastian.granderath@uni-koeln.de <http://www.uni-koeln.de/bio-graduateschool> Sebastian Granderath
 <sebastian.granderath@uni-koeln.de>

UGroningen 2 EvolGenetics

In the Evolutionary Genetics Group, Centre for Ecological and Evolutionary Studies (CEES) in the Faculty of Mathematics and Natural Sciences of the University of Groningen, two PhD positions are available:

1. Ph.D position in evolutionary genetics for studying the genetic basis of inbreeding depression

We are looking for a Ph.D. student for a research project that aims to elucidate the nature of the genes that cause inbreeding depression in model insect species.

Job description Inbreeding depression is currently an important phenomenon in conservation genetics, but is also considered as a main driving force for evolutionary processes such as recombination, the evolution of sex, the evolution of mating systems, etc. Inbreeding depression has been documented to occur in many organisms and has been shown to affect the survival probability of populations. Nevertheless, even today remarkably little is known about the nature of the genes causing inbreeding depression. Considering the new developments in the analyses of complex traits, such as QTL analysis and several omics-techniques, it is now timely to tackle this problem. We like to address a number of basic questions on the genetic architecture of inbreeding depression in two model systems with different reproductive modes, the diploid fruitfly *Drosophila* and the haplodiploid wasp *Nasonia*. Questions will focus on determining the number of genes involved, the nature of these genes (major and minor, dominance vs overdominance), and the mode of expression of these genes (sex specific, epistasis, conditional).

This PhD project will be linked to an ongoing collaborative project with the Department of ecology and Genetics (Prof. V. Loeschcke) of University of Aarhus (DK) on part of the same issues.

Ph.D position for four years We are looking for a masters or equivalent degree in biology with preferably a

strong background in population and evolutionary genetics. The project is expected to be very demanding and asks for a very creative mind. The candidate should have a strong interest in molecular and evolutionary genetics research and affinity with experimental work on insects. Good proficiency of the English language is required. The candidate is supposed to attend a few graduate courses (<10% of time). The project should result in a Ph.D. thesis. We offer a four year position with an annual stipend of Euro 17000. The position is open to all EU members and affiliates, except Dutchmen

The group The Evolutionary Genetics group is part of the Centre for Ecological and Evolutionary Studies (CEES) in the Faculty of Mathematics and Natural Sciences of the University of Groningen. Areas of research include evolution of reproductive systems, conservation genetics and life-history evolution; main model organisms are *Drosophila* and parasitic wasps. Research into the consequences of genetic erosion and inbreeding depression for the persistence of endangered species is a major research line of the group. The group provides a lively, internationally oriented, scientific environment with excellent facilities. The group takes part in the National Research School "Functional Ecology" which offers advanced courses in ecology and evolution.

Information For more information and a detailed description of the research programme: Prof. Dr. Kuke Bijlsma, tel: +31 50 363 2117; r.bijlsma@rug.nl Prof. Dr. Leo W. Beukeboom, tel: +31 50 363 8448 (or 2092), l.w.beukeboom@rug.nl Dr. Louis van de Zande, tel: +31 50 363 2126, email: l.p.w.g.m.van.de.zande@rug.nl <http://www.bio.rug.nl/evogen> applications Send applications, including a detailed CV and names + e-mail addresses of persons that can be approached for references, before March 1 2005 to either one of the above, preferably by e-mail

2. Ph.D position in evolutionary genetics for studying sex determination in *Nasonia*

We are looking for a Ph.D. student for our research project on the genetic mechanisms of sex determination in the haplodiploid wasp *Nasonia*. The project is funded by the Netherlands Scientific Organisation (NWO).

Job description Haplodiploidy is a mode of reproduction that occurs in a number of groups (e.g. Hymenoptera): males are haploid, females are diploid and heteromorphic sex chromosomes are absent. There is a longstanding interest in elucidating the underlying genetic mechanisms of haplodiploid sex determination. In this project, we like to address if sex determination

cascades in Hymenoptera compare to those of other insects. The research will focus on determining the number and nature of genes involved in sex determination of the parasitic wasp *Nasonia*. This species is an emerging model organism for analysing complex traits, is easy to culture and handle, and a number of genetic tools and mutant lines are available. It is to be expected that its entire genome sequence will be available soon. You will use genetic, cytogenetic and molecular

— / —

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>

UHawaiiManoa InsectConservation

Insect Conservation on top of a Volcano Life history, evolution, population structure, and conservation management of the Wekiu Bug

Position Announcement Graduate Research Assistantship in Insect Conservation, Ecology and Evolution
Period: To begin approximately August 15, 2005, for 1 year. Renewable annually for up to 4 years, contingent upon progress.

Background: The wekiu bug (*Nysius wekiuicola*) is restricted to cinder substrate habitat between 11,715 and 13,796 feet on the slopes of the Mauna Kea volcano, Hawaii Island. The current and historic population sizes of the wekiu bug are not known, although lower numbers during recent trapping efforts suggest that the species may be in decline, possibly due to development of Astronomy research facilities. In addition to conservation management, the study system presents many interesting evolutionary questions. The wekiu bug is a flightless predator of dead or dying insects blown up on to the snowfields that blanket the volcano periodically in the winter and spring. A putative sister species occurs on the neighboring Mauna Loa volcano, but both may be independently derived from a lowland, volant, herbivorous ancestor. Because the wekiu bug appears dependent on specific cinder conditions and snowfall, it may be limited to particular sections of the volcano, and persist in genetically substructured populations. Duties: Assess the impacts of habitat alteration on Wekiu bug populations including the development of rigorous quantitative field experiments. Develop laboratory-

rearing protocols and discover natural history traits including fecundity, phenology, and habitat preference. Use molecular techniques to understand evolution and population structure. Will be responsible for designing and conducting laboratory experiments at UH Manoa, and fieldwork on the Mauna Kea Volcano on the Big Island of Hawaii.

Minimum Qualifications Bachelor's degree in a biological science from an accredited university or college with a minimum 3.0 GPA, and competitive GRE scores. A strong background and/or interest in insect biology, and/or molecular biology, population modeling and/or conservation is highly desirable. Student must be in excellent physical condition since fieldwork will occur at very high elevations, and often under cold conditions. Approximately 30 days of fieldwork per year. Must be accepted in the Entomology Graduate Program (MS or PhD) at the University of Hawaii, Manoa. Salary: \$15,558 - \$25,000 per year depending on qualifications and degree pursued (MS/PhD), plus benefits, tuition waiver and field and laboratory research funding, including inter-island travel. To Apply: Must be admitted to the University of Hawaii Graduate School (requires application, GRE, see: <http://www.hawaii.edu/graduatestudies/admissions/html/admissions.htm>). Send letter of application, informal transcript, list of GRE scores (General test), and names and contact information for 3 academic references to Dr. Daniel Rubinoff, Department of Plant and Environmental Protection Sciences, University of Hawaii at Manoa, 3050 Maile Way, Gilmore 310, Honolulu, HI 96822; or, preferably, by email to: rubinoff@hawaii.edu

Closing Date: April 2, 2005

The University of Hawaii is an Equal Opportunity / Affirmative Action Institution

rubinoff@hawaii.edu

ULouisianaMonroe SystMalacology

Masters Student position in systematic malacology

I am looking to recruit one student to do research on the systematics of non-marine snails through the Museum of Natural History at the University of Louisiana at Monroe. The students project will employ morphological and molecular data to study the biodiversity and evolution of either the freshwater genus *Elimia* or the

land snail family Polygyridae. Stipends, paid through teaching assistantships, are available on a competitive basis through the Department of Biology at ULM. The stipend is \$8,000 for nine months and includes a tuition waiver. Interested students are encouraged to apply soon, as assistantships are limited.

Qualifications: Student must be admitted to the Master of Science Degree Program in Biology for the Fall 2005 semester and have an interest in systematics. Experience with generating molecular data (PCR, DNA sequencing, etc.) is required; experience working with snails preferred. Graduate program application materials are available at <http://www.ulm.edu/gradschool/admis.html>. Information on my research can be found at <http://homepage.mac.com/russminton/index2.htm>. Information on the department is at <http://www.ulm.edu/biology>. Russ Minton, Ph.D. Molecular Genetics Lab Coordinator & Curator of Invertebrates Museum of Natural History Assistant Professor, Department of Biology University of Louisiana at Monroe Monroe, LA 71209-0520 ph: 318-342-1795 fax: 318-342-3312 <http://homepage.mac.com/russminton/index2.htm> Russ Minton <minton@ulm.edu>

UManchester PhylogenomicsWorkflow

A WORKFLOW FOR PHYLOGENOMICS: STUDYING AND CAPTURING HOW PEOPLE WORK

A BBSRC-funded* PhD studentship for a bioinformatics project at the University of Manchester (www.manchester.ac.uk) to start September 2005.

Molecular phylogenetics, or phylogenomics when applied to complete genomes, is central to the appropriate analysis of genomic data and in particular to comparative studies, because it is evolution that explains the relationships between divergent genomes. Furthermore, to fully understand the evolution of viruses, genomic data is the only available information for study. Unfortunately, much research effort, often of significant medical importance, is performed on similar data sets by distributed researchers using disparate and occasionally flawed analysis methodologies. Thus, decisions made by a researcher can have an impact on the outcome of the analysis to the extent that conflicting phylogenetic relationships are obtained (for an example see Worobey et al., 2002). The aim of this project is to

implement and standardise a computer-based workflow that captures best practise for the appropriate phylogenetic and statistical analysis of comparative data sets. The implementation and management of the workflow will make use of Grid-enabled middleware, myGrid, an EPSRC e-Science project at the University of Manchester (Stevens et al., 2004).

Informal enquiries can be addressed to the PhD project supervisors: Dr. David Robertson (david.robertson@manchester.ac.uk) or Dr. Robert Stevens (robert.stevens@manchester.ac.uk). MSc in Bioinformatics or Computational Biology preferred, or equivalent experience.

Formal queries and applications should be directed to the Faculty of Life Sciences Graduate School: <http://www.ls.manchester.ac.uk/postgraduate> and Miss Kate Barugh (kate.l.barugh@manchester.ac.uk) at (0161) 275 5608.

References: Worobey M, Rambaut A, Pybus OG, and Robertson DL (2002) Questioning the evidence for genetic recombination in the 1918 "Spanish flu" virus. *Science* 296:211; Stevens RD, Tipney HJ, Wroe CJ, Oinn TM, Senger M, Lord PW, Goble CA, Brass A, and Tassabehji M (2004) Exploring Williams-Beuren syndrome using myGrid. *Bioinformatics* 20 S1:I303-I310.

*See www.bbsrc.ac.uk/funding/training/eligibility.pdf for details on eligibility.

robertson@bioinf.man.ac.uk

UNevadaReno ComputationalEvolBiol

PhD position: Computational Evolutionary Biology

I (Guy Hoelzer) am seeking a new PhD student to work on computational modeling and analysis of the spatial architecture of gene pools. There are a great many open questions to be addressed regarding the influence of isolation by distance on evolutionary dynamics (the rates and localization of evolutionary processes) and spatial self-organization (symmetry breaking in spatially manifested dynamical systems) in biological systems, so there is flexibility in the particular set of questions to be addressed in this student's dissertation. For example, the dissertation could focus primarily either on theory development through the systematic exploration of well-defined, generic conditions, or on specific situ-

ations with a goal of informing ecosystem or wildlife management practices. A blend of both aspects would be ideal.

The dissertation project envisioned for this student is not currently funded by sources external to the university, so the student's stipend would initially be based on a Teaching Assistantship. An NSF grant proposal to support this project, including a Research Assistantship for this student will be submitted this Spring, and we will continue to seek external RA support as needed. Information about the Reno area and our graduate program in Ecology, Evolution, and Conservation Biology (EECB) can be found online at <http://www.eecb.unr.edu/>. For any questions about this PhD position, email hoelzer@unr.edu.

Guy Hoelzer

Department of Biology University of Nevada Reno
Reno, NV 89557

Phone: 775-784-4860 Fax: 775-784-1302

"Guy A. Hoelzer" hoelzer@unr.edu

UNewOrleans ConservationBiol

Regents Fellowship in Conservation Biology at the University of New Orleans

The Department of Biological Sciences at the University of New Orleans announces a Doctoral Fellowship for fall 2005. The fellowship provides support for four years and includes a full tuition waiver, an annual stipend of \$22,000, and an allowance for research supplies and travel. The Department of Biological Sciences offers opportunities for graduate research in ecology, genetics, systematics, evolution, reproductive biology, physiology and biochemistry. Applicants must be U.S. citizens. For more information, send e-mail to biograds@uno.edu or see the website: <http://biology.uno.edu/>. <http://biology.uno.edu/>. Application materials for the PhD program can be obtained online or by writing to: Director of Graduate Studies, Department of Biological Sciences, University of New Orleans, New Orleans, LA 70148. Review of applications will begin February 15, 2005.

Nicola M. Anthony, Assistant Professor, Department of Biological Sciences University of New Orleans 2000 Lakeshore Drive New Orleans LA 70148

Tel. (504) 280-1362 Fax. (504) 280-6121 Email: nan-

thony@uno.edu

UNewcastle BarnacleVariation

NERC CASE studentship available at University of Newcastle, UK.

Only UK students are eligible.

Applications are invited for a NERC Industrial CASE PhD studentship on the causes of variation in the adhesion of barnacles. Understanding how adhesion varies between populations living under different environmental conditions is the main objective of this project and differences in adhesion between different populations will be interpreted in relation to their genetic makeup. This project is a collaboration between the School of Biology (Drs Jeremy Thomason and Kirsten Wolff) and International Paint Ltd (Dr David Williams). We are seeking candidates who will relish learning a wide variety of laboratory methods. Undergraduate or masters level experience of molecular techniques and a good understanding of basic genetics is essential. The closing date for applications is: Friday 1st April and the project will begin in September 2005.

For further information and how to apply, please follow the link: <http://www.ncl.ac.uk/biol/postgrad/jt.phd.1.htm> Best wishes, Kirsten

Dr. Kirsten Wolff Reader in Evolutionary Genetics University of Newcastle, School of Biology Ridley Building, room 461, Newcastle NE1 7RU, UK phone: (+44) 0191 222 5626 fax: (+44) 0191 222 5229 <http://www.staff.ncl.ac.uk/kirsten.wolff/> <http://www.bioprofiles.co.uk/> <http://www.ncl.ac.uk/biol/> Kirsten Wolff Kirsten.Wolff@newcastle.ac.uk

UdeNeuchatel PlantSurvival

The Swiss National Centre of Competence in Research (NCCR) "Plant Survival in Natural and Agricultural Ecosystems"

The NCCR Plant Survival is a network of scientists from different Swiss institutions who work on interdisciplinary subjects, and on the transmission of new basic knowledge into practice.

The structure of the NCCR Plant Survival centres around four Modules each of which is made up of two to three Thematic Groups: Natural and Agro-ecosystems, Disease Resistance and Pest Control in Grapevine, Energy and Resources, and Statistics and Modelling.

Thematic groups: 1) Multitrophic Interactions, 2) Genetic Introgression and Ecological Consequences, 3) Evolution and spread of potentially invasive plants, 4) Grapevine diseases and resistance mechanisms, 5) Development of novel control methods for grape moths based on their sex pheromones and host plant attractants, 6) Plastid Function and Plant Survival, 7) Mycorrhiza development and functioning, and its effect on soil structure, 8) Plant - fungi - bacterial interaction in the Ca - oxalate cycle: relationship with calcite biomineralisation and its consequences on soil properties, and 9) Statistical and Dynamical Modelling.

Women are strongly encouraged to apply. Applications including the letter of motivation, CV, contact details of two referees should be submitted by April 1, 2005. Starting date, Spring 2005, for up to 4 years.

Please indicate which of the 9 thematic groups you are interested working with.

For further information on conditions and individual research projects visit our web site, www.unine.ch/nccr/pages/research/res.jobs.htm NCCR Plant Survival Université de Neuchâtel Emile-Argand 11 2007 Neuchâtel Switzerland plant.survival@unine.ch

UppsalaU ComplexTriats

PHD STUDENT IN BIOINFORMATICS Linnaeus Centre for Bioinformatics, Biomedical Center, Uppsala University, Uppsala, Sweden.

We are seeking a highly motivated individual interested in pursuing a PhD degree in Bioinformatics within an ongoing research project on development of Analytical Methods for Genetic Dissection of Multifactorial traits. A suitable candidate will be offered a four year PhD student position with the full benefits of employees at the University.

Most complex traits and disorders in humans (e.g. diabetes and cardiovascular disease), animals (e.g. growth and fat deposition) and plants (e.g. disease resistance and yield) have a multifactorial rather than monogenic background. A better understanding of the underlying mechanisms of these traits is needed for applications in fields such as medicine, evolutionary biology and agriculture. By studying the associations or linkage between genetic markers and relevant phenotypes, chromosomal segments harbouring genes affecting the phenotype (Quantitative Trait Loci or QTL) can be identified. This PhD student project is part of a larger, ongoing effort to develop novel methods for identifying QTL in various types of populations with an aim to better understand the genetic mechanisms underlying complex trait expression. The project is part of a collaboration between the Department of Genetics and Pathology and the Linnaeus Centre for Bioinformatics at Uppsala University. Currently, four other graduate students and three Post-Doc are active within the project.

Applicants should have an undergraduate degree in genetics, statistics, animal science, bioinformatics, computer science, or a related field. Programming skills in UNIX, FORTRAN or C++, knowledge of QTL mapping, linkage mapping or genetic association studies would be a plus.

The Linnaeus Centre for Bioinformatics offers a superb interdisciplinary working environment located at the heart of biomedical research at Uppsala University. Access is available to the Swedish national supercomputing center. Uppsala is located 40 minutes north of Stockholm by train, 20 minutes from Stockholm's international airport.

Please submit your CV, a letter describing your research interests and skills, relevant reprints, and contact information for three references. Send all materials:

by mail: Linnaeus Centre for Bioinformatics ATTN: Job Code QG (for Quantitative Genetics position) Box 598, Biomedical Center SE- 751 24 Uppsala, Sweden.

by email: qg-app@lcb.uu.se

For more information, please contact Örjan Carlborg (qg@lcb.uu.se, 46 (0) 18 471 6691). Screening of applicants will immediately and will continue until a suitable candidate has been found.

Jobs

Barcelona EvolBiol	22	SouthAfrican NatlBiodiversityInst MolSyst	30
ChicagoBotanicGardens SummerInternships	22	TuftsU MolEvolInfDisease ResAssist	30
ColoradoStateU Genomics	23	UArizona ResTech	30
ColumbiaU Lecturer EcolEvol	23	UChicago ResTech EvolGenetics	31
CornellU MammalianGenomics EvolDisease	24	UDurham SleepEvolution	31
DukeU LabManager EvolGenetics	24	UGroningen MarineBenthicEcolEvol	32
FrenchPolynesia Entomology	24	UGroningen MarineBenthicEcolEvol 2	32
GaterslebenGermany SixMonthInternship	25	UHawaiiHilo PlantEvolGeneticist	33
HollingsMarineLab EvolMolBiol	25	UHawaiiManoa LabTech MarineInvertPhylo	34
ImperialCollege PopulationBiology	26	UMassachusettsAmherst ChairEvolMicrobiol	34
MBL WoodsHole SeniorResAssist	26	USheffield ConservationGenetics	35
MichiganStateU SummerAssist EvolEcol	27	USheffield FieldAssist SparrowStudy	35
NorthCarolinaStateU EvolEcol	27	UVirginia SummerStudent	36
NorthernArizonaU MicrobialPathogenEcolEvol	27	UZurich SystematicBotany	36
NorthernArizonaU MolEvolMicrobialPathogens	28	WesternWashingtonU Minority SummerInterns	37
OldDominionU EvolViralDiseases	28		
Paris AnimalFunctionalGenomics	29		

Barcelona EvolBiol

A three-year lectureship is available at the Evolutionary Biology Unit, Universitat Pompeu Fabra (Barcelona). Teaching duties include (but are not limited to) undergraduate Zoology; courses should be taught either in Catalan or in Spanish.

The successful applicant will undertake his/her research in any of the current areas at the Unit (<http://www.upf.es/cexs/recerca/bioevo/index.htm>), or in any related field such as comparative genetics/genomics or molecular phylogeny.

The position is aimed at a postdoctoral level; a non-tenure-track full-time "Ayudante Doctor" or similar contract is offered, for a maximum of three years.

Applicants should send: * CV * A letter describing their research interests * Two names (with e-mail addresses and phone numbers) of researchers for reference before February 15th, 2005, to cristina.santa@upf.edu

Francesc Calafell <francesc.calafell@upf.edu>

ChicagoBotanicGardens SummerInternships

Summer Field Research for undergrads or recent graduates

Are you interested in gaining field research experience and learning about the ecology and evolution of plant-pollinator and plant-herbivore interactions? We are looking for field assistants (two undergraduates and one recent grad) for an NSF-funded research project on habitat fragmentation of the tallgrass prairie. We are investigating how small plant population size influences inbreeding, pollination, and herbivory in the purple coneflower (*Echinacea angustifolia*).

No experience is necessary, but you must be enthusiastic and hard-working. You will survey natural plant populations, measure fitness and floral traits in experimental plots, hand-pollinate plants, observe & collect insects, and assist in all aspects of research. Housing is included and there is a stipend. There are opportunities for doing an independent project.

If you want more information or wish to apply, please look here <http://www.cbs.umn.edu/~wagenius/jobs/-index.html> or contact Stuart Wagenius. Applications due 14 March 2005.

— Stuart Wagenius, Ph.D. Institute for Plant Conservation Chicago Botanic Garden 1000 Lake Cook Road Glencoe, IL 60022

phone: 847 835 6978 fax: 847 835 5484

email: swagenius@chicagobotanic.org

SWagenius@cbgnt.chicagobotanic.org

ColoradoStateU Genomics

Hi all, We are initiating a search to fill two positions in genomics, broadly defined. We are interested in people using genomics tools to study species interactions and/or biological invasions.

My department is in the Ag. College, and so we are particularly interested in the following types of study organisms or model systems: insects (herbivores and 'natural enemies' in particular, vectors as well), plant pathogens, plants (as they interact with insects, pathogens, competitors), environmental weeds (i.e. invasive plants).

Below is the official short ad. Use the link to get to the longer version. If you have any questions, let me or the search chair know.

Best, Ruth

The Department of Bioagricultural Sciences and Pest Management at Colorado State University invites applications and nominations for two full-time, tenure-track Assistant Professor academic faculty positions in genomics of pests, pathogens, or invasive plants in agricultural or natural systems. Additional information is available at <http://www.colostate.edu/Depts/-bspm/Positions/positions>. Applications and nominations will be considered until the position is filled; however, for full consideration, applications should be submitted by March 25, 2005. Please address inquiries, nominations, and applications to: Dr. Dennis L. Knudson, Search Committee Chair, Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523-1177. Phone: 970.491.5261, Fax: 970.491.3862, Email: Dennis.Knudson@ColoState.edu. Communication via email is strongly encouraged. CSU is an EO/AA em-

ployer.

Ruth A. Hufbauer Assistant Professor <http://lamar.colostate.edu/~hufbauer/> Department of Bioagricultural Sciences and Pest Management Colorado State University Fort Collins, CO 80523-1177 USA

office: C147 Plant Sciences (970) 491-6945 lab: E113/115 Plant Sciences (970) 491-5984 fax: (970) 491-3862 email: hufbauer@lamar.colostate.edu

hufbauer@lamar.colostate.edu

ColumbiaU Lecturer EcolEvol

Lecturer position at Columbia University

Columbia University invites applications for a one-year lecturer position in the Department of Ecology, Evolution and Environmental Biology. PhD required. Successful candidate will have a serious commitment and proven record in undergraduate teaching and advising, and will act as Director of Undergraduate and Post-baccalaureate Studies for 30-40 undergraduate majors and concentrators. Candidate will co-teach introductory course in ecology and evolution, upper-division conservation biology and participate in team-taught senior seminar. Two additional advanced courses in areas of organismal biology will be negotiated based on candidate's specific expertise. Appointment to begin July 2005, pending vacancy. Interested candidates should send CV, statement of teaching experience and interest, and three letters of reference to Chair, Department of E3B, Columbia University, 1200 Amsterdam Avenue, New York, NY 10027. Application review will begin March 18 and proceed until position is filled. Women and minorities are encouraged to apply. Columbia University is an Equal Opportunity/Affirmative Action Employer.

