
E v o l D i r

April 1, 2004

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

Forward

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

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

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Conferences

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Baltimore HapMap Apr18-20

The following meeting may be of interest. Note that enquiries should be directed to Mgray@md.capconcorp.com, not to me.

International HapMap Community Analysis Meeting
April 18-20, 2004 Renaissance Harborplace Hotel 202
East Pratt Street Baltimore, MD, USA

This meeting will be hosted by the McKusick-Nathans Institute of Genetic Medicine/Johns Hopkins University and the National Human Genome Research Institute, to discuss data analysis and methodological issues relevant to the International Haplotype Map Project. This will include approaches to describing linkage disequilibrium, properties of linkage disequilibrium, inference of haplotypes and haplotype frequencies, and methods for utilizing the haplotype map in association and other disease studies. The meeting will provide an important opportunity for a diverse community of investigators (both those involved directly in the project, and those in the broader community) to come together to define and debate a range of issues in the creation of the Haplotype Map resource.

The meeting is scheduled to begin at 6pm on Sunday, April 18, with presentations and a reception and will conclude at approximately 3pm on Tuesday, April 20. The International HapMap Data Analysis Group Planning Committee is pleased to invite you to register for this meeting and encourages the submission of an

abstract. For further information about the HapMap Project and complete details regarding registration, hotel reservations, and guidelines for abstract submission, please visit the International HapMap Project Website at www.hapmap.org and click on the link International HapMap Community Analysis Meeting, or you may go directly to the logistics web site at <http://www.capconcorp.com/hapmap04/>

ColoradoStateU ErnstMayrAward

2004 Ernst Mayr Award from the Society for Systematic Biologists

This award is given to the graduate student or early postdoctoral fellow who gives the outstanding oral presentation of his or her research at the meetings in Colorado this June. The talk should present research completed during the dissertation, rather than postdoctoral research, and the entrants should be graduate students or postdoctoral fellows in the first year of their postdoctoral research. To enter, a 150-word abstract should be sent by email to edwardsadmin@oeb.harvard.edu by April 15 (you must register for the conference and submit your title separately to the conference organizers). From the entrants, the Mayr Award Committee will select 15 finalist whose talks will be given during a special session devoted to the Awards. For more information, please see <http://systbiol.org/info/mayr.html>.

“Scott V. Edwards” <sedwards@fas.harvard.edu>

ColoradoStateU UndergradOpportunities

UNDERGRADUATE OPPORTUNITIES to attend EVOLUTION 2004 in Colorado

For the third time since 2001, 15 undergraduates from diverse backgrounds will be brought to the annual meetings of the Society for the Study of Evolution (June 26-30, 2004, Colorado State U.) to present their work, meet professionals in the evolutionary biology and advance their careers. Additionally, thanks to support from NSF-IBN, a group of undergraduates interested in plant evolution and/or the evolution of developmental mechanisms will also have expenses covered to attend the meeting. Students from both groups will present posters in a special section of the poster session on Sunday June 27 in the Main Ballroom. Information on applications for students in any area of evolutionary biology (due date, April 15) can be found at: <http://www.oeb.harvard.edu/faculty/edwards/diversity> . For students interested in plant evo-devo, contact David Baum at <dbaum@wisc.edu>.

“Scott V. Edwards” <sedwards@fas.harvard.edu>

Fairbanks SSB 2005

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

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

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

FortCollins SSBSEASN Jun26-30 3

The annual meetings of the The American Society of Naturalists <<http://www.amnat.org/>>, Society of Systematic Biologists <<http://systbiol.org/>>, and Society for the Study of Evolution <<http://lsvl.la.asu.edu/evolution/>> is scheduled for June 26-30, 2004, in Fort Collins, Colorado, on the campus of Colorado State University. The web site providing information and access to online registration and contributed post/paper submission can be accessed via links from each of the three societies' web sites, or directly at:

<http://evolution04.biology.colostate.edu/> (NOTE: the incorrect web address has been published on several other web sites).

PLEASE BE AWARE OF THE FOLLOWING DEADLINES:

- Contributed poster/paper submission is March 31, 2004 (registration must be completed before paper/poster submission)
- Early registration is June 1, 2004

OTHER HIGHLIGHTS:

- Information for travel arrangements, housing, and child care (under “accommodations”) can be found on

the web site.

- Conference attendees can come early on June 26 for a course on model fitting being offered by Dr. David Anderson, or for a guided field trip to visit the Pawnee National Grassland (and wildflowers, if it rains between now and then!). Dormitory spaces will be available beginning the night of June 25.