Lourdes Gautier Departmental Administrator Ecology, Evolution, and Environmental Biology Columbia University 1200 Amsterdam Avenue New York, NY 10027 212-854-9987

Lourdes Gautier <lg2019@columbia.edu>

CornellU MammalianGenomics EvolDisease

Faculty Positions in Mammalian Genomics/Genetics of Disease

The Baker Institute for Animal Health at Cornell University has openings for two tenure track faculty. The Institute has a distinguished record of discovery in areas benefiting both animal and human health, and seeks outstanding scientists using genomic approaches to investigate the biological basis of disease consistent with the Institute's mission. Applications at all levels are encouraged from, but not limited to, individuals with interests complementary to the Baker Institute's strengths in infectious disease and immunology, reproductive biology, and musculoskeletal disease. Recruited faculty will be members of an appropriate department in the College of Veterinary Medicine and will have opportunities to participate in the University's campus-wide New Life Sciences Initiative and the newly established Center for Vertebrate Genomics. Successful candidates will be expected to have, or to develop, extramurally funded research programs and to contribute to professional (DVM) and graduate education. The Institute offers competitive start-up packages and new laboratory facilities in a supportive, interactive research environment. For more information, go to: <http://bakerinstitute.vet.cornell.edu/facsearch.html>. To apply, send (preferably as a single PDF file) a cover letter, Curriculum Vitae, names of and complete contact information for three references, and statement of research plans to: John Schimenti, Ph.D. (jcs92@cornell.edu), c/o Charlotte Williams (cw25@cornell.edu), College of Veterinary Medicine, Cornell University, T9014A VRT, Ithaca, NY 14853. Review of applications will begin immediately and will continue until the positions are filled.

Cornell is an Equal Opportunity / Affirmative Action Employer / Educator

Charlotte Williams <cw25@cornell.edu>

DukeU LabManager EvolGenetics

I'm hiring a lab manager to help set up and manage my laboratory, which will be moving to the Duke University Biology Department in May, 2005. Please feel free to write me with any questions, particularly about the research projects: NOOR@DUKE.EDU See also: <http://fds.duke.edu/db/aas/Biology/faculty/noor> ASSOCIATE IN RESEARCH (LAB MANAGER), EVOLUTIONARY GENETICS

An Associate in Research position is available in the Duke University laboratory of Biology Department Associate Professor Mohamed Noor beginning May 1, 2005. Responsibilities: 35% Isolation and molecular analysis of DNA using PCR and other techniques; 30% Maintenance of fruit fly cultures and collection of unmated flies; 15% Supervision of undergraduates; 10% Data entry and analysis of results from molecular and phenotypic assessments; 10% Ordering and laboratory maintenance. Required qualifications: B.S. or B.A. degree in biology or related field, some experience with basic laboratory techniques. Additional qualifications desired: experience with molecular biology protocols, experience with handling of *Drosophila* fruit flies, experience with supervising others. Anticipated hire date is May 1, 2005. Application deadline is April 1, 2005, or until candidate is selected. Submit letter of application and resume to: Dr. Mohamed Noor, NOOR@DUKE.EDU . Duke University is an Equal Opportunity / Affirmative Action Employer.

FrenchPolynesia Entomology

JOB Entomology

Applicants are invited for a technician position in Entomology at the Plant Protection Department of French Polynesia, in the Agricultural Entomology Laboratory.

The successful applicant will be hired as a volunteer for development (CVD: contrat de volontaire au développement de la Polynésie Française). Due to the restrictions of the contract, the post is open to people who originate from French Polynesian or live in French Polynesia for at least 5 years. For more information about eligibility, please visit: <http://www.service-public.pf> The applicant will be involved in the classical biological control program conducted against the glassy-winged sharpshooter (GWSS) *Homalodisca coagulata* (Hemiptera: Cicadellidae), a major exotic pest in French Polynesia. This program is conducted by the

University of California, Berkeley in association with the Plant Protection Department of French Polynesia. This program aims to introduce the exotic mymarid egg parasitoids *Gonatocerus ashmeadi* and *G. trigguttatus* (Hymenoptera: Mymaridae) to control *H. coagulata* populations.

The successful candidate will be primarily responsible for parasitoids mass rearing and will participate to experimental and field work.

The position is 24 months and could be renewable. The successful candidate should have a MS in entomology or ecology with experience in laboratory work. The candidate must be highly motivated, independent, reliable, and a good communicator. Computer skills such as the use of word processing, spreadsheet, and e-mail programs are essential.

For more information or to apply please contact Dr Julie Grandgirard : juliegrandgirard@yahoo.fr. Please send a cover letter, a CV and names and contact information for three references. Applications will be reviewed as received, until the position is filled.

juliegrandgirard@yahoo.fr

GaterslebenGermany SixMonthInternship

I have funding for a 6 month student internship in my research group from the The International Association for the Exchange of Students for Technical Experience (IAESTE; www.iaeste.org). Candidates must be registered at a university or other center for advanced studies in order to qualify for the grant, and furthermore they must provide a letter which shows that they would be returning to their university after this internship.

I am presently setting up a research group to study the evolution of asexual reproduction (apomixis) in the plant genera *Boechera* and *Hypericum*. The proposed internship in my lab would be to primarily work on the optimization and analysis of microsatellite variation in *Hypericum perforatum* (St. John's Wort). The work would include standard laboratory methods (DNA extraction, PCR preparation, etc.) followed by analyses using an automated genetic analysis system. The candidate should also be comfortable with computers since much of the downstream work will involve genetic analysis software.

My lab is found in the department of Cytogenetics

at the Institute for Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany (www.ipk-gatersleben.de). This internationally-recognized institute has a wonderful array of resources in widely different areas of plant research. Gatersleben is a small village found near the Harz Mountains, and is approximately 2 hours from Berlin and 1 hour from Leipzig and Halle. Check out the following web sites for more Harz information:

<http://starfsfolk.khi.is/salvor/fyrstimai/nornir-harz-fjollin.htm>

<http://www.deutsche-welle.de/dw/article/-0,1564,1087191,00.html>

For those who like hiking, mountain biking and skiing, the Harz Mountains are beautiful and have lots to offer.

While knowledge of German would be helpful, it is not required. The internship would begin in late spring/early summer 2005. Please feel free to contact me for further information.

Dr. Tim Sharbel Apomixis Research Group Dept. of Cytogenetics Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) Corrensstraße 3, D-06466 Gatersleben Germany www.ipk-gatersleben.de tel: +049 (0)3948 25608 fax: +049 (0)3948 25137

HollingsMarineLab EvolMolBiol

Molecular Biologist/Biochemist Position Immediate Opening

A contract scientist position is available to assist in scientific and technical oversight of a multi-disciplinary research program using molecular, genetic and biochemical approaches for assessing the health status of marine organisms. The focus of the work will be on scleractinian corals and their associated microbial communities. The research may be conducted collaboratively with investigators from academic, state and other federal institutions. The work location is at the NOAA National Ocean Service, Center for Coastal Environmental Health and Biomolecular Research (CCEHBR), Charleston, SC. Qualifications: Masters Degree with three years of research experience or Ph.D. Degree in Cellular/Molecular Biology, Biochemistry, or other relevant discipline. The candidate must demonstrate technical competency in advanced genomics or proteomics. Experience in developing, planning, and implementing

research projects, as well as communication and interpersonal skills, is also required. Experience in working with invertebrate systems is desirable. Salary: \$50,541 p.a. and includes health benefits. Submit resume and three references via mail or fax (843) 762-8737 to Dr. Cheryl Woodley, NOS/CCEHBR, Hollings Marine Laboratory, 331 Fort Johnson Road, Charleston, SC 29412. Please note that e-mail applications will not be accepted. Closing Date: Applications must be received by February 25, 2005. Position is to be filled on or about March 11, 2005. Inquiries may be made to Dr. Cheryl Woodley at (843) 762-8811 or cheryl.woodley@noaa.gov

– Cheryl Woodley, Ph.D. Coral Health and Disease Program

DOC/NOAA/NOS/NCCOS Center for Coastal Environmental Health and Biomolecular Research Hollings Marine Laboratory 331 Fort Johnson Rd Charleston, SC 29412 843.762.8862 Phone 843.762.8737 Fax cheryl.woodley@noaa.gov

Cheryl Woodley <Cheryl.Woodley@noaa.gov>

ImperialCollege PopulationBiology

Lecturer, Senior Lecturer or Reader in Ecology / Population Biology

Imperial College London Division of Biology Silwood Park

We seek to appoint a permanent staff member who works in the broad area of ecology/ population biology (i.e. including population, community or ecosystem issues using theoretical and/or experimental approaches) to work on plant, animal or microbial systems; and pure or applied problems. We are particularly interested in candidates who will bring new skills to the community of ecologists and population biologists at Silwood Park.

The appointment will be within the Division of Biology, a RAE 5* department in the Faculty of Life Sciences. The division includes the Ecology & Evolution Section and the NERC Centre for Population Biology, both of which are based at Imperial College's Silwood Park campus where research is carried out on a wide range of topics in ecology, evolution and associated fields.

PhD in a relevant subject and a strong research publication record is essential. You will be expected to develop an independent and externally-funded research

programme, and to contribute to teaching at undergraduate and postgraduate levels. The appointment level will depend on experience and we will consider candidates who seek part-time positions.

Salary: Lecturer: £32,620 ? £36,714; Senior Lecturer / Reader: min. £40,118

For further information and application forms contact Mrs Diana Anderson at Division of Biology, Imperial College London, Silwood Park Campus, Ascot, Berks, SL5 7PY (d.anderson@imperial.ac.uk).

Closing date: 11 March 2005 –

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

<http://www.bio.ic.ac.uk/research/iowens/welcome.htm> Ian Owens <i.owens@imperial.ac.uk>

MBL WoodsHole SeniorResAssist

SENIOR RESEARCH ASSISTANT [JBPC SRA], FULL TIME

Josephine Bay Paul Center for Comparative Molecular Biology and Evolution The Marine Biological Laboratory, Woods Hole, MA

Description: The Marine Biological Laboratory is seeking applicants for a full-time year round Senior Research Assistant position with the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution as a Computer Systems Administrator. This is a grant funded position.

Duties: Primary duties will include but not be limited to management of a large and diverse computing environment dedicated to basic biological research. Primary responsibilities include network management (switches, NFS, file synchronization), account and LDAP management, systems security, hardware maintenance, data integrity and back-up strategies, and web site/database development. Secondary responsibilities include telecommunications, including management of PolyCom Video Teleconferencing. Additional responsibilities include basic training of staff in the UNIX operating system.

Education/Experience: The successful applicant should have a B.A. or M.S. and advanced course work in computer science or have extensive experience working as a

Programmer and Systems Administrator. Experience with heterogeneous operating systems required (Linux, Mac OS, Windows, etc). Experience with Sun Grid Engine, beowulf clusters or other forms of parallel computing strongly desired. Scientific programming (C, C++, Perl, Java) and web and database software (SQL, PHP) skills a plus. The successful applicant is expected to have good team skills and be able to work with a high level of independence with broad supervision.

Please apply to: Applicants should submit a cover letter, curriculum vitae, and a list of three references including telephone numbers and email address to: Marine Biological Laboratory, 7 MBL Street, Attn: Human Resources reference code [JBPC SRA], Woods Hole, MA 02543; telephone 508 289 7422; email: resume@mbl.edu An Equal Opportunity/Affirmative Action Employer/Non-smoking workplace.

Deadline: Until a suitable candidate is identified.

MichiganStateU SummerAssist EvolEcol

Summer assistant needed for participating in an NSF-funded research project on the evolutionary ecology of plant-insect interactions. Specifically, I am looking for an undergraduate (or a recent graduate) interested in gaining hands-on research experience in greenhouse and field experiments to evaluate the response of an annual plant to insect herbivory. There is a stipend. For more information please contact Gabriela Bidart-Bouzat. Applications are due March 15, 2005. No previous experience is required but a CV and a letter of reference will be requested. I particularly encourage Minority students to apply.

Gabriela Bidart-Bouzat, PhD Kellogg Biological Station Michigan State University 3700 E Gull Lake Drive Hickory Corners, MI 49060 bidartbo@hotmail.com

“M. Gabriela Bidart-Bouzat”
<bidartbo@hotmail.com>

NorthCarolinaStateU EvolEcol

ECOLOGIST - EPV 01-16-0502

The Department of Zoology at North Carolina State University invites applications for a 12-month tenure-track position at the *ASSISTANT PROFESSOR* level. Applicants should have an outstanding record of research achievement, with expertise at any level of ecology from genes to communities, to complement and enhance existing strengths in the department and college. The successful applicant is expected to establish an energetic, extramurally funded research program and to teach and advise students at the undergraduate and graduate levels. Further information is available on the North Carolina State University *website: <http://www.cals.ncsu.edu/zoology>*. Applicants should submit a curriculum vitae and statements of research and teaching interests and have supporting letters sent from three references to: *Dr. Thurman Grove, Department of Zoology, **Box 7617, North** **Carolina** State University, **Raleigh**, **NC** **27695-7617*. Review of applications will begin 1 March 2005 and continue until an excellent candidate is identified. North Carolina State University is an Equal Opportunity/Affirmative Action employer. NC State welcomes all persons without regard to sexual orientation. Persons with disabilities who need accommodations in the application process should contact Susan Marschalk, Department of Zoology, via telephone at (919) 515-2741, or via e-mail at susan_marschalk@ncsu.edu

NorthernArizonaU MicrobialPathogenEcolEvol

“Assistant Professor- Microbial Pathogen Ecology and Evolution

The Department of Biological Sciences at Northern Arizona University (NAU; <http://www.3.nau.edu/-biology/>) invites applications for a tenure-track position to perform basic research on the ecology, mechanisms of evolution, and host-pathogen interactions of a variety of microbial pathogens, including *Yersinia pestis*, *Bacillus anthracis*, *Francisella tularensis*, *Brucella* spp., *Burkholderia mallei*, *Burkholderia pseudomallei*, and *Coxiella burnetii*. The research will be conducted primarily in a large, state-of-the-art microbial pathogen molecular genetics laboratory (35+ staff and students). In addition to communicating the results of the above research by preparing scientific articles and presenting results at national and international conferences, this position will be expected to develop new

research projects from conception to funding procurement, including preparing grant proposals and writing interim and final reports for funding agencies. Other duties will include training and advising postdoctoral fellows, technicians, and graduate and undergraduate students, as well as assisting with day to day management of the research facilities. Qualifications include a Ph.D. in a relevant field, at least one year of postdoctoral experience in a research setting, and prior experience managing a research group and/or facility. The successful candidate will have knowledge of advanced statistical and phylogenetic methods, including experience at GIS modeling of infectious disease, experience with molecular genetic analysis, field-based handling and sampling techniques of microbial pathogen hosts and vectors and demonstrated success in obtaining grant funding. As this position will be funded from extramural "soft" monies until tenure is granted, success at obtaining extramural funding will be a major criterion for granting tenure. The appointment includes nine months of salary support with additional salary to be generated through extramural funding. Please submit C.V., a description of research interests, a statement of teaching philosophy, a statement that describes your commitment to (and/or evidence of) working effectively with diverse student, faculty, and staff populations, and three letters of recommendation to: Microbial Pathogen Ecology and Evolution Search Committee, NAU, Box 5640, Flagstaff, AZ, 86011-5640. Please visit <http://hr.nau.edu/m/content/view/299/-315/>, vacancy# 554806 for more information. E-mail Paul.Keim@nau.edu if you have questions. Position is open until filled and subject to availability of funding. Review of applications will commence 31-March-2005. NAU is an Equal Opportunity Affirmative Action Institution. Minorities, Women, Persons with Disabilities and Veterans are encouraged to apply. "

James Schupp <James.Schupp@nau.edu>

NorthernArizonaU MolEvolMicrobialPathogens

"The Center for the Study of Dangerous Pathogens at Northern Arizona University (<http://www.kgl.nau.edu/>) has two mid level (Research Specialist) and one entry level (Research Technician) laboratory positions open. The Center conducts research towards characterizing molecular evolutionary mechanisms of microbial pathogens, such as Bacillus

anthracis, Yersinia pestis, Francisella tularensis, among others. The large, 35+ person facility utilizes state-of-the-art methodologies and equipment in pursuit of this research. The ideal candidates for the mid level positions will have a Masters degree in an appropriate field or a Bachelors of Science degree and two years of laboratory research experience. Experience with microbial genotyping, fluorescent DNA fragment analysis, molecular genetic data analysis, and working in a BSL-2 environment a plus. Supervisory experience also a plus. Candidates for the entry level position should have a Bachelors degree in an appropriate field. The Center is located at 7,000 feet above sea level on the mountain campus of Northern Arizona University in Flagstaff, AZ. For more information and application materials, contact the NAU Human Resources Department at 928-523-2223, HR.Contact@nau.edu, or go to the NAU HR Jobs website at <http://hr.nau.edu/m/content/view/3/25/>. Reference Vacancy# 554799 for the Research Specialist positions, and Vacancy# 554805 for the Research Technician position."

James Schupp <James.Schupp@NAU.EDU>

OldDominionU EvolViralDiseases

DESPITE THE GENERIC, MILK-TOAST NATURE OF THIS AD, OUR DEPARTMENT IS VERY INTERESTED IN INDIVIDUALS STUDYING THE ECOLOGICAL AND EVOLUTIONARY ASPECTS OF VIRAL DISEASES USING ANY SYSTEM, PLANT OR ANIMAL. THE INDIVIDUAL HIRED IS EXPECTED TO BE INTERACTIVE WITHIN OUR NEWLY ORGANIZED PROGRAM IN ECOLOGY, EVOLUTION AND INTEGRATIVE BIOLOGY. FEEL FREE TO CONTACT ME FOR ADDITIONAL INFORMATION.

Virologist The Department of Biological Sciences at Old Dominion University invites applications for a tenure-track Assistant Professor for August 2005. Applicants in any area of virology who will strengthen existing programs in the department are especially encouraged to apply. Applicants must have a Ph.D. degree in Microbiology or related field. Postdoctoral training and teaching experience is preferred. The successful candidate will be expected to establish an externally funded research program and participate in teaching in our undergraduate and graduate programs and must possess the communication skills necessary

to be effective teachers. For information about the Department of Biological Sciences and for links to the campus and Old Dominion University, see our website at <http://web.odu.edu/sci/biology/index.html>. Please send curriculum vitae, statement of research interests and teaching philosophy, along with names of at least three references with e-mail addresses, telephone numbers and addresses to Dr. Wayne Hynes, Virology Search Committee Chair, Department of Biological Sciences, Mills Godwin Building, Old Dominion University, Norfolk, VA 23529-0266. Electronic submission of materials to virologist@odu.edu is encouraged. The review of applications will begin on 15 March 2005, and continue until the position is filled. Old Dominion University is an equal opportunity, affirmative action employer and requires compliance with the Immigration Reform and Control Act of 1986.

William J. Resetarits, Jr., Ph.D. Professor Department of Biological Sciences Old Dominion University Norfolk, Virginia 23529 757 683-3763 fax: 757 683-5283

“Truth is born into this world only with pangs and tribulations, and every fresh truth is received unwillingly. To expect the world to receive a new truth, or even an old truth, without challenging it, is to look for one of those miracles which do not occur” (from an interview with Alfred Russel Wallace published posthumously in 1913).

More Ecological Quotes <http://www.unifr.ch/biol/ecology/sayingseco.html> William Resetarits <wresetar@odu.edu>

Paris AnimalFunctionalGenomics

Permanent Assistant Professor position in Animal Functional Genomics, at the Institut national agronomique Paris-Grignon

In France, the Institut national agronomique Paris-Grignon (INA P-G) is the main institution of higher education in the fields of Agriculture and Agri-food. A permanent position in Animal Functional Genomics is open at the “Maître de Conférences” (Assistant Professor) level in the Animal Breeding and Genetics Team, within the Animal Sciences Department of INA P-G.

The position requires 50% teaching and 50% research. The successful candidate will teach (mainly in French) at all levels of the INA P-G 3-year curriculum, in the Animal Genetics and Animal Production Masters, at

the doctoral level, and in professional training sessions. He (she) is expected to develop a new course(s) on Animal Genomics and its applications in Animal Breeding. The research activity will be developed within the INRA/INA P-G joint research unit Animal Genetics and Diversity, in Jouy-en-Josas (close to Paris), and will benefit from the Transcriptomics facilities located in the Jouy INRA centre. Collaborations will be developed with other laboratories within the framework of national programmes (AGENAE) as well as European programmes (RIVAGE) or networks (EADGENE). The research activity will deal with gene expression of animals from local livestock breeds in relation to their environment, as an original contribution to the investigation of the genetical basis of adaptation.

A PhD is required and research experience in the field of functional genomics is necessary. Candidates are expected to be interested by conducting studies with applications in Animal Breeding and Animal Genetic Resources. Ability to work within a predominantly French speaking environment is required. Good skills in speaking and writing English are also necessary.

A full description of the position is available on line: <http://www.inapg.fr/rh/contacts2005.htm> (the present position is the last one in the list). General conditions for application and administrative information are also available at: <http://www.inapg.fr/rh/concours-ens.htm> Deadline for application: August 5, 2005. Discussion with the candidates and practical examination will occur in Paris, between October and December (definitive dates to come). The position will be available on January 01, 2006. For further information, please contact Prof. Etienne Verrier: verrier@inapg.fr

Prof. Etienne VERRIER verrier@inapg.fr

UMR Génétique et Diversité Animales

INA Paris-Grignon / Dépnt. Sciences Animales / GER Génétique Elevage et Reproduction INRA / Dépnt. Génétique Animale

16 rue Claude Bernard, 75235 PARIS cedex 05 Tél. + 33 - (0)1 44 08 17 48 ; Fax. + 33 - (0)1 44 08 86 22 http://www.inapg.fr/ens_rech/dsa/ger_genetique/-gergen.htm

SouthAfrican NatlBiodiversityInst MolSyst

Research leader: molecular systematics/ conservation genetics South African National Biodiversity Institute, Kirstenbosch, Cape Town

The Leslie Hill Molecular Systematics Laboratory at Kirstenbosch is one of the foremost facilities of its kind in Africa and includes a DNA bank for the South African flora. SANBI is seeking a dynamic individual to direct the laboratory and to provide leadership for research. The current research programme, which can be expanded, uses DNA sequencing and AFLP markers to better understand phylogenetic relationships and population/conservation genetics of the South African flora. The successful candidate will be expected to identify key research questions and make links to other projects within SANBI and outside institutions, manage the research programme and DNA bank, contribute to mentoring and capacity building, and source additional funds for research. A PhD with appropriate research experience as well as the ability to lead a research programme are prerequisites for the position.

Additional information, including a job description, can be obtained from www.sanbi.org. The successful candidate will have excellent interpersonal skills, as well as sound oral and written command of English. Command of one other official language would be an advantage. A valid, unendorsed Code B driver's licence is essential.

SANBI offers a salary package of R 193 920.00 per annum, plus additional fringe benefits that include attractive medical and pension schemes.

Please note that applications must be accompanied by a letter of motivation as to why the applicant should be favourably considered for the position.

SANBI reserves the right not to fill this position.

All applications will be considered, with the understanding that, in terms of the SANBI Employment Equity Plan, preference will currently be given to candidates from the designated groups.

Contact Glynnis Oosthuizen on (021) 799 8635 or preferably, forward an abbreviated CV by e-mail to recruitment@sanbi.org or fax (021) 762 3229. Postal applications are to be addressed to The Deputy Director: Human Resources, South African National Biodiversity Institute, Private Bag x7, Claremont, 7735.

Closing date: 25 February 2005

If no response has been received within 21 days after closing date, candidates may assume that their applications were unsuccessful

Gail Reeves <Reeves@sanbi.org>

TuftsU MolEvolInfDisease ResAssist

Research Assistant Position announcement:

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

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

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

Review of applications will begin immediately.