- Conference attendees can stay a day later on July 1 for one of several field trips to visit either Rocky Mountain National Park or the Roosevelt National Forest at Pingree Park, just north of RMNP. Dormitory spaces will remain available an additional day after the conference for these trips.

- Sales of T-shirts will benefit graduate students to travel to meetings planned for New Zealand in 2007. Check out the snazzy "Black Death" shirt, in addition to a shirt with the conference logo on it.

- You will be spared the lugubriousness of yet another conference bag this year, so bring something with you to carry your program and other stuff.

- Michael F. Antolin

Associate Professor of Biology Department of Biology Colorado State University Fort Collins, CO 80523-1878 U.S.A.

e-mail: michael.antolin@colostate.edu Voice: (1)-970-491-1911 FAX: (1)-970-491-0649

Geneva HumanMigrations Jun10-13

An international meeting on Human migrations in continental East Asia and Taiwan Genetic, linguistic and archaeological evidence will be held in Geneva (Switzerland) on June 10-13, 2004 Please find detailed information at <http://geneva.unige.ch/geneva2004/> The organizing committee: Prof. Alicia Sanchez-Mazas Department of Anthropology and Ecology, University of Geneva, Switzerland Dr Marie Lin Mackay Memorial Hospital Taipei, Taiwan Prof. Ilia Peiros, Santa Fe Institute, New Mexico

***** Prof. Alicia Sanchez-Mazas Laboratory of Genetics and Biometry Dpt of Anthropology and Ecology, University of Geneva 12 rue Gustave-Revilliod, CH-1227 Carouge, Geneva Switzerland Tel: ++4122 / 379.6984, FAX: ++4122 / 379.3194 *****

Alicia Sanchez-Mazas <alicia.sanchez-

mazas@anthro.unige.ch>

Netherlands Passerines Oct1-5

*** Hole-breeding Passerines Conference 2004 *** 1 - 5 October 2004, Vlieland, The Netherlands

Although some of you have already received this message, we know that we have missed several others in our previous mailings. Please accept our apologies for any repeat-postings, and feel free to pass this on to anyone you think might be interested.

To celebrate the 50th birthdays of three of our long-term nest-box areas (the Hoge Veluwe, Liesbos and Vlieland), we are reviving the highly successful - but sadly now dormant - series of 'Hole-breeding Passerines' conferences. To mark the anniversary, we are holding the conference a stone's-throw from one of our half-centurion study areas on the beautiful Waddensea island of Vlieland.

Please pre-register before the first of April. To do this, just forward this message to hole-breeding-meeting@nioo.knaw.nl and fill in the form below!

For more information, see <http://www.nioo.knaw.nl/-events/hole-breeding-vlieland> We hope to see you on Vlieland in October! Marcel Visser Kate Lessells Erik Postma Piet Drent Jan Visser

Netherlands Institute of Ecology (NIOO-KNAW) Centre for Terrestrial Ecology Boterhoeksestraat 48, 6666 GA Heteren P.O. box 40, 6666 ZG Heteren The Netherlands

----- Pre-registration form, to be returned by 1st April

Yes, I would like to register for the 2004 Hole-breeding Passerines Conference

Name: University / Institute: Address: E-mail: Position: PhD-student / Post-Doc / Permanent staff / Other: Brief description of research interests (a few keywords): I do/do not wish to offer a poster/spoken presentation with the following title: Preferred accommodation (please delete all but one of the following):
- Will only accept single room in hotel - Prefer single room in hotel, but will accept shared accommodation if

necessary - Prefer shared accommodation but will accept single room if necessary - Will only accept shared accommodation -----

Port Townsend EVO-WIBO Apr16-18

A meeting of the evolutionary biologists of the Northwest, EVO-WIBO, will be held for the first time April 16-18, 2004 in Port Townsend, Washington. Please see the meeting's web-page, <http://www.zoology.ubc.ca/evo-wibo>, for details.

Note that the registration deadline is fast approaching: March 15, 2004. – Michael Whitlock whitlock@zoology.ubc.ca Department of Zoology - University of British Columbia 6270 University Blvd, Vancouver, BC V6T 1Z4 CANADA phone: (604) 822-2069 FAX: (604) 822-2416

Rhode Island Microbial Eukaryotes Jun2

Symposium: Genome Evolution in Microbial Eukaryotes June 2nd, Smithfield Rhode Island

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

Travel funds are available for undergraduates, graduate students and postdocs. These funds will offset costs of those currently working on molecular evolution/genomics of microbial eukaryotes, and those switching into the field. Students and postdocs are encouraged to bring a poster of their work. For more information, visit: http://www.science.smith.edu/departments/Biology/lkatz/SOPgenome_fundsrequest.html

The symposium will take place at this year's Society of Protozoologists meetings.