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

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

UArizona ResTech

Research Technician / Research Specialist

A research position is available in the laboratory of

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

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

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

UChicago ResTech EvolGenetics

Header: Research technician: evolutionary genetics

I am looking for a research technician to work in my laboratory at the University of Chicago. Our research is on the evolutionary genetics of *Drosophila*, concentrating largely on the genetics of speciation. The position is funded through August of 2006, and will continue after that if the current NIH grant is renewed.

The job is full time, with full benefits, and salary depends on qualifications, although a bachelor's degree in biology or the equivalent is required. Some experience with *Drosophila* is preferred but not necessary, as well as familiarity with the standard computer programs (Excel, MS Word, Statview, etc.). Please get in touch with me at j-coyne@uchicago.edu or at 773-702-1105 if you have further questions.

Interested individuals can apply for the position

electronically (and get further information) through the University of Chicago's Employment Website at <http://jobopportunities.uchicago.edu/applicants/jsp/-shared/frameset/Frameset.jsp?time=1107440048272>

Jerry Coyne Dept. Ecology and Evolution University of Chicago 1101 E. 57 Street Chicago, IL 60637 USA

Jerry Coyne <j-coyne@uchicago.edu>

UDurham SleepEvolution

UNIVERSITY OF DURHAM

DEPARTMENT OF ANTHROPOLOGY

POST DOCTORAL RESEARCH ASSOCIATE: PHYLOGENETIC ANALYSES OF SLEEP EVOLUTION

£21,640 - £24,820 per annum depending upon qualifications and experience.

We seek to appoint a post-doctoral research associate to work in the Evolutionary Anthropology Research Group within the Anthropology Department on a two-and-a-half year project funded by the National Institutes of Health. The position is available immediately (and ideally not later than May 2005) and will investigate the evolution of sleep patterns in mammals using phylogenetic methods applied to comparative data. The project will be supervised by Dr Robert Barton in conjunction with Charles Nunn (University of California) and Patrick McNamara (Boston University). The research associate will be involved in collecting and analyzing comparative data on mammalian sleep patterns in relation to life history variables, ecology, physiology and neuro-anatomy.

Post reference number: 0688. Closing date: 1 March 2005.

Further details of the post and an application form are available on our website (<https://jobs.dur.ac.uk>) or telephone 0191 334 6499; fax 091 334 6495. Contact Robert Barton (r.a.barton@durham.ac.uk, tel 0191-334-6171) for informal discussion of the post.

Dr Robert Barton

Reader & Deputy Head of Department

Evolutionary Anthropology Research Group, Department of Anthropology, University of Durham, 43 Old Elvet, Durham DH1 3HN, UK.

Tel +44(0)191-334-6171 Fax +44(0)191-334-6101

robert barton <r.a.barton@durham.ac.uk>

j.l.olsen@rug.nl

UGroningen MarineBenthicEcolEvol

UGroningen MarineBenthicEcolEvol

2

Dear EvolDir Readers:

The University of Groningen, Department of Marine Biology (Centre for Ecological and Evolutionary Studies) has an Assistant Professorship position open under its new tenure track policy.

The job description calls for development of an innovative research programme in marine population genetics/community ecology of benthic organisms. We are especially interested in the development of ecological genomic approaches for studying adaptation, hybrid zones, stress responses, statistical phylogeography... The Department is a participant in the FP6 Networks of Excellence Marine-Genomics-Europe and MarBEF (Marine Biodiversity and Ecosystem Function).

It is the intention that the candidate, having achieved a favorable tenure review, will join the permanent faculty of the university. Our target candidates are senior post-docs with an absolute minimum of 2 years of post-doctoral experience. The candidate will take on a regular faculty role with respect to teaching, grant writing and administrative duties.

The Assistant Professor will join the Benthic Ecology and Evolution Group headed by Prof. Jeanine L. Olsen within the Centre for Ecological and Evolutionary Studies.

Please consult the attached formal advertisement for further details.

If you are interested in the position but are not sure that you fit the profile, please contact Prof. Jeanine Olsen (j.l.olsen@rug.nl) or Prof. Wytze Stam (w.t.stam@rug.nl).

Jeanine Olsen & Wytze Stam

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

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

Tenure Track Position in Marine Benthic Ecology & Evolution

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

The Department of Marine Benthic Ecology & Evolution (MarBEE) and Department of Ocean Ecosystems constitute the Marine Biology cluster within the Centre for Ecological and Evolutionary Studies (CEES) in the Faculty of Mathematics and Natural Sciences of the University of Groningen, and also takes part in the National Research School "Functional Ecology". Areas of research include population genetics and genomics of benthic plants and animals, ecophysiology of marine phytoplankton, and marine behavioral mechanics and energetics of zooplankton, zoobenthos and nekton. The present position is available within the MarBEE group which focuses on the population structure, dispersal, phylogeography and speciation in seagrasses, seaweeds and benthic fish; and also on the speciation of corals and their symbionts. Methods from molecular ecology, genomics and metagenomics are the tools of choice.

The position:

The MarBEE group invites applications for a tenure track position at the Assistant Professor level. We seek a population geneticist/community ecologist with a strong interest and/or background in benthic marine organisms. The successful candidate must have an active interest in the development of ecological genomics. Ideally, we would like to have someone who is both field and laboratory oriented.

Personal profile:

Applicants must have a Ph.D. degree and a strong record of research accomplishments. The successful candidate will actively participate in the teaching and research programmes of the faculty and the Center for Ecological and Evolutionary Studies (CEES). He/she will develop an innovative research programme in marine population genetics and genomics of benthic organisms. The successful candidate will need to have the following qualifications:

A doctorate in the field of marine biology with spe-

cial interest in population genetics, molecular ecology and/or environmental genomics.

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

Excellent research, teaching and organizational qualities

Strong research accomplishments, as expressed in a list of (first author) publications.

Evidence of successful acquisition of external funding.

The University of Groningen can offer you excellent career prospects:

The Faculty of Mathematics and Natural Sciences is offering young, talented researchers positions which are at the level of Assistant Professor via the tenure-track system. Researchers are given the opportunity to develop their own line of research. The faculty's career policy is characterized by flexible personnel management with a focus on the individual. Academic achievements are seen as being central to the academic career, and ample opportunities for professional development and supplementary training and education are offered. Arrangements for training in the area of teaching will be made with all new employees.

The initial appointment is for 6 years. On completion of 5 years of employment (or possibly sooner) there will be an assessment of performance based on established criteria. If the outcome of the assessment is positive, the Assistant Professor will be tenured and promoted to the rank of Associate Professor.

A salary dependent on qualifications and work experience up to a maximum of ? 4580.00 gross per month (scale 12) for a full-time job.

For information, please contact: Prof. Dr. Jeanine L. Olsen, phone +31 (0)50 363 2250, e-mail: j.l.olsen@rug.nl or Prof. Dr. Wytze T. Stam, phone +31 (0)50 363 2252, e-mail: w.t.stam@rug.nl [http://www.rug.nl/biologie/onderzoek/onderzoekinstututen/cees/](http://www.rug.nl/biologie/onderzoek/onderzoekgroepen/-marieneBiologie/) <http://www.rug.nl/biologie/onderwijs/>

[Applications should include: Cover letter, complete CV, and statement of research vision/motivation. Be sure to include the names and full addresses of three persons that are prepared to write letters of recommendation for you. Send to: Prof. J.L. Olsen, Dept. of Marine Biology, P.O. Box 14, 1750 AA Haren, The Netherlands]

Deadline for application materials is 31 March 2005.

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

Dr. Jeanine L. Olsen Professor Department of Marine Biology Biological Centre, RUG PO Box 14 NL-9750 AA Haren The Netherlands tel: +31-50-3632250 (work); +31-50-3131832 (home) fax: +31-50-3632261 e-mail: j.l.olsen@rug.nl

— / —

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>

UHawaiiHilo PlantEvolGeneticist

Assistant Professors of Biology: Plant Evolutionary Geneticist position number 83380, and Community/Ecosystem Ecologist position number 82643, University of Hawai'i at Hilo Department of Biology, tenure-track, 9-mo, general funds, to begin Fall 2005, pending position clearance and funding.

Duties:

Teach undergraduate and graduate courses in areas of specialization; contribute to the Biology Department undergraduate programs and the MS degree in Tropical Conservation Biology and Environmental Science; develop an independent research program in plant evolutionary genetics or community/ecosystem ecology that is supported by extramural funding; advise students, participate in departmental governance and related University and community service.

Plant Evolutionary Geneticist

Minimum qualifications:

Ph.D. in the biological sciences, a record of student training, teaching experience in biological sciences, and research in plant evolutionary genetics. The ability to work with students from diverse cultural backgrounds is essential.

Desirable qualifications:

Demonstrated teaching expertise in some combination of the following: evolution, botany, genetics, cell biology, and general biology; a successfully funded research program in tropical plant evolutionary genetics and the ability to develop a research program in the Hawaiian or Pacific region with the potential to obtain extramural funding.

Community/Ecosystem Ecologist

Minimum qualifications:

Ph.D. in the biological sciences, a record of student training, teaching experience in biological sciences, and research in community or ecosystem ecology. The ability to work with students from diverse cultural backgrounds is essential.

Desirable qualifications:

Demonstrated teaching expertise in some combination of the following: ecology, botany, conservation biology, and general biology. A successfully funded research program in tropical community/ecosystem ecology with a specialization in microbial ecology, plant-animal interactions, or trophic dynamics preferred. The ability to develop a research program in the Hawaiian or Pacific region with potential to obtain extramural funding.

Pay range:

I3 Salary commensurate with qualifications and experience.

To apply:

Submit a cover letter indicating the position title and position number and how you satisfy the minimum and desirable qualifications, a curriculum vitae, and statements of research and teaching interests. In addition, have 3 letters of recommendation mailed directly by the referees.

Application address:

Dr. Donald Price Biology Search Committee Chair, University of Hawaii at Hilo, 200 W. Kawili Street, Hilo, HI 96720; donaldp@hawaii.edu

Inquiries:

Dr. Donald Price: donaldp@hawaii.edu,

Continuous recruitment:

Review of applications will begin on 7-March-2005 and will continue until the position is filled.

University of Hawaii at Hilo is an EEO/AA Employer D/M/V/W.

Donald Price <donaldp@hawaii.edu>

**UHawaiiManoa LabTech
MarineInvertPhylo**

Lab Technician

A Lab Technician position is available immediately in my lab (Dr. David Carlon) at the University of Hawaii's Manoa Campus. The position is funded for 6 months (full time) or one year (half-time) with the possibility of extension depending on extramural funding. The focus of this position will be to develop molecular markers to determine phylogenetic relationships and population structure of tropical marine invertebrates. The successful candidate will have a minimum of a bachelors degree in a related field, and two years of experience in a molecular biology environment in which increasing levels of responsibility were demonstrated. Coursework and practical knowledge of marine invertebrates will be favorably considered, but are not required. Specific responsibilities include DNA isolation, PCR, construction and cloning of gene libraries, sample preparation for automated sequencing, editing sequence data, using genomic data base and searching tools, running phylogenetic and population genetic software, and data interpretation. General responsibilities include maintaining and purchasing laboratory supplies, assisting with grant proposal and manuscript preparation, and assisting with graduate student training. Salary starts at \$31,596/year. To apply send a cover letter describing your interests and qualifications, a CV, and contact information for three references. You can find additional information on this position at:<http://workatuh.hawaii.edu/>, position #00777771T.

David B. Carlon Department of Zoology 2538 McCarthy Mall, Edmondson 152 University of Hawaii Honolulu, HI 96822

e-mail: carlon@hawaii.edu <<http://www.hawaii.edu/zoology/faculty/carlon.htm>><http://www.hawaii.edu/zoology/faculty/carlon.htm> Office: 808-956-9523 Lab: 808-956-4722 FAX: 808-956-9812

Dave Carlon <carlon@hawaii.edu>

**UMassachusettsAmherst
ChairEvolMicrobiol**

The Department of Microbiology at the University of Massachusetts, Amherst invites applications for the position of Head of the Department of Microbiology. We are seeking an individual with an outstanding research record who can provide energetic and creative leadership for the Department. The candidate's research program should be within the broadly defined area of Mi-

crobiology. It is anticipated that the position will include a tenured appointment at the rank of Professor.

The Department currently has 13 faculty representing the diversity of subdisciplines within microbiology and a proven record of excellence in teaching and research. Opportunities exist to develop strong collaborations with faculty in the Five College Consortium (Amherst, Hampshire, Mount Holyoke and Smith Colleges and the University of Massachusetts), the University of Massachusetts Medical School at Worcester, and the Bay State Medical Center.

Review of applications will begin February 15, 2005, and continue until the position is filled. Applicants should send a letter of application, a curriculum vitae, a summary of research interests and future plans, representative publications, and arrange to have at least three letters of reference sent to: Dr Guy Lanza, Chair Search Committee, Department of Microbiology, 203 Morrill Science Center IV North, 639 North Pleasant Street, University of Massachusetts, Amherst, MA 01003. The University of Massachusetts is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups are encouraged to apply.

More information on the department can be found at <http://www.bio.umass.edu/micro/> Jeffrey L. Blanchard Assistant Professor Department of Microbiology University of Massachusetts Amherst, MA 01003 Office and Lab: Morrill I N330 Tel: 413-577-2130 Fax: 413-545-1578 http://www.bio.umass.edu/micro/blanchard/Lab_About.html Jeffrey Blanchard <blanchard@microbio.umass.edu>

USheffield ConservationGenetics

UNIVERSITY OF SHEFFIELD

DEPARTMENT OF ANIMAL & PLANT SCIENCES

The following posts were advertised in New Scientist on 13 February:

1. Research Technician in Molecular Conservation Genetics
2. Field Technician (Botanist)

The post holders will be required to assist with our UKPopNet conservation genetics project: see <http://www.york.ac.uk/depts/biol/units/ukpopnet/projects/proj1c.htm> 1. Research Technician - Molecular Conservation Genetics

The post holder will assist with molecular genotyping.

Applicants should preferably have experience of molecular genetics and have as a minimum qualification an HNC, or equivalent, in Biology or Biochemistry or a related subject. The post is available for one year from 1 April 2005, in the first instance, with the possibility of renewal subject to further funding.

Ref no: S5658

Closing date: 4 March 2005

For further details and how to apply see <http://www.shef.ac.uk/jobs/> 2. Field Technician

The post holder will assist with the field sampling of plant species. Applicants must have as a minimum qualification an HNC, or equivalent, in Biology or Ecology or a related subject. The post is available for 3 months from 13 May 2005.

This post is available for a period of 3 months from 13 May 2005.

SALARY: Within the scale for Technical staff Grade C: from £13,900 per annum.

Ref no S5659

Closing date: 4 March 2005

For further details and how to apply see <http://www.shef.ac.uk/jobs/> INFORMAL ENQUIRIES: Informal enquiries for both positions may be made to Professor Terry Burke, tel: 0114 222 0096 (e-mail: t.a.burke@sheffield.ac.uk).

USheffield FieldAssist SparrowStudy

Field Assistant Needed for Sparrow Study on Lundy Island

FIELD ASSISTANT needed from around early May to early to mid July 2005 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 (required to get along with people on the island and an ability to get up early (very early sometimes)). Daily routines involve checking nest boxes, nest box watch and setting video cameras. Both physically and mentally challenging so be prepared! Travel within UK, camping fee on the island and food will be covered (if from overseas, some of airfare may be covered). The island is a beautiful place with great

wildlife. For more info on the project, you may want to check the website (<http://www.shef.ac.uk/misc/groups/molecol/lundyparttwo.html>). Please send a letter of interest, resume, and names, telephone numbers, and E-mail addresses of 3 references to SHINICHI NAKAGAWA 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@sheffield.ac.uk

UVirginia SummerStudent

PLEASE FORWARD TO YOUR STUDENTS.

Greetings,

The Mountain Lake Biological Station (<http://www.virginia.edu/~mtlake/mlbs.org>, University of Virginia) announces paid research opportunities for undergraduates and university-level credit courses in field biology. We offer students hands-on experience and training in a wide variety of biological field studies. Students are invited to join us for an exciting and unforgettable summer in a beautiful and stimulating teaching and research environment. Scholarships and financial aid for courses are available.

NSF-Funded Research Experience for Undergraduates (REU) Program <http://www.mlbs.org/REU.html> We match undergraduate students with visiting scientists for 10 weeks of advanced, independent research on a project of the student's own design. REU positions come with a stipend of \$3,500 and pay all room and board expenses. Minority students are especially encouraged to apply. Deadline for receipt of applications is March 1.

Field Courses

<http://www.mlbs.org/courses.html>
mlbs<http://www.mlbs.org/courses.html>

1) Field Entomology May 15 - 29. Upper-level undergraduate and graduate course on the ecology and diversity of insects. 2) Field Geology May 31 - June 24. Introduction to field techniques used by geologists. 3) Ecology Of Wildlife Diseases May 31 - June 24. Intro-

duction to the ecology and evolution of parasites in wild animal populations. 4) Plant Biodiversity And Conservation June 27 - July 22. The extraordinary diversity of the Southern Appalachians will serve as a backdrop to explore the world of plants. 5) Evolutionary Ecology June 27 - July 22. Will examine how individuals, populations, and communities respond to their environments and how those responses are influenced by their evolutionary history. 6) Biodiversity In The Southern Appalachians July 25 - Will teach students how historical processes and current land-use patterns shape the compositions of ecological communities. 7) Ecology And Conservation Of Freshwater Fishes July 25 - August 5. An investigation of the ecology and conservation of freshwater fishes through a series of discussions, lectures, lab and field exercises.

Our field station is located on a mountaintop in southwestern Virginia and is home to a lively research, teaching and social community. For details on these programs, full course descriptions, application material, and a list of research areas see our web page:

<http://www.virginia.edu/~mtlake/mlbs.org> Thank you very much for your help.

Contact our office at : Mountain Lake Biological Station , University of Virginia, 238 Gilmer Hall, PO Box 400327, Charlottesville VA 22904-4327, U.S.A. mlbs@virginia.edu 434-982-5486 .

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake Biological Station Assistant Professor, Department of Biology University of Virginia, 238 Gilmer Hall, P.O. Box 400327 Charlottesville, VA 22904-4327 USA Street Address: 485 McCormick Road 434-982-5486 office (540-626-5227 summer office) 434-982-5626 fax (540-626-5229 summer fax) 434-906-3122 cell Email: enagy@virginia.edu
Personal page: <http://faculty.virginia.edu/nagy> Mountain Lake Biological Station: <http://www.mlbs.org/> enagy@virginia.edu

UZurich SystematicBotany

The Faculty of Science (Mathematisch-naturwissenschaftliche Fakultät) of the University of Zurich invites applications for a

Professorship (Ordinarius, Extraordinarius, or As-

sistant Professor with Tenure Track) in Systematic Botany

at the Institute for Systematic Botany, to commence on October 1, 2007. The new professor is expected to establish and lead a successful research group, contribute to the graduate teaching in Systematic Botany, and the undergraduate teaching in Biology. She or he will find an excellent library, herbarium, laboratory infrastructure, and botanical garden, as well as a stimulating environment. The institute is associated with the Zoological Museum, the Palaeontological Institute and other related research institutes in a School of Biology, and with other botanical Institutes of the University, the ETH and the University of Basel in the Zurich-Basel Plant Science Center. Current research interests at the institute include molecular and morphological phylogenetic systematics, comparative evolutionary biology, and biogeography.

We are looking for excellent researchers in systematic botany with an interest in micro-evolution, palaeobotany, reproductive biology, morphology, or other fields that will complement existing research strengths in the institute.

Applicants are invited to submit by April 31, 2005 a curriculum vitae, a publication list, and a summary of their research interests to Prof. Dr. P. Truöl, Dean of the Faculty of Science (MNF), University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland.

The application material should also be submitted in a single Word or PDF file to jobsmnf@zuv.unizh.ch.

For further information, contact Prof. H.P. Linder, Institute for Systematic Botany, phone +41 1 6358410, email: plinder@systbot.unizh.ch, or visit the institute homepage at www.systbot.unizh.ch ContiElena@access.unizh.ch

Western Washington U Minority Summer Interns

“As I’ve done the past two summers, I’m offering research internships for minority undergraduate students, under my NSF-funded program, Minority Opportunities for Research on Evolution (MORE). The research focuses on the evolution of reproductive barriers in a beetle hybrid zone. For further information, visit the MORE website: www.biol.wwu.edu/~peterson/MORE.html .Please let your students know about this opportunity.

Merrill Peterson Biology Department Western Washington University Bellingham, WA 98225”

Merrill Peterson <peterson@biol.wwu.edu>

Other

ABI CEQ opinions	38	DNA collection in the field	43
ABI3700 PeakHeights	38	Effective vs census pop size answers	43
ABI3700 PeakHeights answers	39	Ernst Mayr passing	44
ABI AFLP primer sequences	40	Ernst Mayr Award Syst Biol	45
ALF sequencing	40	Europe Exchange Grants Insect Parasitoids	45
Aggregation tests	40	Genescan	45
Asteraceae samples	40	Genotyper	46
Bremer support TreeRot	41	Individual genetic distances	46
Bremer support TreeRot answer	41	Intelligent Design	46
Chicago Botanic Garden Field Internship	41	Intelligent Design responses	47
Combining Marker Data	42	Isolation by distance answers	48
Creation Evol Debate Impact	42	Isotopes in seawater	50

Kangaroo cDNA	50	SYBR Green I	55
LifeHistory evolution	50	Software BEAST v1 2	56
Liquid Nitrogen	50	Software DataMonkey Update	56
LongnoseDace samples	51	Software PAPA v2	57
MatrixMill extractions	51	Software PASOS v1	57
NestedCladeAnalysis	51	Software TreeScan	58
NestedCladeAnalysis answers	52	Software for micros	58
PopDensity MatingRate	53	SystBiol2006 CallForSymposia	58
RRTree question	53	Trifolium samples	59
Relation s migration	53	UPretoria PopSizeFluctuations	59
Removing 3rdCodon	54	combining marker data	59
Restorase	54		
SSCP DGGE dHPLC answers	54		

ABI CEQ opinions

Dear colleagues,

I'm putting together a proposal to acquire some sort of automated genotyper (for microsatellite analysis), probably either a Beckman-Coulter CEQ 8000 (which I have some experience with) or an ABI Prism 3100 or 3100 Avant (with which I am completely unfamiliar). I would greatly appreciate the opinions/recommendations as to which system people prefer (if anybody is familiar with both systems), and/or how you like the ABI genotyper. My main considerations include reliability, and approximate running cost per sample. superfast throughput is not so important. Please reply to emacdoug@uwo.ca , thanks in advance for any thoughts on this! Cheers, Beth MacDougall-Shackleton

Dr. Beth MacDougall-Shackleton Assistant Professor
Department of Biology, Univ Western Ontario London,
Ontario, Canada N6A 5B7 Office: 340 BGS; Lab: 341
BGS phone: 519-661-2111 ext 81206

ABI3700 PeakHeights

Dear Evoldir members,

We are using several microsatellite loci to estimate outcrossing and gene flow rates in the perennial herbaceous plant, *Aquilegia coerulea*. While examining our data in Genotyper, we have seen a good deal of variation in the

relative peak heights for heterozygotes at our loci. For any given plant, we can find one of three peak height distributions: 1. The shorter allele is taller than the longer allele. 2. The longer allele is taller than the shorter allele. 3. The peaks are equal in height

Ideally, we would like all of our plants to have the third distribution, but some plants have the first, and other plants have the second distribution. Although differing among individual plants, these distributions will stay consistent for particular individuals on repeat runs (including when changing the number of PCR cycles from 40 to 30).

One major problem is that the ratio of tall peak to small peak varies along a continuous gradient, without any obvious cutoff point. This makes it difficult to designate a minimum peak height below which we will ignore a peak (e.g., 1/3 the height of the taller peak), without the designation being arbitrary and without generating a good number of borderline cases.

We're hoping to do paternity analysis and so have little room for error. If anyone has had similar experiences and knows of techniques that might help even out our peak heights, we'd be very grateful.

Brian Dunphy USDA, ARS Vegetable Crops Dept. of Horticulture Univ. of Wisconsin dunphy@wisc.edu

Below are details of our protocol:

DNA EXTRACTION - DNA was extracted from individual seeds (seeds are tiny, about 1 mg each) using the Qiagen DNeasy kit. - Seeds had been lyophilized prior to DNA extraction.

PCR - Settings: 94 deg. C: 10 minutes 40 cycles: 94 deg. C - 30 seconds; 55 deg. C - 30 seconds; 70 deg. C - 60 seconds Final extension: 70 deg. C -30 minutes 4 deg. C hold - MgCl: 2 mM

SEQUENCING - Two of the microsatellite loci have dinucleotide repeats, the third has trinucleotide re-

peats. - Formamide added to PCR product prior to sequencing - Sequencing performed on an ABI 3700 - Rox Ladder - Did not multiplex - Peaks averaged several thousand fluorescent units in height, but varied considerably

Brian Dunphy USDA, ARS Vegetable Crops Dept of Horticulture University of Wisconsin 1575 Linden Drive Madison, WI 53706 dunphy@wisc.edu Ph. 608-263-1129

ABI3700 PeakHeights answers

Thank you to all who responded to my question about unequal peak heights in heterozygotes following sequencing on an ABI 3700. Below is my original question, followed by the answers:

We are using several microsatellite loci to estimate outcrossing and gene flow rates in the perennial herbaceous plant, *Aquilegia coerulea*. While examining our data in Genotyper, we have seen a good deal of variation in the relative peak heights for heterozygotes at our loci. For any given plant, we can find one of three peak height distributions: 1. The shorter allele is taller than the longer allele. 2. The longer allele is taller than the shorter allele. 3. The peaks are equal in height

Ideally, we would like all of our plants to have the third distribution, but some plants have the first, and other plants have the second distribution. Although differing among individual plants, these distributions will stay consistent for particular individuals on repeat runs (including when changing the number of PCR cycles from 40 to 30).

One major problem is that the ratio of tall peak to small peak varies along a continuous gradient, without any obvious cutoff point. This makes it difficult to designate a minimum peak height below which we will ignore a peak (e.g., 1/3 the height of the taller peak), without the designation being arbitrary and without generating a good number of borderline cases.

We're hoping to do paternity analysis and so have little room for error. If anyone has had similar experiences and knows of techniques that might help even out our peak heights, we'd be very grateful.

#1: couple of thoughts on your ABI peak height problem.

If it is consistently in the same marker (and fairly reg-

ular across samples) you can try 1 of 2 possibilities.

1. Reduce the number of PCR cycles in those where the peaks are high...you seem to have a lot (40) of per cycles?...for radio nucleotides I use 30-35(max) for the fluoro I tend to use between 27-30. By over amplifying in the PCR you could be leaving yourself open to other problems too! 2. Try diluting the PCR product of those samples that are too high.

Can I also ask (probably seem like a dumb question but I am not looking at your initial copy), when you place your DNA's in the PCR mix are they all at the same concentration or are you just assuming that after extraction they will all be about the same?

#2: 1. The shorter allele is taller than the longer allele. 2. The longer allele is taller than the shorter allele. 3. The peaks are equal in height

If I can give my opinion about your situation: If you read about 'stuttering?' (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=9300082&dopt=Abstract) and according to my experience with msats on the 377, I would say that the case number one is the heterozyg. It is expected that the shorter allele should be higher because it is amplified faster. Case two: homozyg. for the longer allele. Typical of stuttering Case three: could be any. You could rely on the stutter pattern of the microsat to make your own idea. It's difficult without seeing the pattern for myself.

Hoping I've answered your question. If stuttering is not the problem, well, I tried. I also read your protocols, and I might have a couple of comments if you don't mind me saying: Final extension: 70 deg. C -30 minutes

It seems long. I used only 5 minutes, you could try less than 30 minutes and see if you get the same quality. - Peaks averaged several thousand fluorescent units in height, but varied considerably

There is an option to adjust the sensitivity of the reading. You can adjust it after saving the run and before the analysis. The other solution is, as I do, to dilute the PCR product in water prior to mix it with the loading buffer. You should try to keep the peaks below 1000, as it says in the manual. When you decide to multiplex your PCR products to save gels, the mixing will work as a dilution and your peaks will be lower. #3: We've been doing SSRs on *Aquilegia* seeds for some time now - you may even be using some of our primers (see attachment) or perhaps Gallaghers? In any case, I think that the reason for your seeing differences in the intensity of the bands (shorter versus longer differing between different seeds) is because you have both maternal tissue

as well as progeny tissue in your extraction. You should amplify both of the maternal plants alleles as well as the paternal contribution. So, if the seed is selfed, you will see two bands (assuming the maternal plant was a heterozygote). If the seed is a homozygote, whichever allele it has will be over-represented but the other maternal allele will still show up. With an outcrossed seed,

— / —

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>

ABI AFLP primer sequences

Does anyone happen to know the core sequences of the MseI and EcoRI AFLP amplification primers provided by ABI? I'd like to use the ABI AFLP kits for a pilot study and then be able to synthesize additional quantities of the chosen selective primers at a lower cost elsewhere. Google searches have turned up nothing, and I am left wondering if ABI's primers are the same as/different from those I see detailed on other websites and in published papers.

Thanks in advance,

Andrea Weeks

NRC Postdoctoral Associate US Army ECBC AMSRD-ECB-RT-BM Bldg E3831 5183 Blackhawk Rd. Edge-wood, MD 21010 tel. 410-436-2719

ALF sequencing

Dear All,

I will be going to another lab to use their ALF EXPRESS machine for some sequencing, here we have an ABI3100.

Now although I cannot seem to find a lot of information on the ALF, it appears to be a mid point between running radionucleotide gels, and the ABI set up. From this I have several questions:-

1. Can anybody direct me to any further sources of information on the ALF? 2. Is there any reason why

comparisons cannot be made between the allelic data from one output with the other i.e. comparing populations? I plan to use several good samples that I have run on the ABI as standards (as well as the normal standard). 3. Any other advice that you feel might be useful.

Many thanks,

Eddie

brede@mpil-ploen.mpg.de

Aggregation tests

Dear Colleagues,

We would be very interested in information on statistical tests that are capable of determining whether distributions of objects (cells, animals, bird nests etc.) are distributed randomly or in aggregated manner in the landscape/ surface (we are only interested in 2 dimensions). Our interest is to compare the tendency for aggregation and so we need to have a statistical test that takes into account the distances among objects and their coordinates (location on the surface) and an effect size estimator. Our search of the literature has not yet landed us with exactly what we are looking for and so we would very much appreciate any information that you may be able to provide us with.

Please send any replies directly to the addresses below,

Thank you very much in advance,

Best regards,

Pauline Manhes (pmanhes@ens-lyon.fr)

Else Fjordingstad (Else.Fjordingstad@snv.jussieu.fr)

Nicolas Schtickzelle (schtickzelle@ecol.ucl.ac.be)

pmanhes@ens-lyon.fr

Asteraceae samples

Rubén Torices, José María Gómez and me (Marcos Méndez) are involved in a project to study the evolution of non-hermaphroditic breeding systems in Aster-

aceae (yes, the whoooooole family with over 1500 genera). To carry out such an ambitious project we request your kind help in collecting for us material from some species/areas which we cannot reach ourselves. You can find more information about the project, and the protocol for the harvest at the following homepage, appropriately named SEXAS:

<http://www.escet.urjc.es/biodiversos/eng/science/-sexas/eng/main.htm> We just need you to send us 30 flowering capitula and/or 30 fruiting capitula of any Asteraceae species you can find. Every species is welcome, including *Bellis perennis*. If you plan to go to Africa, Asia, America or Australia, consider to bring some material for us, or forward this message to any potential helper there. Most Asteraceae are hermaphroditic (over 50%) or gynodioecious (35%), so most of the material we will get will be from those breeding systems. We would appreciate if you can additionally target some of the rare breeding systems as monoecy (11%), andromonoecy (7 genera), gynodioecy (2 genera: *Cirsium* and *Bidens* if I remember right) and dioecy (21 genera: *Archibaccharis*, *Baccharis*, *Heterothalamus*, *Antennaria*, *Anaphaloides*, *Parantennaria*, *Cuatrecasiella*, *Pterygoppapus*, *Sinoleontopodium*, *Mniodes*, *Loricaria*, *Podanthus*, *Hymenoclea*, *Petrobium*, *Bidens*, *Brachionostylum*, *Robinsonia*, *Chersodoma*, *Endocellion*, *petasites*, *Tugarinovia*, *Cirsium*, *Serratula*, *Tarchonanthus*, *Gochnatia*, *Lycoseris*, *Brachylaena* and *Crastystylis*).

Help us also to spread this help request by forwarding it to any potentially interested person.

Thank you in advance for your help.

Best regards,

Marcos

– Marcos Méndez Área de Biodiversidad y Conservación Universidad Rey Juan Carlos c/ Tulipán s/n. E-28933 Móstoles (Madrid) Spain - España (La Banana Mecánica - Fusklandet) Phone:+34 91 488 8249 Fax: +34 91 664 7490 E-mail (NEW!!!): marcos.mendez@urjc.es

Bremer support TreeRot

Hi,

I have been trying to use TreeRot to obtain Bremer

support on a morphology based tree. However, I'm experiencing a problem. In the end of the execution of the *.constraints file (in PAUP), I receive the following message:

“using random trees as a starting point for branch swapping is not allowed when enforcing topological constraints”.

I have tried running the example Duck tree file but the result was the same. I have also tried using different Addition Sequence methods (instead of random) and got always the same message.

Does anyone know how to overcome this problem? Or maybe you know about another program who can also calculate decay indexes... Help with be most appreciated.

Thanks in advance, Antonio.

My email: A.PereiraPagarete@student.uva.nl

Bremer support TreeRot answer

Fellow colleagues,

It turned out that the problem was easier to solve than I thought. In PAUP there's is an option, under Parsimony Settings, which allows us to turn of the use of random trees. Once I did it the program TreeRot ran without any problem. Thanks to those how answered back for your suggestions.

António

A.PereiraPagarete@student.uva.nl

ChicagoBotanicGarden FieldInternship

Below is an advertisement for research internship to work in conjunction with Bureau of Land Management and the National Parks Service offices; predominately in the Western States. This internship provides a invaluable opportunity to gain a wide breath of field experiences and to work in some interesting areas of the country. If you could pass it onto any interested parties or advertise it within your respective departments,

it would be much appreciated. For applications and any additional inquiries please contact Dr Lara Jefferson (ljefferson@chicagobotanic.org)

Cheers

Chicago Botanic Garden's Conservation and Land Management Mentoring Program

Offered in partnership with the Bureau of Land Management and the National Parks Service

Are you interested in conservation biology and natural resource management?

Would you like to gain hands-on experience through a paid internship?

Chicago Botanic Garden's conservation and land management mentoring program is seeking to place twenty outstanding college graduates for five-month paid internships to assist professional staff at Bureau of Land Management (BLM) state and field offices or National Parks. We are recruiting suitable applicants who have skills in one or more of the following areas: GIS Insect ID Forestry Map and compass Reptile ID Soils/geology Plant ID Mammal ID Fieldwork Bird ID Applied ecology Technical writing Species monitoring Wetland ecology Conservation policy Archaeology GPS Endangered Species Act

Each intern will receive training on the Endangered Species Act and related conservation issues at a one-week course. Travel and lodging for the course will be provided. After training, interns will be assigned to work with a mentor at priority BLM or NPS sites throughout the United States; most offices are in the western states. The stipend for the internship is \$1650 per month.

To apply, send a letter of interest, transcripts, resume, and three letters of recommendation to the address below by February 15, 2005 (extended to March 7, 2005). Applicants must have a visa authorized for employment in the United States of America. Interns will be selected by April 15, 2005. The training course is in late-May and internships begin immediately afterward.

Dr. Lara Jefferson Chicago Botanic Garden
1000 Lake Cook Road Glencoe, IL 60022
ljefferson@chicagobotanic.org

<http://www.chicagobotanic.org/-research/conservation/blm/index.html>

Lab@cbgnt.chicagobotanic.org

Combining MarkerData

Hi,

is there somebody who can give some hint on how to - reasonably - combine data from AFLP, microsats and mtDNA to obtain overall estimates of population differentiation? My three dataset provide a very congruent picture of the differentiation between populations, and I would like to present results in a compact way.

Thanks in advance. Lorenzo Zane

Dipartimento di Biologia Università di Padova via G. Colombo 3 I-35121 Padova Italy

phone: +39 049 8276250 +39 049 8276222 fax: +39 049 8276209

lorenz@mail.bio.unipd.it lorenz@mail.bio.unipd.it

CreationEvolDebate Impact

Dear colleagues,

The cross-Canadian University newspaper, University Affairs, is investigating the impact that the creationist-evolution debate has had on the "doing" of science in the United States.

If you have any insights or personal stories about the negative or positive impact of this debate on your academic work (e.g., altering how you describe your research, the sorts of grants that you write, pressures from within your University, inspiration to write more in the public sphere, etc.), could you please contact:

Léo Charbonneau <lcharbon@ucc.ca> Deputy Editor/Rédacteur en chef adjoint University Affairs/Affaires universitaires Association of Universities and Colleges of Canada/ Association des universités et collèges du Canada 613-563-3961 x 323

Many thanks, in advance, for your help, Sally Otto –

Dr. Sarah P. Otto (nickname: Sally)
otto@zoology.ubc.ca <http://www.zoology.ubc.ca/~otto>
Department of Zoology University of British Columbia Vancouver BC V6T 1Z4 Canada (604) 822-2778 (604) 822-2416 (FAX)

DNA collection in the field

Hi all

I'm trying to find field manuals (web based preferably) relating to the collection of DNA samples (blood/tissue/feather/etc.) aimed at field workers or wildlife officers without no genetic or lab experience.

Covering issues such as types of sample/storage media, maintaining DNA integrity, contamination etc.

Also again at the non-genetic-specific experienced level relating to collecting wildlife samples for forensic purposes, including chain-of custody/evidence procedures etc.

Thanks

Tee

Dr Tiawanna Taylor School of Biological and Conservation Sciences University of KwaZulu-Natal Private Bag X01 Scottsville 3209 KwaZulu Natal South Africa

Email: taylort@ukzn.ac.za Tel: +27 (0) 33 260 6032
Tel: +27 (0) 33 260 6032

Effective vs census pop size answers

On January 28, 2005, I sent the following to EvoDir:

Dear colleagues,

I vaguely recall seeing a paper some years ago, perhaps 10-15, which suggested that the ratio of N_e/N is smaller the larger is N . Can anybody give me this reference?

Many, many thanks to all who responded! The responses I received are given below for the benefit of all.

Bill

1. (This message actually identified the paper I vaguely recalled:)

From: Charles Goodnight
<charles.goodnight@uvm.edu>

Yup. That would be me (among others) that wrote that. It turns out that there is a strong negative re-

lationship between N and N_e/N . We confirmed this experimentally, and found qualitative agreement with published data (although differences in methodology among studies precluded convincing quantitative comparisons). Aside: Note the census numbers for the galleon populations. Those counts almost killed me. Pray, L. A., C. J. Goodnight, L. Stevens, G. Yan, and J. M. Schwartz. 1996. The effect of population size on effective population size. *Genetical Research* 68:151-156.

2. From: Paul Moran <paul.moran@noaa.gov>

Is that Frankham 95 *Genetical Research* 66:95-107? It seems, however, that the apparent influence of N is related to mixing harmonic and arithmetic means rather than an inherent biological phenomenon. Robin will check my interpretation on that. He wrote about this issue in a recent book chapter, and he and Steven Kalinowski published a paper in *Conservation Biology* (16:129-136).

3. From: Robin Waples Robin.Waples@noaa.gov

Perhaps you are thinking of Vucetich and Waite 1998 *Conserv Biol.* 12:1023-1030 or Vucetich et al. 1997 *Evolution* 51:2015-2019. They showed that N_e/N declines to an asymptote as one considers a longer time series. However, this is the case only if one defines long term N_e/N as the harmonic mean N_e divided by the arithmetic mean N . Hedgecock (1994) suggested N_e/N might be very small in some marine species. This hypothesis is controversial, but some recent genetic estimates of N_e in marine species support this idea. N_e and Tajima (1981) suggested N_e/N might be low in species with large N such as insects, but I don't think they provided any data.

Hedgecock, D. 1994. Does variance in reproductive success limit effective population sizes of marine organisms? Pp. 122-134 in A. R. Beaumont, ed. *Genetics and evolution of aquatic organisms*. Chapman and Hall, London.

4. From: Paul Moran <paul.moran@noaa.gov>

Thanks, Robin. As an example of your point about N_e in marine populations (other than oysters), Lorenz Hauser's work on New Zealand snapper showed a really small N_e/N ratio (I've forgotten just how small, but I remember being impressed when I saw him present those data).

Hauser L, Adcock G.J., Smith P.J., Bernal Ramirez J.H., Carvalho G.R. (2002) Loss of microsatellite diversity and low effective population size in an overexploited population of New Zealand snapper (*Pagrus auratus*). *Proceedings of the National Academy of Sciences* 99, 11742-11747.

5. From: Masatoshi Nei <nxm2@psu.edu>

Dear Bill,

Maybe you are referring to the Nei and Graur paper, which was published in *Evolutionary Biology* in 1984. In this paper we estimated the census size in a crude way and effective size from average heterozygosity. You can get a copy of this paper from my website, which is given at the bottom of the signature page of this email. You can see that N_e/N ratio is smaller for large N .

6. From: Nicky Rivers <bgyngm@leeds.ac.uk>

Dear Bill

regarding your question below, I dont know the paper but would be interested to know of the reference if you find it - could you post the replies on evoldir? However there is a useful section in R. Frankham, J.D. Ballou and D.A. Briscoe's book 'Introduction to Conservation Genetics' which talks about the influences on N_e/N (p241-251), however it doesnt say that larger N per se influences the ratio, but does say fluctuations in popn size, overlapping generations, unequal sex ratio, variations in family size and outbreeding are important factors influencing the N_e/N ratio, so perhaps it is not as simple as the larger the N , the smaller the N_e/N ratio?

Nicola Rivers

7. From: Rich Strauss <Rich.Strauss@ttu.edu>

No, but to the extent that N_e is roughly constant among populations (or time), then N_e/N and N are proportional to reciprocals.

Rich Strauss

C. William Birky, Jr. Professor of Ecology and Evolutionary Biology Member, Graduate Interdisciplinary Programs in Genetics Biological Sciences West 1041 E. Lowell University of Arizona Tucson, AZ 85721 Office phone: 520-626-6513 Lab phone: 520-626-5108 Fax: 520-621-9190 Email: birky@u.arizona.edu

birky@u.arizona.edu

Ernst Mayr passing

Ernst Mayr, perhaps the most influential evolutionist in the world during the 20th century, died on Thursday, February 3, 2005. He was well into his 100th year, enjoying good health until near the end. In hand were several more manuscripts that he would have published

had he lived longer.

Mayr's influence was wide and deep. His two major works on evolution and systematics (Mayr 1942, 1963) are still read today. He was a constant innovator of systematic nomenclature (Mayr 1978). Mayr's books on the history of biology (Mayr and Provine, 1980, Mayr 1982), and on the philosophy of biology (Mayr 1988) had a major influence on both fields. Between Mayr and Richard C. Lewontin, Harvard's Museum of Comparative Zoology became the center of training for young historians and philosophers of biology.

Mayr was a forceful writer, and never hesitated to challenge his colleagues. Naturally, he had many detractors, whom he relished. His ideas endured much criticism from me, but he never wavered as a friend and advisor. The worst thing, he claimed, was being ignored. After roundly criticizing the contributions of population genetics to evolutionary biology (Mayr 1959), Mayr later nominated Sewall Wright for the Balzan Prize, and attended the award ceremony in Italy when Wright won the prize. When Theodosius Dobzhansky published his *Genetics and the Origin of Species* in 1937, Mayr pointed out to him with glee that the figure of a cell division on the spine of the book had the chromosomes backward (Dobzhansky was an accomplished cytologist, and had not noticed).

Finally, no notice of his death has mentioned his prodigious production of correspondence over his lifetime. He answered nearly every letter that reached him, and initiated much correspondence. His influence through correspondence will have to be evaluated in the future and I predict it will be immense.

Best wishes to all on Evoldir, Will Provine

Mayr 1942. *Systematics and Origin of Species*. New York: Columbia University Press.

Mayr, 1959. *Where are We?* Cold Spring Harbor Symposia of Quantitative Biology 24, 1-14.

Mayr 1963. *Animal Species and Evolution*. Cambridge: Harvard University Press.

Mayr 1978. *Origin and History of Some Terms in Systematic and Evolutionary Biology*. *Systematic Zoology* 27, 83-88.

Mayr and Provine, eds. 1980. *The Evolutionary Synthesis*. Cambridge: Harvard University Press.

Mayr 1982. *The Growth of Biological Thought: Diversity, Evolution, and Inheritance*. Cambridge: Harvard University Press.

Mayr 1988. *Toward a New Philosophy of Biology: Observations of an Evolutionist*. Cambridge: Harvard

University Press.

William Provine <wbp2@cornell.edu>

ErnstMayrAward SystBiol

ERNST MAYR AWARD IN SYSTEMATIC BIOLOGY

General Information. The Ernst Mayr Award is given to the presenter of the outstanding student paper in the field of systematics at the annual meetings of the Society of Systematic Biologists, as judged by the Ernst Mayr Award Committee. The award consists of \$1000.00 and a set of available back issues of the journal.

Who is Eligible. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. Students wishing to participate should register and submit titles for the SSB Meeting in Fairbanks, Alaska (<http://www.evolution05.uaf.edu/>), and notify the current awards chair (Kelly Zamudio, krz2@cornell.edu) of your interest. Please include in your e-mail, your name and complete contact information, and a 400-word abstract of your talk (in the body of your e-mail text). Based on the submitted abstracts, the Mayr Awards committee (appointed by the Awards Chair) will select the best 15 for inclusion in the actual competition at the meetings, which will be held at a single venue in a separate session. Deadline for abstract submission is March 31, 2005. Previous winners are not eligible.

Judging. Papers will be judged on creativity, quality, excellence of research, and quality of presentation. Abstracts should clearly indicate methods used, the relevance to systematics and the conclusions. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

Co-Authors. The paper may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenting the paper and the intention is that person will be senior author on the published version of the paper.

Notification of Winner. The winner of the award will be announced during the banquet at the annual meetings, and an announcement will be published in Systematic Biology.

For details on this and other SSB Student and Researcher Awards please visit the SSB website: <http://systbiol.org/> -

Kelly R. Zamudio Associate Professor Faculty Curator of Herpetology Dept. of Ecology and Evolutionary Biology E209 Corson Hall Cornell University Ithaca NY - 14853-2701

phone: (607) 254 4212 FAX: (607) 255 8088

<http://www.eeb.cornell.edu/zamudio/KZhome.html>
krz2@cornell.edu

Europe ExchangeGrants InsectParasitoids

Information on the new ESF Programme BEPAR (Behavioural Ecology of Insect Parasitoids - from theoretical approaches to field applications) is now available at <http://www.esf.org/bepar> BEPAR announces a Call for Applications for Short Visit and Exchange Grants, deadline 29 April 2005. Further information and access to the online application forms at the above address.

If you wish to be included in the BEPAR email mailing list to receive regular updates on Programme activities, please send an email to jgoetz@esf.org.

Thanks in advance.

Joanne Goetz Life, Earth and Environmental Sciences (LESC) & ESF Database Coordinator European Science Foundation (ESF) BP 90015 1 quai Lezay-Marnésia 67080 Strasbourg Cedex France

Tel: +33 3 88 76 71 22 (Direct Line) Fax: +33 3 88 37 05 32 Email: jgoetz@esf.org <http://www.esf.org>
Joanne Goetz <jgoetz@esf.org>

Genescan

Hello,

I am looking to acquire Genescan (PC, v. 3.7 preferred) to analyze files generated at a core facility. As many of you are aware, ABI no longer supports the software. However, their alternative GeneMapper, is beyond my budget. Please let me know if you or anyone you know

could put me in contact with a group that has recently upgraded and/or has an extra copy for sale.