More information about the symposium: http://www.biology.uiowa.edu/workshop/SOP_symposium.html More information on the SOP meetings: http://www.uga.edu/protozoa/meetings/sop_meeting.html http://www.uga.edu/protozoa/meetings/sop_meeting.html http://www.uga.edu/protozoa/meetings/sop_meeting10.html

Scheduled Speakers

Recent Studies on Eukaryotic Genome Evolution Paddy Patterson, University of Sydney, Australia/Marine Biological Laboratory, USA The changing face of protozoan taxonomy

Jessica Kissinger, University of Georgia, USA Parasite genome evolution

Andrew Roger, Dalhousie University, Canada Genome and cell evolution in anaerobic protists: Inferences from EST data

Kenneth Stuart, University of Washington Comparative genomics in kinetoplastids

Laura Katz, Smith College, USA Evolution and implication of genome rearrangements in ciliates

Uwe Maier, University of Marburg, Germany Organelles and endosymbiosis

Debashish Bhattacharya, University of Iowa, USA Genome evolution in photosynthetic eukaryotes

Workshop On Data Acquisition and Analysis Jane Carlton, TIGR, USA Protist genome sequencing projects and comparative genomics: from genome to populome

Martin Embley, University of Newcastle, UK Challenges and pitfalls in reconstructing eukaryotic relationships

Amy Driskell, UC Davis, USA Exploiting large sequence databases to build the trees of life

Poster Session: Molecular Evolution and Genomics TBA

Keynote Address Martin Embley, University of Newcastle, UK Genomes, organelles and the demise of the Archezoa

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Laura A. Katz, Associate Professor Department of Biological Sciences College Road Smith College Northampton, MA 01063 Phone: 413-585-3825 Fax: 413-585-3786 <http://www.science.smith.edu/departments/Biology/lkatz/>

“Laura A. Katz” <LKatz@smith.edu>

**StonyBrookU George C Williams
Apr24**

SYMPOSIUM IN HONOR OF GEORGE C. WILLIAMS

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

Registration for the symposium begins at 8:30 am on April 24 and the talks will run from 9:15 am until 5:00 pm. After the symposium, there will be a reception and banquet in George's honor.

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

GEORGE BARLOW (To be determined). HELENA CRONIN - Adaptation. MARTIN DALY and MARGO WILSON - Facultative modulation of risk-taking and future discounting in Homo sapiens. STEVEN FERRARO - Red-letter days. MART GROSS - Sex ratio theory. DAVID HAIG - Reflections on pregnancy and Darwinian medicine. BOBBI LOW - Women's lives in evolutionary perspective. RANDOLPH NESSE - Maladaptation and natural selection. MARY JANE WEST-EBERHARD - What George Williams said about sex but didn't really believe.

Please pre-register for the symposium and banquet. Attendance of the symposium will be \$60 (\$30 for students), and the banquet will be \$50. For further details and on-line registration, please go to <http://life.bio.sunysb.edu/ee/williams>. Inquiries can be sent to GCW_symp2004@life.bio.sunysb.edu.

Michael A. Bell Department of Ecology and Evolution State University of New York Stony Brook, New York 11794-5245, USA Phone: (631) 632-8574 (lab) (631) 632-8600 (dept.) Fax: (631) 689-6682

"Michael A. Bell" <mabell@life.bio.sunysb.edu>

**Toronto GeneticsSocietyCanada
Jun17-20**

GSC CONFERENCE 2004 The 47th Annual Conference of The Genetics Society of Canada University of Toronto June 17 to 20, 2004 <http://www.thesnidersweb.com/gsc2004/>

The Genetics Society of Canada's annual meeting will be held this year in Toronto. Plenary sessions will include a tribute to Professor Margaret Thompson on Medical Genetics, a session on genetically modified organisms and one on functional genomics. There will be workshops, platform and poster sessions, award winner lectures and a dinner at the Kortwright Centre.

Register before April 7th for early booking discounts.