Thanks, Mark

Mark A. Jordan Assistant Professor Department of Biology Indiana University-Purdue University 2101 E. Coliseum Blvd. Fort Wayne, IN 46805-1499 Phone: 260-481-6315 FAX: 260-481-6087 Email: jordanma@ipfw.edu Web: <http://users.ipfw.edu/-JordanMA/index.htm>

Genotyper

Hi all,

I just saw Mark Jordan's request for Genescan, and I have a similar problem. I'd like a copy of Genotyper, but ABI doesn't support it anymore. I called them up, and they said the only way I could get a copy was if someone was willing to sell/give me an old copy. So if anyone out there has a copy they wouldn't mind selling or something, please let me know!

Thanks, Alisa

PS Mark, I'd let you have one of our copies but we use MACs, older version.

Alisa P. Ramakrishnan Portland State University Department of Biology SB2 rm 246 1719 SW 10th Ave Portland, Oregon 97201 (503)332-4641 aramakris@yahoo.com

Individual genetic distances

Hi there, I'm currently trying to finish my master's thesis and I've run into a problem with my analysis. I have microsatellite data for 9 loci for a single population that contains 1) bisexual species and 2) related unisexual hybrids. I want to generate a genetic distance matrix at an individual level for my multi-locus genotype data, that will allow me to compare graphically the genetic relatedness between the hybrids and sympatric bisexuals. However, I can't seem to find a program that will allow me to generate a genetic distance matrix for genotype data at an individual level (as compared to a sub-population level through allele frequencies). I've

hit a wall here and so if anyone can help me figure out how to do this analysis, I'd be super appreciative. Thanks so much in advance! Cadhla

Cadhla Ramsden M.Sc Candidate Department of Integrative Biology University of Guelph N1G 2W1 cramsden@uoguelph.ca

Intelligent Design

Look who's on the NYT Op-ed page. "But they do not doubt that evolution occurred. And intelligent design itself says nothing about the religious concept of a creator." Actually, many of them do; Behe is one of the few who sort of accepts evolutionary history. And that's after just reading the first two paragraphs.

Evan

New York Times, February 7, 2005 OP-ED CONTRIBUTOR Design for Living By MICHAEL J. BEHE

Bethlehem, Pa. - IN the wake of the recent lawsuits over the teaching of Darwinian evolution, there has been a rush to debate the merits of the rival theory of intelligent design. As one of the scientists who have proposed design as an explanation for biological systems, I have found widespread confusion about what intelligent design is and what it is not.

First, what it isn't: the theory of intelligent design is not a religiously based idea, even though devout people opposed to the teaching of evolution cite it in their arguments. For example, a critic recently caricatured intelligent design as the belief that if evolution occurred at all it could never be explained by Darwinian natural selection and could only have been directed at every stage by an omniscient creator. That's misleading. Intelligent design proponents do question whether random mutation and natural selection completely explain the deep structure of life. But they do not doubt that evolution occurred. And intelligent design itself says nothing about the religious concept of a creator.

Rather, the contemporary argument for intelligent design is based on physical evidence and a straightforward application of logic. The argument for it consists of four linked claims. The first claim is uncontroversial: we can often recognize the effects of design in nature. For example, unintelligent physical forces like plate tectonics and erosion seem quite sufficient to account for the ori-

gin of the Rocky Mountains. Yet they are not enough to explain Mount Rushmore.

Of course, we know who is responsible for Mount Rushmore, but even someone who had never heard of the monument could recognize it as designed. Which leads to the second claim of the intelligent design argument: the physical marks of design are visible in aspects of biology. This is uncontroversial, too. The 18th-century clergyman William Paley likened living things to a watch, arguing that the workings of both point to intelligent design. Modern Darwinists disagree with Paley that the perceived design is real, but they do agree that life overwhelms us with the appearance of design.

For example, Francis Crick, co-discoverer of the structure of DNA, once wrote that biologists must constantly remind themselves that what they see was not designed but evolved. (Imagine a scientist repeating through clenched teeth: "It wasn't really designed. Not really.")

The resemblance of parts of life to engineered mechanisms like a watch is enormously stronger than what Reverend Paley imagined. In the past 50 years modern science has shown that the cell, the very foundation of life, is run by machines made of molecules. There are little molecular trucks in the cell to ferry supplies, little outboard motors to push a cell through liquid.

In 1998 an issue of the journal *Cell* was devoted to molecular machines, with articles like "The Cell as a Collection of Protein Machines" and "Mechanical Devices of the Spliceosome: Motors, Clocks, Springs and Things." Referring to his student days in the 1960's, Bruce Alberts, president of the National Academy of Sciences, wrote that "the chemistry that makes life possible is much more elaborate and sophisticated than anything we students had ever considered." In fact, Dr. Alberts remarked, the entire cell can be viewed as a factory with an elaborate network of interlocking assembly lines, each of which is composed of a set of large protein machines. He emphasized that the term machine was not some fuzzy analogy; it was meant literally.

The next claim in the argument for design is that we have no good explanation for the foundation of life that doesn't involve intelligence. Here is where thoughtful people part company. Darwinists assert that their theory can explain the appearance of design in life as the result of random mutation and natural selection acting over immense stretches of time. Some scientists, however, think the Darwinists' confidence is unjustified. They note that although natural selection can explain some aspects of biology, there are no research studies indicating that Darwinian processes can make molecular machines of the complexity we find in the

cell.

Scientists skeptical of Darwinian claims include many who have no truck with ideas of intelligent design, like those who advocate an idea called complexity theory, which envisions life self-organizing in roughly the same way that a hurricane does, and ones who think organisms in some sense can design themselves.

— / —

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>

Intelligent Design responses

I have pasted below a number of responses (letters to the NYT editor) to Behe's NYT Op-ed piece. Feel free to add one of your own.

<http://www.nytimes.com/ref/membercenter/help/lettertoeditor.html> 'Intelligent Design'

Published: February 12, 2005

To the Editor:

In "Design for Living" (Op-Ed, Feb. 7), Michael J. Behe quoted me, recalling how I discovered that "the chemistry that makes life possible is much more elaborate and sophisticated than anything we students had ever considered" some 40 years ago. Dr. Behe then paraphrases my 1998 remarks that "the entire cell can be viewed as a factory with an elaborate network of interlocking assembly lines, each of which is composed of a set of large protein machines."

That I was unaware of the complexity of living things as a student should not be surprising. In fact, the majestic chemistry of life should be astounding to everyone. But these facts should not be misrepresented as support for the idea that life's molecular complexity is a result of "intelligent design." To the contrary, modern scientific views of the molecular organization of life are entirely consistent with spontaneous variation and natural selection driving a powerful evolutionary process.

In evolution, as in all areas of science, our knowledge is incomplete. But the entire success of the scientific enterprise has depended on an insistence that these gaps be filled by natural explanations, logically derived from confirmable evidence. Because "intelligent design" the-

ories are based on supernatural explanations, they can have nothing to do with science.

Bruce Alberts President National Academy of Sciences Washington, Feb. 9, 2005

Published: February 9, 2005

To the Editor:

Re "Design for Living," by Michael J. Behe (Op-Ed, Feb. 7):

The basic principle of intelligent design is that life is just too complicated to occur by chance, and thus there must be some intelligent entity guiding the process.

A much more likely explanation is that our inability to comprehend these phenomena that appear "designed" merely reflects our own limitations as a species. We only recently discovered fire and the wheel and remain a basically savage society. Why not recognize our own limited capacity to understand complexity?

Our perception of complexity derives from our sense of scale in daily events. Is it any surprise that from this perspective, the evolution of life is beyond our grasp to comprehend? Intelligent design, like other creation myths, is just another way for us to make sense of our world.

A simpler alternative is to embrace our limited ability to comprehend and move on from there.

Richard W. Grant, M.D. Boston, Feb. 7, 2005

-

To the Editor:

I, like most working scientists, remain extremely skeptical that intelligent design can yet claim to be part of science. Writers such as the evolutionary theorist Richard Dawkins have pointed out the philosophical and scientific weaknesses in design arguments.

For me, the telling point is that the proponents of design cannot answer how it was supposed to have happened. Was it from divine intervention, visits by space aliens, magic?

Design will be a real science when we have testable answers for these questions.

Donald Terndrup Columbus, Ohio, Feb. 7, 2005 The writer is an associate professor of astronomy, Ohio State University.

-

To the Editor:

Michael J. Behe is right that the general public is free to accept intelligent design. This idea may be psychologi-

cally or spiritually attractive and even consistent with the world we see around us.

But the doctrine of intelligent design does not produce falsifiable (or disprovable) statements that are susceptible to testing. This rigorous testing process is the central element of the modern scientific method.

Assertions about intelligent design fall into an area of faith and belief outside the scope of science.

Karen Rosenberg Newark, Del., Feb. 7, 2005 The writer is chairwoman of the department of anthropology, University of Delaware.

-

To the Editor:

Michael J. Behe does an important service by taking the theory of intelligent design out of the hands of much of the faith-based community - where, unfortunately, it is equated with creationism - and providing its scientific underpinnings.

It is important to add that Darwin was not an atheist who set out to disprove that God created life. Rather, he set out to disprove that every single living thing was "specially created" by God and show instead that most living things evolved from other living things.

Darwin believed that God created life and "set in motion" the "laws of the universe" - including evolution - but did not tinker with them.

Dr. Behe says that many scientists "see roles for both the messiness of evolution and the elegance of design." One could argue

— / —

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>

Isolation by distance answers

Thank you very much to everyone who replied to my isolation-by-distance question. There was, of course a mistake in my original posting- Slatkin proposes using $F_{st}/(1-F_{st})$ where distances are linear, not $1/(1-F_{st})$ as I stated.

My original question was:

I wish to test for isolation-by-distance amongst popu-

lations of a stream-dwelling salmonid. In many published papers this is approached by testing for a positive correlation between F_{st} and distance. However, other authors perform this test using $1/(1-F_{st})$ instead of F_{st} , following Rousset (1997). Can someone advise me which is the correct test statistic, and why?

The answers:

1. The correct quantity is $F_{ST}/(1-F_{ST})$, which varies from zero to infinity (F_{ST} just varies from zero to one). So if you are looking for a linear relationship between genetic and geographic distance (which varies from zero to infinity) you want to use $F_{ST}/(1-F_{ST})$.

Rousset also makes good points about whether to use untransformed or log transformed distances. For salmon, you'd probably want to use untransformed distance, measured along the stream course, since streams are essentially one dimensional.

Slatkin's 1993 Evolution paper is also good, as are his other papers on gene flow.

2. I suggest you read :

Castric V. et Bernatchez L. 2003. The rise and fall of isolation by distance in the anadromous brook charr (*Salvelinus fontinalis* Mitchill). *Genetics*, 163: 983- 996

Castric V. et Bernatchez L. 2004. Individual assignment methods reveal restricted dispersal despite no detectable increase of genetic differences with distance in Atlantic salmon *Salmo salar* and brook charr *Salvelinus fontinalis*. *Molecular Ecology*:

Whitlock M. C. et McCauley D. E. 1999. Indirect measures of gene flow and migration: F_{st} not equal to $1/(4Nm+1)$. *Heredity*, 82: 117-125

3. A few bits cut & pasted from my PhD thesis:

Rousset (1997) devised a method to use F_{ST} estimators and geographic distances to test for a linear association between these two quantities. Representation of data is a plot of estimates of $F_{ST} / (1 - F_{ST})$ against distance in one dimensions (i.e. linear as in a river bank or the coast of Chile) or log distance in two dimensions (i.e. a lake).

The pairwise F_{ST} values were additionally used to test for a linear association between genetic differentiation and geographic distances between the respective populations (isolation by distance; Rousset, 1997) using Genepop (Ver 3.1) (Raymond & Rousset, 1995). The Mantel test (Mantel, 1967) was used to examine whether a correlation existed between the pairwise F_{ST} values and the corresponding pairwise geographical distances. The linearised genetic differentiation and geographic distance matrices were permuted 10,000

times to generate a null distribution between the two variables. A Spearman rank correlation coefficient was calculated and a one-tailed test of significance was performed to determine whether this coefficient was statistically outside the null distribution.

The equation of the linear regression produced will be in the form $y = a + bx$, where a is the intercept and b is the slope of the regression. Rousset (1997) showed that the slope of the linear regression can be used to estimate 'neighbourhood size' (N_b):

$\llcorner \llcorner \dots \text{OLE.Obj} \dots \gg \gg$ Where: $\llcorner \llcorner \dots \text{OLE.Obj} \dots \gg \gg$
Slope of regression

N_b is the effective number of individuals within a circle of radius $2\sigma_x$ (variance of the dispersal distribution). It is a dimensionless ratio, which determines the relative strength of gene flow and drift, the continuous population equivalent of N_m (Slatkin & Barton, 1989).

4. The Rousset correction is performed because F_{st} is limited in the values it can take (it only varies between 0 and 1) which is strictly not comparable with geographical distance which can increase from zero indefinitely. The converted distance also scales between 0 and infinity which allows it to be more correctly compared with geographic distance. I think the correction is $F_{st}/(1-F_{st})$ not $1/(1-F_{st})$ as you wrote. Also if you have a lot of geographic distances that vary in scale, (eg lots of distance around 10-20 km then a jump to >200km for example) a log conversion of geographic distance might be more appropriate.

5. I guess the answer in Rousset's paper. However a first point: there is a difference between testing for IBD (which can be done using a Mantel-like test, implemented in Genepop and other softwares; note that you can in principle use any kind of distance for running such a test) and using Rousset's method. What F. Rousset has shown, based on explicit population genetics theory, is a linear relationship between $F_{st} / (1 - F_{st})$ and distance (or its log, depending on the number of dimensions) under specific circumstances (e.g. on σ^2). The strong aspect is that, if you think that you are under these circumstances, the slope

— / —

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>

Isotopes in seawater

Hello all

Would someone be able to point me to a protocol to get N-15 and C-13 analysis done in seawater samples? The laboratory where I send my samples here in Australia say that they cannot measure stable isotopes from seawater. I have raked through the literature and could not find pertinent information. Any pointers to my email sasidiver@yahoo.com.sg would be greatly appreciated.

Cheers

Sasi

Sasi Nayar, Ph.D

Research Scientist Environmental Assessment and Rehabilitation SARDI Aquatic Sciences 2 Hamra Ave., West Beach Adelaide, South Australia

Postal address : PO Box 120, Henley Beach, SA 5022

Sasi Nayar <sasidiver@yahoo.com.sg>

Kangaroo cDNA

We are working on a project characterizing some novel human genes. To study the evolution of these genes it would be crucial to us to have some kangaroo RNA or cDNA. Then we could test for gene expression and sequence the kangaroo genes present. So far I have not seen anyone offering this commercially and therefore we are trying this way to find someone who might be willing to help us out.

We will of course pay the transportation costs and will acknowledge the gift in any resulting communication.

Best wishes Thomas

Thomas Arnesen Department of Molecular Biology University of Bergen Norway Tel: +47 55584539 / Fax: +47 55589683

Thomas Arnesen <Thomas.Arnese@mbi.uib.no>

LifeHistory evolution

Dear all,

I'm looking for source references for a couple of life history evolution hypotheses, which I'm sure I've come across before but can't remember where. Any help would be most appreciated:

1. Is there known or thought to be a trade-off between evolution of increased fecundity in mothers and evolution of offspring traits that increase their survival probability (such as physical defences)? If yes, is this a smooth relationship or is there a cut-off point in terms of survival probability, below which increased fecundity is selected for and above which increased survival is selected for?
2. Is intraspecific resource competition known or thought to cause temporal intraspecific polymorphisms in resource use, possibly between life stages within a generation but more importantly (for me) between generations?

Best wishes to all

Richard Bailey.

r_1470@yahoo.co.uk

Liquid Nitrogen

Dear all,

Does anyone have any advice on the use of liquid nitrogen to keep samples frozen over long periods? I'm going to be working remote in West-Australia, and liquid N would be the safest solution. However, I have no idea where I might be able to buy it, or where to start looking, what kind of container to use and above all whether I need a permit for its use/transport in WA. Any pointers much appreciated!

Best wishes Anne -

Dr Anne Peters Max Planck Institute for Ornithology Vogelwarte Radolfzell Schlossallee 2 D-78315 Radolfzell Germany

Ph +49 (0)8157- 932 337 Fax: +49 (0)8157 932 400

peters@orn.mpg.de

LongnoseDace samples

Hi.

I am a PhD student working on a phylogeography of the longnose dace (*Rhinichthys cataractae*), a common cyprinid of North American rivers. I have performed an extensive sampling of the Quebec rivers (Quebec, Canada) and in order to confirm the post-glacial origin of those populations, I need samples from Missouri/Mississippi or Great Lakes watersheds, from the northeastern part of Ontario as well as from the Atlantic region (Canada and/or USA).

I would be grateful if anyone would be able to provide me with DNA and/or conserved tissue/specimen (preferably in 95% ethanol) from those localities. If you are able to provide me with any of the above samples or know of anyone that might be able to help, I would appreciate your feedback.

Please contact me to the address given below.

Thank you very much for your help!

Philippe Girard M. Sc. Département des Sciences Biologiques Université de Montréal Courriel: philippe.girard@umontreal.ca Tél. (514) 343-6111 poste 1051

philippe.girard@UMontreal.CA

MatrixMill extractions

Hi

We are thinking of buying a Matrix Mill (as manufactured and supplied by Harvester Technology Inc of Lansing, NY, USA) to use for DNA extraction of plant material in 96well plates and I wondered if anyone had experience using the equipment and could advise us.

It seems from their blurb that they recommend their equipment for extracting DNA that is going to be used immediately for PCR but not for extracting DNA that may need to be stored for analysis later on. We want to do both and wondered if anyone had used this and

stored the DNA for any length of time or alternately had used this equipment for grinding but then used a modified CTAB extraction or other DNA extraction method subsequently.

Advice please! Thank you in advance.

Pamela Biss p.m.biss@open.ac.uk

Pamela Biss Department of Biological Sciences The Open University Walton Hall Milton Keynes MK7 6AA
"P.M.Biss" <P.M.Biss@open.ac.uk>

NestedCladeAnalysis

Dear All, I want to apply nested clade analysis to mtDNA sequence data, and am looking for suggestions of how to get multiple disconnected parsimony networks to connect into a single network (actually, two disconnected networks would be okay, but beyond that, the correct higher-level clade nesting order becomes uncertain). Below are a few details about my particular case, a list of the approaches I have tried, and the outcomes: 570-bp mtDNA COI fragment, 69 haplotypes from 200 animals (springtails) - up to 12% uncorrected p sequence divergence. Collected from 70 localities (fine-scale sampling at approx. 2-3 km intervals) spanning the species' entire known geographic range. End up with two parsimony networks that contain the majority of haplotypes (40 and 10 haplotypes, respectively), one very small network (5 haplotypes), and the remainder are either groups of two haplotypes or single unlinked haplotypes. Gives a total of 9 disconnected networks.

- Tried converting 3rd positions to transversions only, then used 1+2+3tv to build the parsimony network.

- Tried removing 3rd positions altogether, then used 1+2 to build the parsimony network.

- Tried cutting the full length sequence (arbitrarily) in half, then used each of the two 285-bp fragments separately.

- Tried reducing the 95% confidence setting in TCS down to 90%.

- Tried the approach suggested by Templeton & Sing (1993) i.e. build a Maximum Parsimony tree in PAUP (but constrain haplotypes within each of the networks that do connect at 95% confidence, so you're just resolving inter-network relationships), reconstruct DNA sequences of nodes that represent shared mutational

pathways among two or more of the disconnected networks, then re-run TCS with these inferred ancestral nodal haplotypes included.

The end result has been one (or two) of the following:

- Formerly disconnected networks still fail to form one or two networks... the number of networks I end up with is roughly proportional to the amount of information that is being discarded by the particular method used.

- Homoplasy (reflected by reticulation or closed loops within networks) becomes quite prevalent.

- The incorporation of reconstructed nodal haplotype sequences does not create any new linkages among the disconnected networks, at 95% confidence.

Any ideas would be most appreciated.

cheers, Ryan Garrick E-mail: r.garrick@latrobe.edu.au

Ryan Garrick Department of Genetics Biological Sciences Building 1 La Trobe University Bundoora, VIC 3086 AUSTRALIA E-mail: r.garrick@latrobe.edu.au <mailto:r.garrick@latrobe.edu.au>

NestedCladeAnalysis answers

Dear Evoldir members,

Below are the responses I received to my recent question regarding how best to deal with disconnected parsimony networks when performing NCA with relatively highly divergent intraspecific mtDNA sequence data (up to 12% uncorrected p). Thanks to everyone who offered advice... your comments were very helpful & informative.

cheers,

Ryan

1. Your data seems quite divergent. I am not sure what is your problem with the constrained MP approach, or with the reduced confidence setting approach but at worst you could claim that you have nine clades at the last nesting level.

David Posada

- 2.

This is a common “problem” with accompanying misconceptions. I would first ask if the different networks represent groups of allopatric haplotypes? If so, any

further efforts to join them would seem rather pointless to me. Moreover, it should be understood that the network NCA approach is really only meant for closely related lineages, and the inference key for “almost” exclusively intraspecific interactions. Of course, every gene has a different mutation rate, and we rarely have a good idea what it is, so each network constructed with a different gene reflects a different level of temporal resolution, a point which I think most people understand, but few comment on, or take into consideration when drawing inferences, or comparing data sets. If your data set is really about one species, with some level of interaction among many of the populations in the recent past (e.g. the last few 100,000 years or so), then it would seem that the COI in this species is mutating too fast to provide the best data set for NCA across the species range. By trying to remove 3rd positions, etc., you are reducing the genetic resolution (in a temporal sense) and that should help, but if it does not, and/or results in more and more reticulate branches than it would seem to me that you simply have too much homoplasy.

If these different networks represent allopatric populations that have been isolated for long periods of time, then there seems little point in wanting to “connect” them, to support inferences other than “fragmentation”, which can be simply concluded, in any case (and perhaps the notion that you have different species). I see no problem in conducting the analysis on your larger networks independently (the ones with 40 and 10), and simply inferring long-term fragmentation for the other smaller networks, which I presume are located on peripheral edges of the distribution and/or in specific refugia or areas that have undergone bottlenecks accompanied with isolation.

Lastly, if these different networks do not represent allopatric groups of haplotypes, it is more complicated, and you need to first establish through other genetic marker systems if you are indeed looking at one or more species before considering other approaches to the problem

steven.weiss

- 3.

In the new version of TCS (1.18), you can fix the connection limit to a defined number of steps, instead of using the 95 or 90% connection limit. So you can just increase this number of steps, until all your haplotypes are connected in a single network.

Best wishes, Patrick

- 4.

I think you might need to just set TCS's connection

limit (not a confidence limit) down much lower. My understanding of that is that if you have 12% difference, then to get them into one clade, you need to go down to below that, e.g. below 88% connection limit. You might need to go lower, though. From what you're saying, I'm not entirely certain (my ignorance here) whether 12% is the maximum distance between two animals. It's that max you should use. Also be sure that the sequences are all aligned exactly.

Good luck! Ruth

5.

Could you constrain the groups found in Paup and get that to recover the best phylogeny of the disconnected groups? If I was forced to analyse the data that way I would do it. However, realize that you have some deep diversity issues which probably violate assumptions of the NCA and/or some other process like cryptic speciation might be in play.

Joe

6. I have never encountered your problem....my major problem with networks have always been intragenomic variation and homoplasy. I attach you a paper that might be useful. But in your case I think I would approach it this way:

I would construct the network in the classic way, i.e. 95% confidence. Because you don't want to lose power. If the result is whatever number of disconnected networks, I think you have to deal with this by discussing it in your paper: what could explain this pattern? You should definitely calculate what is/are the nearest connection/s (less mutation steps) between your disconnected networks and haplotypes, and then join them together in the shortest way in order to get the whole picture. You will probably get loops that you also will have to deal with them....but that might be easy as there are some rules to resolve

— / —

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>

PopDensity MatingRate

Dear all

A quick question: does anyone know of any published

data from any species of animal describing mating rates at differing population densities?

Any contributions gratefully received.

Rob Knell

Biological Sciences, Queen Mary, University of London

RRTree question

Hi,

Anybody familiar with the program RRTree (<http://pbil.univ-lyon1.fr/software/rrtree.html>)? I use this software to calculate Ks - number of synonymous substitutions per synonymous site- for coding sequences. But the program could not calculate the Ks for some of my sequences (relative to the outgroup). The error message says "Ks not computable". But why it does calculate the Ks for other sequences in the same alignment?

Regards,

Tuo

Tuo Shi Environmental Biophysics and Molecular Ecology Institute of Marine and Coastal Sciences Rutgers University 71 Dudley Road, New Brunswick, NJ 08901 Phone: (732)-932-6555 x332 Fax: (732)-932-4083

Tuo Shi <tuoshi@imcs.marine.rutgers.edu>

Relation s migration

I have two questions concerning the relationship between the selective advantage of an allele (s) and the rate at which it migrates over geographic distance.

For those of you interested in the background: we can model, or measure, the selective advantage associated with alleles conferring drug resistance in malaria, so have estimates of 's', but the alleles appear to occur very rarely and have subsequently migrated around the world.

Intuitively, there must be a positive relationship but has it been quantified? On the basis that Fisher/Haldane/Wright sewed up most of population

genetics in the 1920s to 1940s I tried there and was not disappointed:

Fisher, R. A. (1937). The wave of advance of advantageous genes. *Ann.Eugen* 7: 355-369.

who found that rate of advance was proportional to the square root of 's'. This paper appears to be cited only rarely (at least in this context; it is used a lot in chemistry as a basis for the diffusion of reactions) so my first question is whether it was flawed, overlooked, or was simply superseded by later work?

My second question pertains to island and stepping stone models: has anyone investigated the relationship between 's' and migration rate from these models? Apologies if they have, but I haven't located it among all the work looking at more complex questions like maintenance of clines, genetic variability etc.

I realise I could probably do it myself using stepping models but there is the (non-negligible) risk I would get it wrong, it is superfluous if it has been done already, but most importantly I just need to cite the result in a review and don't want to have to prove it in an appendix.

As a technical point, malaria is haploid so we need not worry about dominance.

Thanks to those who can comment.

Regards,

Ian.

Ian Hastings, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool L3 5QA phone: 0151-705-3183 fax: 0151-705-3371

hastings@liverpool.ac.uk

Removing 3rdCodon

Hello Colleagues, I am looking for a easy way -software- to get rid of the 3dn position of the codons in an alignment. Any ideas? Many thanks Colomban

vargas@imcs.marine.rutgers.edu

Restorase

Dear Evoldir members:

I was told that a new revolutionary enzyme called Restorase has been developed for specially damaged or fragmented DNA from archival specimens. This enzyme is supposed to restore DNA templates for PCRs. Does anyone know how does it exactly work? Which are the criteria to bind fragments from DNA templates? Can this enzyme recognize fragments and array them correctly, I mean, in the same order as they were before being degraded?

Any information would be much appreciated.

Thank you in advance

Regards,

Javier Sánchez-M. Fontenla PhD Student Centre d'Estudis Avanats de Blanes (CSIC) C/ d'accés a la Cala Sant Francesc, 14 17300 Blanes, Girona (Spain) Ph: 0034 972336101 Fax: 0034 972337806 E-mail: javisan@ceab.csic.es Web: <http://www.ceab.csic.es> javisan@ceab.csic.es

SSCP DGGE dHPLC answers

Sorry for the delay in getting these responses out. Thanks to all who offered advice!

George

I am a bit in the same situation as you are. I send you a reference (below) on SSCP technique that may help you. I am currently doing tests with SSCP and it works fine so far, but I am gonna lean DGGE method in January and compare it to SSCP with the same set of individuals. I can inform you of my conclusions. Please, let me know what kind of responses you have, good luck, Mélanie

Sunnucks P., Wilson A. C. C., Beheregaray L. B., Zenger K., French J. et Taylor A. C. 2000. SSCP id not so difficult: the application and utility of single-stranded conformation polymorphism in evolutionary biology and molecular ecology. *Molecular Ecology*, 9: 1699-1710

This information is probably of no help, but in case it is... I did similar work for my PhD research. Here is one method that did not work, just in case you were thinking of it. I thought if I digested the PCR product with a restriction enzyme that only cut one allele, I could cut out the undigested band from an agarose gel

and sequence it to get the haplotype phase. But it was always still heterozygous. I think it was because in the later stages of PCR you produce a lot of heteroduplex dsDNA as the two haplotypes denature and reanneal. The enzyme won't cut the heteroduplex DNA, and it runs with the larger (undigested) band. It should work if you cut out one of the smaller bands and sequence it, so that may be worth a try. Restriction enzymes are cheap and the methodology is simple. I never tried DGGE because it seemed like too much work to set up the gel pouring. The first time I tried SSCP I nearly burned down the lab. I did have success with allele-specific PCR for haplotyping, and with TA-cloning of PCR products, although with the latter I did see some in vitro PCR-recombination, or jumping PCR, or whatever they call it these days.

Good luck, Mike

Just to chuck another idea into your pot RSCA (reference strand conformation analysis) is based on a similar idea to SSCP but you bind your sample on to a known sequence reference strand, and run this without denaturing it. The main advantages should be that by using different reference strands you should get different patterns of separation in your products. Therefore you can be sure that each of your products has only one sequence (and aren't mixed products that are migrating together). There are a couple of references that you might like to check out:

Addie DD, Kennedy LJ, Ryvar R, Willoughby K, Gaskell RM, Ollier WER, Nart P, Radford AD (2004) Feline leucocyte antigen class II polymorphism and susceptibility to feline infectious peritonitis *Journal of Feline Medicine and Surgery* 6 (2): 59-62 Arguello JR, Little AM, Bohan E, Goldman JM, Marsh SGE, Madrigal JA (1998) High resolution HLA class I typing by reference strand mediated conformation analysis (RSCA) *Tissue Antigens* 52 (1): 57-66 Arguello R, Pay AL, McDermott A, Ross J, Dunn P, Avakian H, Little AM, Goldman J, Madrigal JA (1997) Complementary strand analysis: A new approach for allelic separation in complex polyallelic genetic systems. *Nucleic Acids Research* 25:2236-2238 Drake GJC, Kennedy LJ, Auty HK, Ryvar R, Ollier WER, Kitchener AC, Freeman AR, Radford AD (2004) The use of reference strand-mediated conformational analysis for the study of cheetah (*Acinonyx jubatus*) feline leucocyte antigen class II DRB polymorphisms *Molecular Ecology* 13 (1): 221-229 Kennedy LJ, Ryvar R, Brown JJ, Ollier WER, Radford AD (2003) Resolution of complex feline leukocyte antigen DRB loci by reference strand-mediated conformational analysis (RSCA) *Tissue Antigens* 62 (4): 313-323

Sarah Helyar

I guess you do not want to clone, because it is kinda expensive and time consuming. I've never used other techniques than cloning, and it worked really well for me, especially because you get to know the specific alleles of your polymorphisms. Anyway, I attach you a pdf article of a study where we had to deal with multi-copy nuclear region (ITS) and where cloning helped a lot (*Molecular Ecology* 2004, 13, 109-122)

Good luck and all the best, Sandra

I have been using SSCP to score nuclear genotypes, and also as an alternative to cloning alleles for sequencing. We use isotope incorporation (alpha 33P dATP), and visualise by autoradiography. If you staple your film to the gel, you can then excise single-stranded DNA and use it as template for reamplification / sequencing (see Sunnucks et al. 2000. *Molecular Ecology* 9: 1699-1710 for the procedure).

Time commitment: If you have (i) a large number of individuals to screen (say >250), and/or (ii) a large number of alleles at a locus (say >10), this can require a fairly big time commitment. After your initial run, it is usually essential to reshuffle samples within that gel so that samples with apparently the same SSCP gel

— / —

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>

SYBR Green I

Dear Evoldir members:

I am interesting in rapid screening of microsatellite markers for polymorphism using SYBR Green I and a gel (ALF Express) or capillary (ABI 3100) automated DNA sequencer. I am wondering whether people have some experiences and the protocol employed.

Thank you in advance,

M Belén Gómez Pardo Departamento de Genética Facultad de Veterinaria Universidad de Santiago de Compostela Campus de Lugo 27002 Lugo Spain Tel and Fax n: 34 982 254681

pardobg@lugo.usc.es

Software BEAST v1.2

A new version of BEAST (v1.2) is now available from the BEAST website:

<http://evolve.zoo.ox.ac.uk/beast/> This version features some new demographic models:

* The Bayesian Skyline demographic model is now available in BEAUti & BEAST. The Bayesian skyline plot is a new method for estimating past population dynamics through time from a sample of molecular sequences without dependence on a pre-specified parametric model of demographic history.

This model is described in the following paper:

<http://mbe.oupjournals.org/cgi/content/abstract/-msi103v1> * We have also added the Logistic demographic model which can be selected within BEAUti.

In order to analyse either of these models in Tracer, you will require the latest Tracer package (v1.2.1):

<http://evolve.zoo.ox.ac.uk/software/tracer/> For more information see the following site:

<http://evolve.zoo.ox.ac.uk/beast/help/> This contains tutorials, documentation and FAQ. There is also a section of the website where users can contribute information, ask questions and the like.

Andrew Rambaut & Alexei Drummond, February 25th, 2005

Software DataMonkey Update

Dear EvolDir,

We are pleased to announce an update to DataMonkey (<http://www.datamonkey.org>; [1]), a web-based interface to HyPhy (<http://www.hyphy.org>; [2]), a sophisticated software package for phylogenetic modeling of sequence variation.

DataMonkey estimates nonsynonymous and synonymous substitution rates, dN and dS, in coding sequences alignments on a codon-by-codon basis, in order to detect sites under positive or negative selection [3].

Three methods are offered; the first is a counting based method (up to 150 sequences), similar to that of Suzuki and Gojobori (1999, [4]), but which uses maximum likelihood ancestral reconstruction; the second is a fixed effects type model (up to 50 sequences), in which dN and dS are estimated on a site-by-site basis using maximum likelihood, similar to that of Suzuki (2004, [5]) and Massingham and Goldman (2005, [6]), except that variation in dS across sites is permitted; and the third is a random effects type model (up to 25 sequences), in which a distribution of rates across sites is performed, with empirical Bayes estimation of sites under selection, similar to the models of Nielsen and Yang (1998, [7]) and Yang et al. (2000, [8]), except that these models also place a distribution on dS as well as a distribution on dN. All methods can use one of 203 underlying reversible nucleotide models, to accommodate complex patterns of nucleotide substitution bias. The methodology is now published in advance access in *Molecular Biology and Evolution* (<http://mbe.oupjournals.org/cgi/content/abstract/msi105v1>).

Results output includes estimates of dN and dS on a codon-by-codon basis, generation of plots in PDF or PNG format, and for the counting method, site-by-site inferred substitutions, which can be graphically mapped onto a phylogeny. These methods take advantage of our Linux cluster, and so will run significantly faster than using a stand-alone version of HyPhy on a desktop computer. Our server reports cluster load, and the progress of each submission in a queue.

Please visit <http://www.datamonkey.org> for further details of these methods. These analyses, and many more, can be implemented within HyPhy, the current build of which can be found at <http://www.hyphy.org/current/index.php>. Suggestions on how we can improve and expand both Datamonkey and HyPhy can be posted on our message board, <http://www.hyphy.org/cgi-bin/yabb/yabb.pl>. Bugs can be posted separately on <http://www.hyphy.org/Bugzilla>. Enjoy! Sergei L. Kosakovsky Pond and Simon D.W. Frost UCSD Antiviral Research Center San Diego, CA, USA

References

- [1] S.L. Kosakovsky Pond and S.D.W. Frost "Datamonkey: rapid detection of selective pressure on individual sites of codon alignments." *Bioinformatics Advance Access* published online on February 15, 2005 *Bioinformatics*, doi:10.1093/bioinformatics/bti320.
- [2]. Sergei L. Kosakovsky Pond, Simon D. W. Frost, and Spencer V. Muse "HyPhy: hypothesis testing using phylogenies." *Bioinformatics Advance Access* published on October 27, 2004, DOI 10.1093/bioinformatics/bti079.

[3] S.L. Kosakovsky Pond and S.D.W. Frost. "Not so different after all: comparison of various methods for detecting amino-acid sites under selection" *Mol. Biol. Evol.* MBE Advance Access published on February 9, 2005. doi:10.1093/molbev/msi105

[4] Suzuki, Y., and T. Gojobori. 1999. "A method for detecting positive selection at single amino acid sites." *Mol. Biol. Evol.* 16:1315-1328.

[5] Suzuki, Y. 2004. "New methods for detecting positive selection at single amino acid sites." *J. Mol. Evol.* 59:11-19.

[6] Massingham, T. and N. Goldman. "Detecting amino acid sites under positive selection and purifying selection" *Genetics* 2005; published ahead of print on January 16, 2005 as doi: 10.1534/genetics.104.032144

[7] Nielsen, R., and Z. Yang. 1998. "Likelihood models for detecting positively selected amino acid sites and applications to the HIV-1 envelope gene." *Genetics* 148:929-936

[8] Yang, Z., R. Nielsen, N. Goldman, and A. M. K. Pedersen. 2000. "Codon-substitution models for heterogeneous selection pressure at amino acid sites." *Genetics* 155:431-449.

in a clear and convivial way. PAPA 2.0 now accepts genotypes of as many as 50 loci (21 previously). A User Guide is provided which describes possible user scenarios for PAPA 2.0, a large set of questions and answers inspired by past interactions with users, and an Appendix containing definitions of all technical expressions found in the User Guide as well as in the PAPA 2.0 interface. We believe that PAPA 2.0 is now a more complete, easier to use and better documented program.

Reference: DUCHESNE, P., M.-H. GODBOUT, L. BERNATCHEZ.. 2002. PAPA (Package for the Analysis of Parental Allocation) : A computer program for simulated and real parental allocation. *Molecular Ecology Notes*. 2 : 191-194.

Louis Bernatchez

Titulaire de la Chaire de recherche du Canada en conservation génétique des ressources aquatiques

Département de biologie Pavillon Charles-Eugène Marchand Université Laval, Quebec QC G1K 7P4 Canada

Tél: 418 656-3402 Fax: 418 656-2043 Courriel: Louis.Bernatchez@bio.ulaval.ca Web: <http://www.bio.ulaval.ca/louisbernatchez/>

Louis.Bernatchez@bio.ulaval.ca

Software PAPA v2

Dear evoldir members, we wish to announce the latest version of the parental allocation program PAPA (2.0) available free of charge at: http://www.bio.ulaval.ca/louisbernatchez/files/-PAPA_2.0_USER.zip http://www.bio.ulaval.ca/louisbernatchez/files/PAPA_2.0_USER.zip PAPA is designed for parental allocation in closed systems i.e. when all parental genotypes have been collected. If you suspect some parents are missing, use PASOS 1.0 instead (see separate evoldir message). This version adds several new features to the preceding ones (1.0, 1.1). It is now possible to simulate crossing/matching plans with resulting offspring mixed together. This should prove especially useful in aquaculture contexts and also in natural settings when some putative reproducers are known a priori not to have mated together. Error modelling is now done simply by typing in the transmission probabilities instead of fixing values for intermediate parameters as previously. We also added to the simulation output files a Summary file, which for most uses is self-contained and shows the main results

Software PASOS v1

Dear evoldir members,

we wish to introduce the first version of the parental allocation program PASOS (1.0). PASOS is a program written in C++ and designed to assess parentage from collected parents and progeny based on individual multi-locus genotypes while detecting the proportion of missing parents when some have not been collected from the population. It was specifically designed for parental allocation in open systems i.e. when some parental genotypes are missing. If you are convinced that all parental genotypes have been collected, use PAPA 2.0 instead (see separate evoldir message). Another purpose of PASOS is to calculate and output reliable estimates of the probability that allocations are correct. This second goal is achieved through simulations. A third goal of the PASOS program is to allow the use of subsets of the available loci in order to find those of minimal number of loci which provide enough power to reach the desired rates of allocation and

correctness. This is also achieved by means of the simulator. Finally, PASOS provides sufficient information to estimate the rates of scoring errors of various sizes. The PASOS interface is very similar to the one found in PAPA, its closed system counterpart (Duchesne et al. 2002). PASOS can be downloaded free of charge at: <http://www.bio.ulaval.ca/louisbernatchez/files/PASOS_1.0_USER.zip>http://www.bio.ulaval.ca/louisbernatchez/files/PASOS_1.0_USER.zip Reference: DUCHESNE, P., CASTRIC, T. L. BERNATCHEZ. 2005. PASOS (parental allocation of singles in open systems): A computer program for individual parental allocation with missing parents. *Molecular Ecology Notes*. 6: (in press)

Louis.Bernatchez@bio.ulaval.ca

Software TreeScan

Dear all,

We have implemented a new program called TreeScan, to test for association between clades and continuous traits, using haplotype trees according to the method introduced by Templeton et al. (2005).

This program is available at <http://darwin.uvigo.es> Source code and a makefile is provided for compilation in any OS with a C compiler. Executables for Windows (DOS) and MacOS X are also included.

Program citation: Posada D, Maxwell TJ, Templeton AR. TreeScan: a bioinformatic application to search for genotype/phenotype associations using haplotype trees. *Bioinformatics*: in press

Method description: Templeton AR, Maxwell T, Posada D, Stengård JH, Boerwinkle E, Sing CF. 2005. Tree scanning: a method for using haplotype trees in genotype/phenotype association studies. *Genetics* 169: 441-453.

Applications: Chasman, DI, Posada D, Subrahmanyam L, Cook NR, Stanton VP and Ridker PM. 2004. A pharmacogenetic study of statin therapy and cholesterol reduction. *Journal of the American Medical Association* 291: 2821-2827

Best wishes,

David.

– David Posada Facultad de Biología Campus Universitario 36310 Vigo

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

dposada@uvigo.es

Software for micros

Hi fellow Microsatters,

Does anybody know of a software programme which will allow you to estimate the number of microsatellite loci that are required to identify all individuals within a population? Presumably you would need to give an indication of allele frequency distributions.

Any help would be much appreciated. Thanks in advance

Bill

Please reply to w.f.hutchinson@hull.ac.uk

Dr Bill Hutchinson Department of Biological Sciences Cottingham Road University of Hull Hull HU6 7RX U.K. 01482 465804 w.f.hutchinson@hull.ac.uk

H.R.Wilcock@hull.ac.uk

SystBiol2006 CallForSymposia

Call for 2006 Symposia. The Society for Systematic Biologists invites proposals for symposia at the 2006 SSB meeting to be held at the State University of New York, Stony Brook. The meeting will be held jointly with the American Society of Naturalists and the Society for the Study of Evolution. Proposals 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 funding is available. The target date for receipt of proposals is May 15, 2005. Proposals will be discussed and two will be selected at the SSB Council meeting during the 2005 annual meeting in Fairbanks, Alaska. Soon after, organizers will be notified of the status of their proposals. Proposals should be sent by email to the Program Chairperson, George D. Weiblen, gweiblen@umn.edu (Department of Plant Biology, University of Minnesota, 1445 Gortner Avenue, Saint Paul, Minnesota 55108).

George Weiblen

Assistant Professor, Department of Plant Biology Curator of Flowering Plants, Bell Museum of Natural History University of Minnesota 250 Biological Sciences 1445 Gortner Avenue Saint Paul, MN 55108 USA

Office: 612-624-3461 Lab: 612-625-8749 Fax: 612-625-1738 Email: gweiblen@umn.edu Web: <http://-geo.cbs.umn.edu> gweiblen@umn.edu

Trifolium samples

Dear evoldir-members

we are currently working on the molecular evolution of flowering genes in the genus *Trifolium*. The idea is to try to couple phenotypic variation between and within species to variation (either molecular sequence variation and/or gene expression variation). Right now we are sequencing flowering genes in a lot of *Trifolium* species, some of which are allopolyploids (e.g. *Trifolium repens*). To check for the origin of within individual variation in sequences in these allopolyploids, we would like to obtain material from the alleged parent species. Therefore we need material from the following species: *Trifolium nigrescens* *Trifolium uniflorum* *Trifolium occidentale*

These species should be present in Southern Europe and *nigrescens* also in southeastern USA.

If anyone could help us obtain samples of these species, we would be most grateful! Please contact me on details of how to sample and store material.

Thank you very much In advance!!!!!!

Joop Ouborg

Dr. N.J. Ouborg Assistant professor Department of Molecular Ecology University of Nijmegen the Netherlands <http://www.eco.sci.kun.nl/popbiol/welcom1.htm>

Attention: new mail address is j.ouborg@science.ru.nl; please adjust this in your address book

j.ouborg@science.ru.nl

UPretoria PopSizeFluctuations

Hello all, I have searched for this using various engines, so I am now posing this question to evoldir. I am looking for some information regarding the effects of annual population size fluctuations on population genetic data, specifically microsats. I work with a species that is both continuous and eruptive, with annual population size differences of several orders of magnitude. Specifically I am interested in the inference of migratory estimates for continuous populations, such as neighbourhood size, from such data. My best logical interpretation is that population size fluctuations will tend to homogenise genetic variability across localities as a result of increased numbers of homozygotes. However, this homogenising effect would be explicitly dependent on the dispersal ability of the species, and could under low dispersal rates cause divergence as a result of genetic drift. Has anyone done, or does anyone know of, work that is a simulation model of this process. I'd appreciate any comments or suggestions. thanks ./w

Wayne Delpoit Molecular Ecology and Evolution Programme Department of Genetics University of Pretoria Pretoria South Africa

wdeploit@postino.up.ac.za

combining marker data

Hi, sorry but I forgot to put my e.mail on first posting of this message.

Here is the original message. Hi,

is there somebody who can give some hint on how to - reasonably - combine data from AFLP, microsats and mtDNA to obtain overall estimates of population differentiation? My three dataset provide a very congruent

picture of the differentiation between populations, and I would like to present results in a compact way.

Thanks in advance.
lorenz@civ.bio.unipd.it

Lorenzo Zane

Dipartimento di Biologia Università di Padova via G. Colombo 3 I-35121 Padova Italy

phone: +39 049 8276250 +39 049 8276222 fax: +39 049 8276209

PostDocs

ArizonaStateU MolEvolGenetics	60	UEdinburgh PineFungalEndophytes	66
Cologne EvolGeneRegulation	61	UFribourg EvolPlantEcol	66
IowaStateU SexDetermination	61	UMiami MolEvolMicrobiology	67
KonzaPrairieBiolStation GenomicsClimateChange .	62	UNewSouthWales PathogenEvol	67
MarieCurieResearchNetwork SEXASEX 2	62	UParis11 MolEvolGenetics	68
MaxPlanck AvianEvolEcol	63	USDA Peoria MicrobialGenomics	69
Philadelphia CancerEvolution	64	USussex DistFitnessEffects	69
QueensCollegeCUNY Bioinformatics	64	UTennessee EvolBioinformatics	69
UBritishColumbia CDC MathModelingDisease	65	UWalesBangor AntarcticFish	70
UC SantaBarbara SexualConflict	65	UWesternAustralia EvolBiol	70
UCambridge HumanSettlementHistory	65	YaleU ModelReproductiveBehaviour	70
UCopenhagen Theory Statistics	66		

ArizonaStateU MolEvolGenetics

ARIZONA STATE UNIVERSITY

Postdoctoral Research Associate Position - Molecular Evolutionary Genetics

A two-year Postdoctoral Research Associate position is immediately available in the Center for Evolutionary Functional Genomics at the Biodesign Institute and School of Life Sciences at Arizona State University. The main focus of research is to examine patterns of population diversity in humans and other primates using comparative genomic and statistical approaches. The candidate must have earned a doctoral level degree with a research emphasis in population genetics or molecular evolution. Preference will be given to candidates with a background in population genetic theory, statistical genetics, evolutionary bioinformatics, and have experience in molecular biology, including standard DNA

techniques (PCR and sequencing). Ideally, the candidate will be involved in various on-going projects in the lab, but also, he or she would be encouraged to design and be responsible for independent research that involves the collection, analysis and publishing of data. The anticipated start date for this position is fall of 2005.