For more details and registration forms visit the meeting web site at <http://www.thesnidersweb.com/gsc2004/>

For further information contact Doreen Ostrowski at Tel. 416-465-8756 or e-mail at doreen.gsc2004@sympatico.ca

Doreen <doreen.gsc2004@sympatico.ca>

ULeicester EGG Mar29-31

Ecological Genetics Group Annual Meeting

The 48th meeting of the Ecological Genetics Group (EGG) is to be held at the University of Leicester from Monday 29th March to Wednesday 31st March 2004. EGG is an international group of scientists in the fields of ecology and genetics, and is a specialist interest group of the British Ecological Society.

We hold our annual meeting at Easter each year, which is an ideal informal stage for anyone from first presentations by postgraduate students early in their research career to academics and research scientists. Bookings still being taken.

For further details visit our web page <http://www.le.ac.uk/biology/staff/cf12/egg/egg2004.html> or Email to Colin Ferris: cf12@le.ac.uk

Dr Colin Ferris Postgraduate Tutor Department of Biology University of Leicester LE1 7RH Tel: 0116 2525152 Fax: 0116 2523330

UOregon EvolGeneRegulation Mar12-14

This conference is coming up at the end of next week for those who might still be interested in attending:

Symposium Announcement:

THE EVOLUTION OF GENE REGULATION

March 12-14, 2004 at the University of Oregon

Fourth annual symposium on Evolution, Development and Genomics sponsored by the joint NSF-IGERT training of the University of Oregon and Indiana University.

Conference details available at <http://evodevo.uoregon.edu> The goal in of this symposium is to reach across fields to foster discussion of emerging issues related to the detection, functional significance, and evolutionary consequences of gene regulation and regulatory regions.

Plenary lecture: John Postlethwait, University of Oregon

Introduction and Overview: Patrick Phillips, University of Oregon

Invited Speakers:

Duccio Cavalieri, Harvard University "Evolution of regulatory networks in natural populations of *S. cerevisiae*"

Manolis Dermitzakis, University of Geneva (soon at the Sanger Institute) "Dissecting regulatory variation and evolution in the human genome"

John Finnerty, Boston University "Surprising complexity in the genomic regulatory systems of cnidarians."

Michael Freeling, UC Berkeley The evolution of regulatory complexity in higher plants

Veronica Hineman, Cal Tech Developmental gene regulatory network architecture across 500 MYA of echinoderm evolution

Thom Kaufman, Indiana University "A comparison of segmentation and limb development in long and short germband insects. Is *Oncopeltus* the new *Drosophila*?"

Mike Levine, UC Berkeley "Whole-genome analysis of *Drosophila* gastrulation"

Michael Ludwig, University of Chicago Enhancer evolution

Simon Malcomber, Univ. Missouri, Saint Louis Heterogeneous expression patterns and separate roles of *SEPALLATA*

genes in grasses (Poaceae)"

Steve Proulx, University of Oregon: Evolution of regulatory specificity

Trisha Wittcopp, Cornell University: "The genetic basis of divergent gene expression in *Drosophila*: cis and trans"

Logistics:

The symposium will begin on the evening of March 12 with a reception at 6 pm and the plenary lecture at 7:30 pm. The symposium will end on the morning of March 14 at 11 am with a brunch. The symposium will be held at the Valley River Inn in Eugene, Oregon, right on the Willamette River, near the University of Oregon.

UToronto EcolEthol May10-12

CALL FOR ABSTRACTS

OEEC 2004 ONTARIO ECOLOGY AND ETHOLOGY COLLOQUIUM UNIVERSITY OF TORONTO MISSISSAUGA, ONTARIO 10-12 MAY 2004 www.oeec.ca ABSTRACT SUBMISSION DEADLINE: 26 MARCH 2004

For the past 34 years, graduate and undergraduate students, post-docs, and faculty from Ontario and beyond, have gathered in the spring for the Ontario Ecology and Ethology Colloquium (OEEC). This annual conference is a forum for students and post-docs to present research in a constructive and friendly atmosphere (small, 150-200 registrants) and for faculty to recruit promising young researchers. Although originally conceived as a venue to present research in ecology and behaviour, OEEC has since broadened to include such diverse topics as evolution, genetics, psychology, conservation and environmental science. This year the OEEC will be held on 10-12 May 2004 at the Mississauga campus of the University of Toronto.