Deadline for applications is March 1, 2005: if not filled, weekly thereafter until search is closed. Applicants may address any specific questions to brian.verrelli@asu.edu. Please send curriculum vitae, a brief statement of research interests, and names and mailing addresses (e-mail) of three references to:

Biodesign Institute Arizona State University PO Box 875001 Tempe, AZ 85287-5001

Arizona State University is an Equal Opportunity/Affirmative Action Employer.

Brian C. Verrelli, Ph.D. Center for Evolutionary Functional Genomics, The Biodesign Institute Assistant Professor, School of Life Sciences Address: Life Sciences C-344 Arizona State University Tempe, AZ 85287-4501

E-mail: brian.verrelli@asu.edu

Brian.Verrelli@asu.edu

Cologne EvolGeneRegulation

Postdoc: Evolution of gene regulation in Cologne, Germany

A postdoc position is open at the Max Planck Institute for Plant Breeding Research in Cologne, Germany; starting in October 2005 to join a newly funded group in the department of Genetics and Plant Breeding (dir. Prof. Maarten Koornneef). The position is for two years with possible extension of an additional year.

Applicants with a strong background in evolutionary biology (either applied or theoretical) and with interest in functional and molecular studies of diversity are invited to apply. Application from skilled molecular biologists with a strong interest in evolution will also be carefully considered. A background in plant biology and/or gene regulation are not a prerequisite.

Our group is interested in evaluating the role played by cis-regulatory regions in adaptative evolution. For this, we are undertaking an analysis of nucleotide and functional evolutionary dynamics of promoter regions within and among closely related species of the *Arabidopsis* genus. Our ultimate goal is to relate this diversity to its ecological role in natural environments. Cis-regulatory evolution remains largely unexplored and there is plenty of room for investigating novel evolutionary concepts and ideas. Thus, specific interests of the successful applicant can easily be integrated into our research questions and approaches.

The Max Planck Institute offers an outstanding environment for carrying out ambitious and innovative research. The Department of Genetics and Plant Breeding brings together plant molecular biologists, quantitative geneticists and evolutionary biologists to investigate the causes and consequences of plant natural variation. The Institute benefits from a superb interdisciplinary scientific community, with world class molecular biology being performed and active contacts with outstanding evolutionary geneticists located in the nearby University of Cologne.

Cologne, the metropolis on the Rhine, has just over one million inhabitants and is the fourth-largest city in Germany. It offers plenty of cultural and recreational activities. The city further benefits from its cen-

tral location in the european travel network. Train go directly from downtown Cologne to Frankfurt International Airport. Low cost air companies operate at the local airport (Köln-Bonn) and can take you anywhere in Europe in a couple of hours.

Applicants are encouraged to consult the Institute/Departmental websites at <http://www.ice.mpg.de/tmo/research/RegEvol.htm> or <http://www.mpiz-koeln.mpg.de>. Review of applications will begin on March 15th 2005 and continue until the position is filled. Please provide a cover letter, curriculum vitae and contact information for two referees and submit to: Juliette de Meaux <jdemeaux@ice.mpg.de>. The position is open to non-german citizens only. Don't hesitate to contact J. de Meaux if you have specific questions about this announcement.

Juliette de Meaux, Post doc Dept of Genetics and Evolution Max Planck Institute of Chemical Ecology Winzlerstraße 10 07745 Jena Germany

tel: + 49(0)3641 57 14 15 e-mail: jdemeaux@ice.mpg.de
e-mail: jdemeaux@ice.mpg.de

IowaStateU SexDetermination

Postdoctoral Researcher: the Molecular Basis of Sex Determination Iowa State University

I seek a postdoctoral researcher to participate in an ongoing study of the molecular basis of temperature-dependent and genotypic sex determination in reptiles. This position synergizes with existing molecular, field, and evolutionary studies of turtles in the laboratory of Nicole Valenzuela, Department of Ecology, Evolution, and Organismal Biology, Iowa State University. Primary responsibilities for this position include: 1) cDNA library construction and screening, 2) gene expression analysis, 3) sequence analysis, 4) analyzing data and writing manuscripts, and 5) assisting with undergraduate projects related to the research. For additional information concerning this and other research projects, please refer to the laboratory web site (<http://www.public.iastate.edu/~nvalenzu>).

Qualified applicants should have a Ph.D. in evolution, genetics, molecular biology, developmental biology, or a related field, and have expertise in one or more of the molecular techniques mentioned above. Salary is \$35,000 plus benefits, and funds are available for two

years pending satisfactory progress. The position can begin immediately. Review of applications will continue until a candidate is selected.

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

ISU is an equal opportunity/affirmative action employer.

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

KonzaPrairieBiolStation GenomicsClimateChange

Two positions at the postdoctoral research associate or research assistant level are available immediately. The postdoctoral research associates/research assistants will work as part of an interdisciplinary team in a new research initiative, Bridging the Divide: Linking Genomics to Ecosystem Responses to Climate Change. This DOE-funded project focuses on the linked study of gene expression and physiological responses in two dominant tallgrass prairie plant species to simulated climate change (<http://per.ornl.gov/PERProjects.html>).

The postdoctoral research associates/research assistants will be responsible for gene expression analyses using microarrays and for gene characterization in natural populations of the two grasses *Andropogon gerardii* and *Sorghastrum nutans*.

This is a collaborative project with Yale University, Kansas State University, Colorado State University, and the University of Minnesota. The postdoctoral research associates/research assistants will interact with a team of researchers with expertise in ecology, physiology, and genomics. The field component of the research will be conducted at Konza Prairie Biological Station, a NSF Long Term Ecological Research site (<http://www.konza.ksu.edu>). Gene expression analyses will be conducted at the KSU Gene Expression Facility (<http://www.ksu.edu/gene-exp>). This project benefits from interactions with a community of researchers working in ecological genomics as part of the Kansas

Ecological Genomics Initiative (<http://www.ksu.edu/ecogen>).

A degree in plant molecular biology or a related field is a requirement for the positions. Applicants for a postdoctoral research associate position should have a Ph.D. in the area and applicants for a research assistant position should have a B.S. or M.S. in the area. Experience in recombinant DNA techniques is required and experience in gene expression analysis, plant physiology or biochemistry, and an interest in ecology are desirable. Part-time employment is a possibility.

To apply, please email a letter of application, CV, and contact information for three professional references to both Dr. Karen Garrett (kgarrett@ksu.edu) and Dr. Melinda Smith (Melinda.smith@yale.edu). Review of applications will begin 1 March 2005 and continue until the positions have been filled.

Dr. Karen Garrett Department of Plant Pathology Kansas State University Manhattan, KS 66506

Dr. Melinda Smith Department of Ecology and Evolutionary Biology Yale University New Haven, CT 06520

Kansas State University is an equal opportunity, affirmative action employer and actively seeks diversity among its employees

Steve Travers Department of Plant Pathology Kansas State University Manhattan, KS 66506 785-532-1340 travers@ksu.edu <http://www-personal.ksu.edu/~travers/index.html> travers@ksu.edu

MarieCurieResearchNetwork SEXASEX 2

Marie Curie Research training network (MRTN) SEXASEX - postdoctoral position available in molecular genetics

Researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to apply for a research position in the European Union Marie Curie Research Training Network SEXASEX, which is coordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. One postdoctoral position remains to be filled, out of a total of 10 positions. Criteria of eligibility include: EU citizenship, less than 10 years for Experienced Researchers (ER), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolution-

ary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. This appointment will be for 3 years.

The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview: Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (YR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The network's theoretical and empirical research will apply 13 major approaches, including novel genetic and cytogenetic approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition. Please refer to <http://www.naturalsciences.be/EVIRENS/> for more information.

postdoctoral position: Molecular Genetic and Cytogenetic approaches to the causes and consequences of asexual reproduction. Starting date: 1st May 2005 or as soon as possible thereafter Duration: 36 months Salary: country-specific plus tax-free mobility allowance Scientists in charge: Dr Stefan Müller, Dr Renate Matzke, Germany Prof. Dr Jan Zima, Czech Republic Prof. Dr Roger Butlin, UK Locations: München, Germany, Brno, Czech Republic &

Sheffield, UK (12 months funded in each location but the final arrangements are open to negotiation with the appointee) Places of work: 1) Ludwigs-Maximilians-Universität München, Department Biology II, Section Anthropology and Human Genetics & Dept. of Geo- and Environmental Sciences, Section Palaeontology; 2) Academy of Science, Institute of Vertebrate Biology & Charles University, Department of Zoology; 3) University of Sheffield, Department of Animal and Plant Sciences Approach and methods to be applied: Sex determination mechanisms in freshwater ostracods in general and in *E. virens* in particular remain elusive: are they chromosome based (XY or XO systems), environmentally cued or are other factors at play? What genetic changes underlie the transition to asexual reproduction and what changes accumulate as a result of long term asexuality? We will investigate these questions with a range of modern genetic and cytogenetic approaches. Correlations between chromosomal architecture and/or other cytological factors and reproductive mode will be examined, using fluorescence in situ hybridization techniques. Gene expression will be examined with Suppression Subtractive Hybridisation (SSH). This will be used to search for genes that are expressed differently in sexual females and asexual females (from young or old lineages) to identify genes involved in the transition to asexual reproduction and the

— / —

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>

MaxPlanck AvianEvoEcol

Post-doc opportunity Max Planck Intitute for Ornithology, Radolfzell location

Applications are invited for a post-doc to study aspects of plumage coloration in relation to season, sex steroids, immune and other health parameters in songbirds. This research is aimed at a better understanding of trade-offs and proximate mechanisms involved in production and maintenance of sexual signals. We are looking for a highly motivated scientist, interested in tackling questions in behavioural ecology from an interdisciplinary approach, able develop their research independently, while working in a team. It is highly desirable to have experience or the willingness and ability

to learn and/or develop independently some of the following skills: modern immune function estimates, bird ringing and blood sampling, the analysis of colour reflectance spectra, classical biochemical assays, hormone analysis and manipulation.

The successful candidate will be part of a newly-started 5-year research program on the behavioural ecology of sexual signalling based at the Max Planck Institute for Ornithology, at the Vogelwarte location in Radolfzell. We offer superb logistical support, including extensive, fully-manned, permanent and seasonal mist netting systems for year-round captures of residents and migrants, complemented by ample aviary facilities. At the Seewiesen location there is access to molecular and endocrinological laboratories. The working language is English, but knowledge of German is advantageous. There are no teaching obligations, but the institute has active connections to the Universities of Konstanz, Freiburg and Munich. This position is initially for one year, but can be extended upto 3(5) years. Remuneration is a tax-free stipend of the Max Planck Society, commensurate with age and family circumstances. Starting date is flexible but a start in April is preferred.

Candidates should send a curriculum vitae, pdfs of max. three key publications, a letter with a brief statement of research achievements and interests plus full contact details of three referees, to peters@orn.mpg.de. To ensure full consideration, applications should arrive before 28 February, aiming for a starting date in Spring.

For further information, please contact Dr. Anne Peters (peters@orn.mpg.de).

The Max Planck Society is an independent, non-profit organization that promotes research in its own institutes. The MPS is an Equal Opportunity Employer

peters@orn.mpg.de

Philadelphia CancerEvolution

There is an opening for a post-doctoral fellow beginning on or after April 2005, to study clonal evolution in carcinogenesis and cancer prevention. Expertise in evolution, phylogenetics and ecology desirable. The projects will involve phylogenetic reconstruction in human tumor samples as well as cell/tissue culture competition experiments. Successful completion of the projects will lead to fundamental discoveries in cancer biology and the opening of new fields in cancer prevention.

A successful candidate will have a Ph.D. or M.D./Ph.D. in the biological or related sciences. For consideration, send inquiries and applications to: cmaley@wistar.upenn.edu. An application should consist of a CV, brief cover letter and contact information for three references. EOE/AA/M/F/D/V

– Carlo C. Maley, Ph.D. Assistant Professor The Wistar Institute 3601 Spruce St. Philadelphia, PA 19104

phone: 206-667-4615 fax: 206-667-6132 cell: 206-355-7425

http://www.wistar.upenn.edu/research_facilities/-maley/research.htm cmaley@fhrc.org

QueensCollegeCUNY Bioinformatics

Dear All, I would like to bring your attention to the following ad which appeared in Science. There are 2 Howard Hughes supported post-doctoral fellowships available at Queens College, CUNY. Research areas include genomics, molecular evolution and ecological modeling. If interested apply asap.

Stephane Boissinot, Ph.D. Department of Biology Queens College, CUNY 65-30 Kissena boulevard Flushing, NY 11367-1597

Postdoctoral Positions (2) in a Howard Hughes Medical Institute funded Research-Teaching Postdoctoral program will be available in the fields of Neuroscience and Bioinformatics at Queens College, CUNY starting fall 2005. In order to prepare post-doctoral fellows for the challenges they will face as researchers/educators they will be situated in an appropriate research lab as well as being paired with a faculty teaching mentor. Research areas include; neurophysiology, neuroanatomy, behavioral neuroscience, pharmacology, genomics, molecular evolution and ecological modeling. For a complete list of research mentors and projects please consult (www.qc.edu/HHMI.htm). In order to better prepare the fellows for future faculty positions, they will initially assist in teaching lower division undergraduate courses and, in consultation with their teaching mentor, will design and teach a course in their specialty during their second year on campus. Salary is \$36,000 per year.

Please send a letter of application, stating preference(s) for research mentor and teaching interests to:

Dean Thomas C. Streckas Division of Mathematics

and Natural Sciences Queens College-CUNY Remsen
Hall/Rm 125 Flushing, NY 11367

SBoissin@qc1.qc.edu

UBritishColumbia CDC MathModelingDisease

Postdoctoral Research Position University of British
Columbia Centre for Disease Control (UBC CDC)

Applications are invited for a postdoctoral research position in the newly-formed Division of Mathematical Modeling (DMM) at the University of British Columbia Centre for Disease Control. UBC CDC is a research and training Centre which assures that health practitioners and the public have ready access to the best people with the latest knowledge and the Centre plays a leading role in Canada in applying research to protect people from infectious diseases. One of the primary objectives of the DMM is to develop and apply new mathematical and computational tools to study the transmission dynamics of communicable diseases and to devise and evaluate strategies to control the spread of disease in populations. We are, therefore, interested in candidates working in the fields related to the mathematical modeling of infectious disease. Preference will be given to applicants with expertise in network theory. This position is for one year, with a possible renewal for a second year, contingent on performance and funding. Successful candidates will have the opportunity to interact and work with researchers in a multidisciplinary environment, nationally and internationally.

Interested applicants should, before March 11, 2005, send a curriculum vitae, research statement and three letters of recommendation to: Dr. Babak Pourbohloul, University of British Columbia Centre for Disease Control, 655 West 12 th Avenue, Vancouver, BC V5Z 4R4.

Lauren Ancel Meyers The University of Texas at Austin Integrative Biology 1 University Station C0930 Austin, Texas 78712-0253 Ph (512) 471-4950 Fax (512) 471-3878 laurenmeyers@mail.utexas.edu <http://cluster3.biosci.utexas.edu/research/meyers/> "Lauren A. Meyers" <laurenmeyers@mail.utexas.edu>

UC SantaBarbara SexualConflict

SUBJECT HEADER: Postdoc: sexual conflict

Postdoc in Evolutionary Genetics of Inter-locus Sexual Conflict

I have an opening for a one-year postdoc to study the evolutionary genetics of inter-locus intersexual conflict in the *D. melanogaster* laboratory model system. A strong background in both evolutionary genetics (theory and/or empirical/experimental, ideally both) and genetic analysis of *D. melanogaster* is preferred, although persons with training in related fields (e.g., animal behavior) may be considered. Please send curriculum vitae and three references to Bill Rice: electronically at rice@lifesci.ucsb.edu (preferred), or for the electronically-challenged, via snail-mail to Bill Rice/Department of EEMB/UC-Santa Barbara/CA 93106. The University of California is an Equal Opportunity/Affirmative Action Employer.

UCambridge HumanSettlementHistory

Position: Research Associate (£19,460 - £29,127 pa);
Department of Genetics, University of Cambridge

A three-year BBSRC funded postdoctoral position in human population genetics is available in the lab of François Balloux (<http://www.gen.cam.ac.uk/newdept/-research/labs/balloux.htm>).

The aim of the project is to use neutral genetic markers to reconstruct past human settlement history, with particular emphasis on the genetic legacy of early Neolithic farmers. A possible development of the project would be to use the resulting demographic models for disentangling between the relative effect of past demography and natural selection on the current geographic distribution of specific genes (e.g. disease or nutrition genes).

The project is generously funded and the lab well equipped. An exciting aspect of the project is the availability of an exceptional dataset of 2,500 blood samples

from the eastern part of the Fertile Crescent (mostly Iran).

The ideal candidate would have strong interest in past human settlement history and human genomics as well as demonstrated competencies in quantitative aspects of population genetics and is expected to focus on the more advanced aspects of data analysis. The selected candidate will be working in close collaboration with a technician and a PhD student.

For more information please contact Francois Baloux, e-mail: fb255@mole.bio.cam.ac.uk . Full applications, including a completed PD18 Cover Sheet (available at <http://www.admin.cam.ac.uk/offices/personnel/forms/pd18/>), a covering letter, CV and contact details of two referees, should be sent to: Mrs. T N Oakley, Dept of Genetics, Downing St, Cambridge CB2 3EH, email: t.oakley@gen.cam.ac.uk . Closing date: 21 March 2005.

fb255@mole.bio.cam.ac.uk fb255@mole.bio.cam.ac.uk

UCopenhagen Theory Statistics

Postdoc in Theoretical Population Genetics/Molecular Evolution

We seek a postdoctoral researcher for up to two years to work on statistical methods in population genetics and molecular evolution at the University of Copenhagen, Denmark. The applicant should have a Ph.d. in the biological or mathematical sciences and an interest in statistical methods in molecular ecology, population genetics, molecular evolution and/or phylogenetics. The postdoc will be supervised by Rasmus Nielsen at the Center for Bioinformatics. There is a wide variety of possible research projects available and research topics will be determined in discussions between the supervisor and the successful applicant. The Center for Bioinformatics is located near the center of Copenhagen at the Institute of Biological Sciences.

Starting salary is approx. \$3,800/month + 15% in retirement for a new Ph.d. graduate and larger for applicants with more experience. Applicants should contact Rasmus Nielsen (rasmus@binf.ku.dk).

rasmus@binf.ku.dk

UEdinburgh PineFungalEndophytes

Fungal Endophytes of Pine: Population Ecology and Interactions with a Related Parasite

Applications are invited at postdoctoral level for a 7 month NERC funded project based at the Institute of Evolutionary Biology, University of Edinburgh with Dr. Richard Ennos. The aim of the project is to develop a set of research tools (species-specific ITS and microsatellite markers) for three pine needle inhabiting fungal species of the genus *Lophodermium* whose life styles span the continuum from endophyte to pathogen. These molecular tools will be used to study the comparative ecology of, and interaction among the three *Lophodermium* species in order to understand the role of endophytes in reducing pathogen damage.

For applications and further information about the project please contact Dr. R. A. Ennos, IEB, University of Edinburgh, Ashworth Building, King's Buildings, Mayfield Rd., Edinburgh EH9 3JT, Scotland. Tel. 0131 650 5411.

Email: rennos@ed.ac.uk

Richard Ennos Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh Ashworth Building King's Buildings Mayfield Rd Edinburgh EH9 3JT Scotland

Tel + 44 131 650 5411 Fax + 44 131 650 6564

email rennos@ed.ac.uk

UFribourg EvolPlantEcol

POSTDOCTORAL POSITION IN EVOLUTIONARY PLANT ECOLOGY

Rationale: The European knapweed *Centaurea maculosa*, introduced from Central Europe into North America during the late 19th century, where it covers now an area larger than Switzerland, has become a model for research on the ecological and evolutionary causes and consequences of invasions. We aim to explore the role of rapid evolutionary processes in the invasion success of *C. maculosa*. This involves the analysis of selec-

tion exerted by herbivorous insects (biocontrol agents) on plant life-histories in different environments and the study of genetic factors (especially polyploidisation) underlying evolutionary change in the exotic range.

We seek a highly motivated person to lead surveys in both Europe and North America, conduct field and greenhouse experiments, and various lab studies (molecular markers, flow cytometry, phenotypic markers, etc.). New ideas and complementary studies are of course highly invited.

Requirements - doctoral degree in experimental plant ecology or evolution, or related disciplines; - knowledge of, and experience in one or several of the following areas of research is highly desirable: population ecology, population genetics, plant-herbivore interactions, experimental design and statistics.

Salary and conditions Salary dependent on age and status (gross salary in the first year about CHF 67'000). Start date: preferentially on 1 April 2005. The position will also include support of research activities of our group. The position is for 2 years, but may be extended depending on funding.

Applications Applicants should send their CV, including the publication list, a short summary of research experience and interests, and the names of two professional referees to the address below (preferably by e-mail).

For further information, please contact: Prof. Dr. Heinz Mueller-Schaerer, Département de Biologie, Unité Ecologie et Evolution, Université de Fribourg, Chemin du Musée 10; CH-1700 Fribourg, SWITZERLAND. tel: + (41) (0) 26-300 88 35 direct, ++ 50 secr., fax: + (41) (0) 26-300 96 98; e-mail: heinz.mueller@UNIFR.CH; <http://www.unifr.ch/biol/ecology/> This is a joint position between H. Müller-Schärer, Thomas Steinger (Uni Fribourg) and Urs Schaffner (CABI Bioscience, Delémont) within the National Centre of Competence in Research (NCCR) Plant Survival, funded by the Swiss National Science Foundation.

UMiami MolEvolMicrobiology

Closing date: Jul 15 2005

Position Title: Postdoc, Molecular Environmental Microbiology

Position Location: U Miami, CIMAS

Position Description: Postdoctoral Associate position in Environmental Microbiology. Research areas include the application of molecular biology to improving water quality monitoring. Incumbent will develop molecular biological probes for detection, quantification, and source tracking of fecal contamination in coastal waters. Requires solid molecular biology experience, and microbiological or related skills. Experience with Luminex strongly desired. Experience with qPCR and sequencing preferred. Doctoral degree in Biology, Molecular Biology, Environmental Science, or related field required. For more information regarding the position contact Dr. Kelly Goodwin, kelly.goodwin@noaa.gov or Dr. Jack Fell jfell@rsmas.miami.edu. Please supply a statement of interest, curriculum vitae, and three letters of recommendation. Employment through the Cooperative Institute for Marine and Atmospheric Studies (CIMAS) of the University of Miami in cooperation with NOAA.

- Kelly D. Goodwin, Ph.D. National Oceanographic and Atmospheric Administration Atlantic Oceanographic and Meteorological Laboratories Ocean Chemistry Division 4301 Rickenbacker Cswy Miami, FL 33149 305 361 4384 FAX 305 361 4447 <http://www.aoml.noaa.gov/ocd/people/goodwin/> Kelly Goodwin <Kelly.Goodwin@noaa.gov>

UNewSouthWales PathogenEvol

POSTDOCTORAL POSITION IN MODELLING PATHOGEN EVOLUTION The University of New South Wales, Sydney, Australia

Postdoctoral Research Fellow SCHOOL OF BIOTECHNOLOGY & BIOMOLECULAR SCIENCES REF. 3338

FIXED TERM: - Salary: \$55,763 - \$59,637 per year (plus up to 17% employer superannuation plus leave loading.) This salary includes a superable UNSW academic loading of \$3,000 per annum payable to all academic staff (pro rata for fractional academic staff).

An ARC-funded post-doctoral position is available at UNSW from early 2005. The successful applicant will be part of a team modelling the evolution and epidemiology of infectious diseases, and constructing methods to analyse genetic variation in pathogen isolates. Responsibilities include taking an active role in the the-

oretical development of mathematical models, and the design and implementation of statistical methods and simulations. Essential criteria: PhD in a quantitative discipline such as theoretical biology, mathematics, physics or computer science; demonstrated ability in mathematics or statistics; an interest in infectious diseases; excellent communication skills; ability to work effectively in a team as well as independently; understanding of equity and diversity principles; commitment to OHS responsibilities and attending relevant OHS training. Desirable criteria: proficiency with Linux and C/C++; experience in computational Bayesian methods; expertise in epidemiology, genetics and/or evolutionary biology. This is a fixed term position for up to three years from early 2005. For more information contact Dr Mark Tanaka email: m.tanaka@unsw.edu.au or telephone (02) 9385 2038 or Dr Andrew Francis email: a.franis@uws.edu.au or telephone (02) 9852 4152.