Early Registration Fees: \$25 (students and post docs), \$40 (faculty)

We are delighted to welcome the following plenary lecturers:

John Alcock, Arizona State University Michael Ruse, Florida State University Anurag Agrawal, University of Toronto Maydianne Andrade, University of Toronto

For more information, visit: <http://www.oeec.ca> (or <http://www.utm.utoronto.ca/~w3oeec>)

Email: Mark Fitzpatrick or Kevin Judge at: oeec@utm.utoronto.ca

UToronto EcologyEthology May10-12

OEEC EARLY REGISTRATION & ABSTRACT SUBMISSION DEADLINE HAS BEEN EXTENDED

OEEC 2004 ONTARIO ECOLOGY AND ETHOLOGY COLLOQUIUM UNIVERSITY OF TORONTO MISSISSAUGA, ON CANADA 10-12 MAY 2004 <http://www.oeec.ca> EXTENDED DEADLINE: 05 APRIL 2004

For the past 34 years, graduate and undergraduate students, post-docs, and faculty from around Ontario and beyond, have gathered in the spring for the Ontario Ecology and Ethology Colloquium (OEEC). This annual conference is a forum for students and post-docs to present research in a constructive and friendly atmosphere (small, 150-200 registrants) and for faculty to recruit promising young researchers. Although originally conceived as a venue to present research in ecology and behaviour, OEEC has since broadened to include such diverse topics as evolution, genetics, psychology, conservation and environmental science. This year the OEEC will be held on 10-12 May 2004 at the Mississauga campus of the University of Toronto.

Early Registration Fees: \$25 (students and post docs), \$40 (faculty) After April 5th: \$35 (students and post docs), \$50 (faculty)

We are delighted to welcome the following distinguished plenary lecturers:

John Alcock, Arizona State University Michael Ruse, Florida State University Maydianne Andrade, University of Toronto Anurag Agrawal, University of Toronto

For more information, go to: <http://www.oeec.ca> or email Mark Fitzpatrick or Kevin Judge at: oeec@utm.utoronto.ca

GradStudentPositions

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LundU AnimalMigration 2	10	ULaval SalmonidEvol	14
MaxPlanck EvolEcol	11	ULeicester L1 Evol	15
MichiganStateU StatGenetics	46	UNeuchatel 2 PlantInsect interactions	15
Newcastle MolEvol	11	UNewcastle EvolBiol	16
PennStateU MammalianMolEvol	12	UVictoria EvolEcol	16
RoslinInst ComplexTraits	12	VirginiaTechU EvolFishImmuno	17
SimonFraserU PlantEvol	13		
TexasTechU TropicalTreeEvol	13		

ImperialCollege PopEcol

PHD STUDENTSHIP

NERC CENTRE FOR POPULATION BIOLOGY Imperial College London, Silwood Park

Population ecology of bird-mosquito-virus interactions in the wild

Host-vector interactions lie at the heart of many emerging diseases, but we know very little about their basic ecology. This project will use birds as a model host system to test a series of theories on viral population biology. The aim of the first part of the project will be to collect field data to parameterize existing host-vector-virus models and then use these models to predict viral population dynamics. In the second part of the project the student will focus in detail on the effect of both the vectors and the virus on bird populations, looking at both genetic and environmental components of parasite resistance.

This studentship is supported by the NERC Centre for Population Biology, a national centre for ecological research, and the student will be registered at Imperial College London. The student will be based at Silwood Park, which is home to a large group of ecologists and evolutionary biologists. The student will be supervised by Profs Ian Owens and Charles Godfray.

The studentship is available from October 2004. There is no formal deadline for applications and we will start to review applications as soon as they arrive.

For further details please see the websites of the NERC Centre for Population Biology (<http://www.cpb.bio.ic.ac.uk/>) and Imperial's Department of Biological Sciences (<http://www.bio.ic.ac.uk/>). For further information please contact Mrs Diana Anderson by email d.anderson@imperial.ac.uk.

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Ian P. F. Owens Department of Biological Sciences Imperial College London Silwood Park Ascot, Berkshire SL5 7PY UK

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

InstZoology Baboons

Foraging rules in social animals: an empirical study in desert baboons

A NERC Studentship is available to carry out research into the foraging decisions made by individual members of baboon groups in relation to social factors, such as dominance and kinship, and to ecological factors, such as food availability and distribution. This studentship is offered by the Institute of Zoology (Zoological Society of London), in collaboration with University College London. Fieldwork will take place at an established site in Namibia, as part of the wider Tsaobis Baboon Project.

The closing date for applications is 10am Monday 5 April 2004.