Applications close 15 March 2005.

APPLICATION PROCEDURE Applicants must include a completed UNSW application form, resume and application letter, addressing the selection criteria, QUOTING REF NUMBER and details of 2 referees. Applications may be submitted by email: jobapplications@unsw.edu.au, facsimile: (02) 9662 2832 or post to: Recruitment, Human Resources, UNSW Sydney 2052 by the application close date. On-line/email applications are encouraged and will receive confirmation of receipt. <http://www.hr.unsw.edu.au/employment.htm> — Mark Tanaka Quantitative and Computational Biology School of Biotechnology and Biomolecular Sciences University of New South Wales Sydney NSW 2052 Australia

<http://www.bioinformatics.unsw.edu.au/~markt>

UParis11 MolEvolGenetics

Position Title: Postdoc, Molecular Evolutionary Genetics

Position Location: U Paris 11 (Orsay) France

Position Description: A two years CNRS post doc position is available in the lab Ecologie, Systematique et Evolution in the University of Paris 11 (Orsay). The targeted starting date is September 1, 2005, but is flexible. Our lab works on a broad range of projects in evolutionary biology, e.g. host-parasite co-evolution, biological invasions, reproductive systems, genome evolution,

using experiments as well as mathematical modelling.

The project aims at detecting and studying the evolution of genes involved in the specialization and the speciation of a model parasite, *Microbotryum violaceum*. This fungus causes a sexually transmitted disease, and constitutes a complex of sibling species, specialized on different Cayophyllaceae. This project aims at detecting genes that have rapidly evolved, and differently between close species, assuming that these genes will have important functions in speciation, specialisation, host-parasite co-evolution. EST libraries are under construction for 5 sibling species of *Microbotryum*. Signatures of positive or diversifying selection will be investigated by comparing orthologs among these genomes, e.g. using the ratio of synonymous vs non synonymous mutations. These genes will then systematically be sequenced in the whole species complex, and their genealogies will be compared to those of conserved genes. The variability of these genes will also be analysed within populations and compared to neutral markers (microsatellites, SNP, ..).

For this position, a Ph.D. in evolutionary biology, host-parasite ecology, or related field is required. Preference will be given to candidates with a background in population genetic theory, statistical genetics, evolutionary bioinformatics, and have experience in molecular biology, including standard DNA techniques (PCR and sequencing). Ideally, the candidate will be involved in various on-going projects in the lab, but also, he or she would be encouraged to design and be responsible for independent research that involves the collection, analysis and publishing of data. Knowledge of the French language is not required.

For more information regarding the position contact Dr. Tatiana Giraud tatiana.giraud@ese.u-psud.fr or Jacqui Shykoff jacqui.shykoff@ese.u-psud.fr. Please supply a statement of interest, curriculum vitae, and letters of recommendation.

Tatiana Giraud

Chargée de recherches Laboratoire Ecologie, Systématique et Evolution UMR 8079 CNRS-UPS-ENGREF Bâtiment 360 Université de Paris-Sud 91405 Orsay cedex France

phone:+33 1 69 15 56 69 + 33 6 68 27 46 85 fax: +33 1 69 15 46 97

<http://www.ese.u-psud.fr/bases/upresa/pages/-Giraud/index.html> <http://www.ese.u-psud.fr/> Tatiana Giraud <Tatiana.Giraud@ese.u-psud.fr>

USDA Peoria MicrobialGenomics

The Microbial Genomics Research Unit, USDA-ARS, Peoria, Illinois, is seeking a POSTDOCTORAL RESEARCH ASSOCIATE, (Geneticist) for a 2 year appointment. Research will focus on molecular evolution of virulence determinants, the phylogenetic history and population genetics of microbial pathogens, and comparative analyses of genome evolution. Candidates for this position should have a strong research background in molecular genetics, with expertise in molecular evolution, population genetics, and/or phylogenetic analyses. Ph.D. in Genetics or related field is required. Salary is commensurate with experience, \$50,541 - \$65,704 per annum, plus benefits. There are some citizenship restrictions. Refer to www.ars.usda.gov/careers for the full text vacancy announcement, RA-05-060H and complete application instructions. Please send curriculum vitae and names of three references to Dr. Todd J. Ward, NCAUR/ARS/USDA, 1815 N. University Street, Peoria, IL 61604 or e-mail (wardtj@ncaur.usda.gov). USDA/ARS is an equal opportunity provider and employer.

WARDTJ@ncaur.usda.gov

USussex DistFitnessEffects

A 3-year post-doc position is available to work at the University of Sussex with Adam Eyre-Walker on developing and applying methods to estimate the distribution of fitness effects from DNA sequence data. The project is funded by the BBSRC and has a salary of £19,460 to £29,128. Applicants should send a CV with the names and email addresses of three referees to Adam Eyre-Walker at a.c.eyre-walker@sussex.ac.uk

Adam Eyre-Walker Centre for the Study of Evolution & School of Biological Sciences University of Sussex Brighton BN1 9QG

tel : 01273 678480

a.c.eyre-walker@sussex.ac.uk

UTennessee EvolBioinformatics

Postdoctoral Research Position: Evolutionary Bioinformatics Department of Ecology & Evolutionary Biology University of Tennessee Knoxville

Applications are currently being accepted for an 18-month postdoctoral position in the laboratory of Michael A. Gilchrist in the Department of Ecology & Evolutionary Biology at the University of Tennessee, Knoxville. The position is to help develop, integrate and test mechanistic models of intra-cellular processes with large scale databases on the yeast proteome, genome, and transcriptome within an evolutionary framework.

The emphasis of the laboratory is to use relatively simple deterministic and stochastic models to analyze complex, heterogeneous datasets to answer biologically motivated questions. The research associated with this position draws upon a wide range of scientific disciplines including: cellular biology, evolutionary theory, differential equations, and probability/likelihood. Consequently, the ideal candidate would have a Ph.D. in biology, mathematics, or statistics and whose training includes work in at least two of these three areas. The researcher is expected to collaborate closely with the PI (Michael Gilchrist) in on-going lab projects as well as initiate new areas of research.

Additional areas of research conducted by the lab include: host, parasite, and saprophytic fungal life-history evolution as well as macro-ecology. The laboratory itself is part of a dynamic and growing Department, located in a medium sized city with relatively mild weather and many opportunities for cultural and outdoor recreation.

Review of applications begins immediately and will continue until the position is filled. The start date is flexible but the position is available immediately. The position employment period is 18 months, but may be extended if additional funding becomes available.

To apply, please submit curriculum vitae, brief statement of research interests, up to 3 relevant manuscripts and 3 professional references either via email or postal mail to:

Michael A. Gilchrist, Ph.D. Department of Ecology & Evolutionary Biology 569 Dabney Hall University of Tennessee Knoxville, TN 37996-1610

email:mikeg@utk.edu

Additional information can be found at <http://eeb.bio.utk.edu/gilchrist.asp> The University of Tennessee is an Equal Opportunity/Affirmative Action Employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

Michael A Gilchrist <mikeg@utk.edu>

Informal enquiries can be made by contacting Professor Gary Carvalho, e-mail: g.r.carvalho@bangor.ac.uk tel: +44 (0)1248 382100; or Dr Helen Wilcock, e-mail: h.r.wilcock@hull.ac.uk, tel: +44 (0)1482 465542.

Dr Helen Wilcock Department of Biological Sciences Cottingham Road University of Hull Hull HU6 7RX U.K. 01482 465542/465536 h.r.wilcock@hull.ac.uk

UWalesBangor AntarcticFish

UNIVERSITY OF WALES, BANGOR SCHOOL OF BIOLOGICAL SCIENCES

Postdoctoral Researcher in Molecular Ecology

Starting Salary: £19,460 - £24,820 p.a. (on R&A Grade 1A)

A NERC-funded three-year Postdoctoral position is available to work in the Molecular Ecology & Fisheries Genetics Group at the University of Wales, Bangor to investigate the contributions of life history variation and oceanographic variability on gene flow in Antarctic fishes. The project, jointly funded with the British Antarctic Survey in Cambridge and University of Hull, integrates molecular genetic analysis (microsatellites, DNA sequencing) with oceanographic modelling of dispersal. The appointee will participate in Antarctic sampling and will join a large, thriving team to investigate the origins and significance of population and species biodiversity in animals.

Applicants should have a broad interest in Evolution and Ecology and should have demonstrated the ability to work on a complex and demanding project. Some experience in the application of molecular genetic markers is essential and knowledge of microsatellite development would be advantageous. Applicants should possess a PhD in molecular ecology or associated areas, be physically fit enough and willing to participate in sampling cruises in the Southern Ocean, together with a strong commitment to timely publication and collaborative research.

Application forms and further particulars should be obtained by contacting Human Resources, University of Wales, Bangor, Gwynedd LL57 2DG; tel: (01248) 382926/388132; e-mail: personnel@bangor.ac.uk

Please quote reference number 05-4/139 when applying.

Closing date for applications: Friday 11th March, 2005.

UWesternAustralia EvolBiol

University of Western Australia

Evolutionary Biology Research Group, School of Animal Biology

Postdoctoral Research Associate (Level A step 6)

To work on an ARC funded research project on Sperm Competition and the Evolution of Ejaculates in Australian Frogs. The successful applicant will have a PhD in a closely related area, extensive field experience, a demonstrated capacity to undertake microsatellite DNA analysis, and evidence of an ability to publish in high ranking international journals. The position will be for 3 years in the first instance, with the possibility for extension.

For details of the EBRG: <http://www.zoology.uwa.edu.au/staff/lsimmons> Applicants should submit electronically a written application addressing the above requirements together with a full CV to

Professor Leigh W. Simmons: lsimmons@cyllene.uwa.edu.au -

Professor Leigh W. Simmons Zoology Building School of Animal Biology (M092) The University of Western Australia Nedlands Tel: +61 8 6488 2221 WA 6009 FAX: +61 8 6488 1029 Australia

<http://www.zoology.uwa.edu.au/staff/lsimmons> lsimmons@cyllene.uwa.edu.au

YaleU ModelReproductiveBehaviour

Postdoctoral Position Available To Model Alternative Reproductive Behaviors

A postdoctoral position is currently available in the lab of Suzanne Alonzo (PI) at the department of Ecology and Evolutionary Biology at Yale University to study the evolution of alternative reproductive tactics. The successful candidate will use mathematical models to develop novel theory on the evolution and ecology of alternative reproductive behaviors in both males and females.

For this position, a Ph.D. in evolution, ecology, mathematical theory or related field is required. Prior experience developing mathematical models is necessary as well as knowledge of behavioral and evolutionary ecology. Prior experience with some of the following theoretical approaches is desirable: game theory, genetic algorithms, individual-based simulations, quantitative genetics, population genetics or adaptive dynamics. The postdoctoral researcher will work independently and in collaboration with the PI to develop new theory. Field or laboratory work is possible but not required.

Review of applications begins immediately and will continue until the position is filled. Start date is flexible

but the position is available immediately. The position is for two years and is renewable contingent on the availability of funding. Please submit curriculum vitae, brief statement of research interests, up to 3 relevant manuscripts and 3 professional references to Suzanne H. Alonzo by email (Suzanne.Alonzo@Yale.edu) or mail (Department of Ecology and Evolution, Yale University, P.O. Box 208106, New Haven, CT 06520-8106).

Yale University is an Equal Opportunity/Affirmative Action Employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

Suzanne H. Alonzo Department of Ecology and Evolutionary Biology Yale University P.O. Box 208106 New Haven CT 06520-8106 phone (203) 432 0690 fax: (203) 432 3854 www.eeb.yale.edu

(please note new contact information) Suzanne H. Alonzo Department of Ecology and Evolutionary Biology Yale University P.O. Box 208106 New Haven CT 06520-8106 phone (203) 432 0690 fax: (203) 432 3854 www.eeb.yale.edu Suzanne.Alonzo@Yale.edu

WorkshopsCourses

Auckland SMBE YoungInvestigators Jun24-26	71
Ireland Shorebirds Oct6-10	72
PortalAZ Ants Aug4-14	73
UEdinburgh EvolAdaptiveImmunity	74
UEdinburgh EvolAdaptiveImmunity correction	74

Auckland SMBE YoungInvestigators Jun24-26

Dear All,

We are recruiting US participants for the 2005 SMBE Tri-National Young Investigators' Workshop.

The Society for Molecular Biology and Evolution announces the third Tri-National Young Investigators'

Workshop, 24-26 June 2005, to be held in conjunction with our annual meeting in New Zealand (19-23 June). Senior graduate students and postdoctoral researchers from the US are hereby invited to apply. Participants in the workshop will be awarded travel funds for our annual meeting, as well as for the workshop itself. While the workshop is open to all fields of molecular evolution, individuals working in the five following subject areas are especially encouraged to apply:

- 1) Epigenetics and adaptive evolution ? transcriptomes and proteomes
- 2) Connections between phenotype and genotype
- 3) Phylogeny, phylogeography, and geology
- 4)

Hominid evolution 5) Genome evolution and complexity

The application deadline is 10 March. Applications consist of a short research statement, including the importance of this meeting to future research and career goals; a CV; and a letter of support from either the current major professor or postdoctoral advisor detailing the intellectual skills, creativity, and originality of the applicant. A paper from each participant will be required by 30 June for publication in a special, peer-reviewed proceedings volume of *Molecular Biology and Evolution*. Up to seven applicants from each country will be selected by a multi-national selection committee.

Please send US applications to Marta L. Wayne (mlwayne@zoo.ufl.edu).

SMBE is committed to international intellectual partnerships, and to diversity as a component of excellence in science.

Workshop Organizers: Marta L. Wayne and Laura Katz, US Yoko Satta and Naoyuki Takahata, Japan Mike Hendy and David Penny, NZ

Marta L. Wayne P.O. Box 118525 Department of Zoology University of Florida Gainesville, FL 32611-8525 (courier: B30 Bartram Hall) vox: 352-392-9925 fax: 352-392-3704 <http://www.zoo.ufl.edu/mlwayne> "Marta L. Wayne" <mlwayne@zoo.ufl.edu>

Ireland Shorebirds Oct6-10

A workshop in Ireland at the Annual Conference of the International Wader Study Group, 6-10 October 2005
Title: "Why do wader populations decline globally? Merging population ecology theory with field data"

A call for contributions

We will be organizing a workshop in Ireland next fall intended to bring together theoretical ecologists and evolutionary biologists with field workers, in order to create a stimulating working group aimed at explaining the ecological, evolutionary and anthropogenic basis for the observed worldwide decline of shorebirds. Read the call for contributions below, and visit the webpage of the congress (<http://wsg.ucc.ie/>) for further information.

Organizers: Pablo Almaraz (e-mail: palmaraz@gmail.com; webpage: <http://www.almaraz.org>)
Tamas Szekeley (e-mail: t.szekeley@bath.ac.uk; webpage:

<http://www.bath.ac.uk/bio-sci//tamas.html>)

Almost half of the known wader populations are declining globally. At the 2003 WSG Congress it became clear that this global decline occurs in many species with different geographic distribution, ecology and lifestyle. However, the ecological and evolutionary factors that influence population declines, and population trends in general, remain largely unknown. We urgently need studies to reveal the intrinsic biological traits and extrinsic human-induced threats driving population trends in waders.

To address these top priority issues we are organising a Workshop at the 2005 WSG Conference in Cork. We will invite a handful of wader-researchers, and have left a number of slots open for contributions. We are aiming at creating a stimulating and multidisciplinary atmosphere by bringing together fieldworkers, theoreticians and policy makers.

The Workshop has four major objectives:

- 1) to reveal how theoretical ecology and population dynamics may help us to understand, predict and possibly reverse the declining trend of wader species and populations;
- 2) to identify the key population variables we need to measure in the field;
- 3) to encourage researchers to investigate population ecology of waders worldwide, and mobilise long-term datasets on wader populations for theoretical research;
- 4) to emphasize the value of population viability analyses (PVAs) implementing both environmental and demographic variation for an effective conservation strategy.

We welcome contributions, both talks and posters, from researchers, conservationists and policy-makers on a topic related to population dynamics and PVA of waders. We specially encourage contributions on long-term time-series of population counts and/or demographic rates of waders throughout the world.

Please send an abstract of your proposed contribution to the organisers: Pablo Almaraz (palmaraz@gmail.com) and Tamas Szekeley (t.szekeley@bath.ac.uk). The abstract should include the title of contribution, authors, contact addresses, and description of work (max 250 words). Deadline of abstract submission: 1 May 2005. Please note that we only have a limited number of slots, so it may not be possible to accommodate all offers. Also note that we welcome comments and suggestions for improving the workshop and its scope.

–

Pablo Almaraz García Estación Biológica de Doñana (CSIC) Pabellón del Perú, Avda. M Luisa s/n E-41013 Sevilla SPAIN

e-mail: palmaraz@gmail.com webpage: <http://www.almaraz.org> palmaraz@gmail.com

PortalAZ Ants Aug4-14

ANT COURSE 2005

<http://www.antweb.org> DEADLINE FOR APPLICATION: April 1, 2005

Southwestern Research Station (SWRS), Portal, AZ, August 4-14, 2005

COURSE OBJECTIVES. ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy. Emphasis is on the classification and identification of more than fifty ant genera of North America. Lectures will include background information on the ecology, life histories and evolution of ants. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment/supply vendors, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the major ant genera of North America; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the biological diversity of ants, and 4) experience keying to the species level.

SPONSORS. California Academy of Sciences and Harvard University's Museum of Comparative Zoology, with partial funding from The E.O. Wilson Foundation.

BACKGROUND INFORMATION. ANT COURSE will be taught from August 4-14, 2005 at the Southwestern Research Station (SWRS) in Portal Arizona (<http://research.amnh.org/swrs/>). The station is centered amid the richest ant fauna in North America. This is an ongoing course, offered annually.

PARTICIPANT ACCEPTANCE CRITERIA. ANT COURSE is open to all interested individuals. Priority will be given to those biologists for whom the course will

have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 25 participants

COSTS. Tuition for the 10-day COURSE is \$475 for current students and \$675 for non-students. In addition, Southwestern Research Station (SWRS) fees for this period, covering dormitory room and board, are estimated at \$440. Transportation costs between home and Tucson (air) or SWRS (auto) are to be borne by all participants.

FELLOWSHIPS. Four fellowships are available for 2005. Two fellowships cover tuition fees and two fellowships cover station fees. Foreign students may apply for additional fellowships to assist in travel. Those interested in attending the course should seek all possible avenues to secure funding for the course. You should only apply for the Ant Course fellowship if you can not find other support and it is essential for your participation in the course. Beware that if you apply for an ant course fellowship and you are not selected for a fellowship, you might not be accepted into the course. Please notify the course if your funding request changes before the application due date.

INSTRUCTORS: 2005 Brian Fisher (Coordinator), Dept. of Entomology, California Academy of Sciences, 875 Howard Street, San Francisco, California 94103; mail to: bfisher@calacademy.org Stefan Cover (Coordinator), Museum of Comparative Zoology, Harvard University, LeeAnne Alonso, Rapid Assessment Program, Conservation International Gary Alpert, University Entomologist, Harvard University - EH&S Department Lloyd Davis, Gainesville, FL Mark Deyrup, Archbold Biological Station André Francoeur, Université du Québec Bob Johnson, Dept. of Biology, Arizona State University Jack Longino, Evergreen State College Mike Kaspari, Dept. of Zoology, University of Oklahoma Andrew V. Suarez, University of Illinois, School of Integrative Biology, Departments of Entomology and Animal Biology Phil Ward, Department of Entomology, University of California

Special Guests Roy Snelling, Raymond Mendez, Howard Topoff

TA Alex Wild, Department of Entomology, University of California

Brian Fisher Assistant Curator and Chairman Entomology California Academy of Sciences 875 Howard

Street San Francisco, CA 94103-3009
 Phone: 415 321 8314 FAX: 415 321 8640
 bfisher@calacademy.org

<http://www.icapb.ed.ac.uk/people/little.html>
<http://daphnia.cgb.indiana.edu/> Tom Little
 <tlittle1@staffmail.ed.ac.uk>

UEdinburgh EvolAdaptiveImmunity

One Day Research Workshop

The evolution of adaptive immunity: genetic and functional relationships between adaptive and innate systems

Organisers: Tom Little (tom.little@ed.ac.uk) and Mark Blaxter (mark.blaxter@ed.ac.uk)

15 April, 2005 University of Edinburgh Ashworth Laboratories, Lecture Theatre 3 Kings Buildings EH9 3JT Edinburgh http://zeldia.cap.ed.ac.uk/evo_adaptive_imm <http://www.icapb.ed.ac.uk/> Confirmed Speakers Jim Kaufman. Institute for Animal Health, Compton Laboratory, Newbury, UK Valerie Smith. Comparative Immunology Group, University of St. Andrews, UK Kenneth Soderhall. Department of Comparative Physiology, EBC, Uppsala, Sweden Mike Siva-Jothy. Department of Plant and Animal Sciences, Sheffield, UK Gary Loake. Institute for Plant Sciences, University of Edinburgh, UK Tom Little. Institute for Evolutionary Biology, University of Edinburgh, UK Francis Jiggins. Institute for Evolutionary Biology, University of Edinburgh, UK Andrew Read. Institute for Infection and Immunology Research, University of Edinburgh, UK Judith Allen. Institute for Infection and Immunology Research, University of Edinburgh, UK Andrew MacDonald. Institute for Infection and Immunology Research, University of Edinburgh, UK

Registration is free for all interested parties and we'll provide lunch.

Please send me (tom.little@ed.ac.uk) an email if you plan to attend (this is just to get the numbers correct for catering).

Schedule and other details to be posted soonish on our web page.

Please see: http://zeldia.cap.ed.ac.uk/evo_adaptive_imm
 Tom Little Institute of Evolutionary Biology School of Biological Sciences, University of Edinburgh Edinburgh EH9 3JT, UK

tom.little@ed.ac.uk tel: 0131 650 7781 fax: 0131 650 6564

UEdinburgh EvolAdaptiveImmunity correction

One Day Research Workshop: The evolution of adaptive immunity: genetic and functional relationships between adaptive and innate systems

Wrong web address in previous posting. Corrected address is:

http://zeldia.cap.ed.ac.uk/evo_adaptive_imm.html Organisers: Tom Little (tom.little@ed.ac.uk) and Mark Blaxter (mark.blaxter@ed.ac.uk)

15 April, 2005 University of Edinburgh Ashworth Laboratories Kings Buildings EH9 3JT Edinburgh

Confirmed Speakers Jim Kaufman. Institute for Animal Health, Compton Laboratory, Newbury, UK Valerie Smith. Comparative Immunology Group, University of St. Andrews, UK Kenneth Soderhall. Department of Comparative Physiology, EBC, Uppsala, Sweden Mike Siva-Jothy. Department of Plant and Animal Sciences, Sheffield, UK Tom Little. Institute for Evolutionary Biology, University of Edinburgh, UK Francis Jiggins. Institute for Evolutionary Biology, University of Edinburgh, UK Andrew Read. Institute for Immunology and Infection Research, University of Edinburgh, UK Judith Allen. Institute for Immunology and Infection Research, University of Edinburgh, UK Andrew MacDonald. Institute for Immunology and Infection Research, University of Edinburgh, UK Gary Loake. Institute for Plant Sciences, University of Edinburgh, UK

Registration is free for all interested parties, but please let me know if you are attending (need to get rough numbers for catering)

Please see our web page for further details:

http://zeldia.cap.ed.ac.uk/evo_adaptive_imm.html
 Tom Little Institute of Evolutionary Biology School of Biological Sciences, University of Edinburgh Edinburgh EH9 3JT, UK

tom.little@ed.ac.uk tel: 0131 650 7781 fax: 0131 650 6564

<http://www.icapb.ed.ac.uk/people/little.html>
<http://daphnia.cgb.indiana.edu/> Tom Little

<tittle1@staffmail.ed.ac.uk>

Instructions

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

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

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

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

Afterward

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