Application details are available at: www.zoo.cam.ac.uk/ioz/PhD_studentship.2004.htm. Candidates unable to access this website should contact Guy Cowlshaw on 020 7449 6697 or via e-mail guy.cowlshaw@ioz.ac.uk.

Ireland PlantDiversity

PhD research studentship in plant breeding and evolutionary genetics

'Evaluation of the extent of genetic diversity in Irish perennial ryegrass and its potential for breeding'

(Funded by Teagasc Walsh Fellowship Scheme)

Department of Botany, University of Dublin, Trinity College, Ireland Teagasc, Crops Research Centre, Oak Park, Carlow, Ireland

Perennial ryegrass (*Lolium perenne* L.) is presently the most important forage species in Ireland and most temperate climate zones of the world. It has been assumed that perennial ryegrass has grown on the islands of Ireland and Britain for approximately 300 years but information about its introduction and routes of introduction are lacking. Because of its open-pollination combined with a strong self-incompatibility system both

ecotypes and cultivars of *Lolium* are highly heterogeneous and Irish adapted material might hold a broad range of rare alleles. These rare alleles may have been lost during selection and the breeding process in modern cultivars. Rare alleles could however contribute to a better adaptation to abiotic and biotic stresses in changing environmental conditions and contribute to improved quality and disease resistances. To exploit the potential of this material for breeding and to estimate its value, it needs to be further characterised by means of molecular markers and biochemistry. The frequencies of alleles at microsatellite loci will be estimated in locally adapted old Irish material and currently used popular varieties. The Irish material has not been grouped in the context of further European wild material and contemporary widely grown cultivars to date. Quality assessments on sugars (HPLC and NIRS) and protein (LECO) contents on the plant material will be included in the study. The geographic origin of perennial ryegrass will be investigated with plastid microsatellite markers that will be developed during this project. These markers could also be useful to distinguish among perennial and Italian ryegrass for seed purity testing.

This project is a collaboration between molecular laboratories at the Department of Botany, Trinity College Dublin (TCD) and Teagasc Crops Research Centre Oak Park and will be jointly supervised by Dr Trevor Hodkinson (TCD; www.tcd.ie/Botany/staff/-THodkinson) and Dr Susanne Barth (Teagasc, <http://www.teagasc.ie/oakpark/plantbiotechunit.htm>). The researcher will be based at Teagasc, Oak Park, Carlow but will benefit from interactions with both institutes as the student will be registered at TCD and some research time will be spent at there. The student will receive an annual tax free stipend of 15,000 Euro for maintenance and to cover university fees. Fees are approximately 4,000 Euro for EU students or 8,000 Euro for non-EU students. There will be opportunities to earn additional money teaching and demonstrating on undergraduate courses and invigilating examinations.

Applicants must have a first or second class (preferably upper) Bachelors, or Masters, degree in a biological science or relevant subject. To apply or to obtain further information, please send a CV including research interests and contact details of two referees and a letter of motivation to trevor.hodkinson@tcd.ie and sbarth@oakpark.teagasc.ie by April 9th 2004.

– Dr Trevor Hodkinson.

Lecturer in Botany Head of Molecular Laboratory Department of Botany Trinity College Dublin 2 Ireland

Phone: 00 353 1 6081128 Fax: 00 353 1 6081147

email:hodkinst@tcd.ie

LundU AnimalMigration 2

Dear All,

Please note that there will be an international PhD student course on the topic “The Ecology of Animal Migration” at the Department of Animal Ecology, Lund University, in Sweden 14-23 April 2004. The tentative program of the course is exposed at the Bird Migration Group home page (see address below), and include a large number of lectures of international experts in the fields Locomotion, Orientation and Navigation, Eco-physiology, Genetics of migration, Migration patterns and Genetics of migration. There will be ample time for discussions, presentations of own work, excursion and own projects trying various methods used to study migration during the course. To cover part of the costs for the course we will have to take a course fee of 2000 SEK, which will be paid upon arrival. The logistics and food will have to be paid by the students, but we can help to arrange for low cost rooms with kitchen available.

If you are interested to attend the course, please contact Rachel Muheim (Email: Rachel.Muheim@zooekol.lu.se). For further information you may contact Susanne Åkesson. Please assign for the course no later than 20 March.

Please, do spread the word to your colleagues and students.

Very Welcome to Lund!

With best wishes,

Susanne Åkesson and Thomas Alerstam

Susanne Åkesson PhD, Docent Department of Animal Ecology Lund University Ecology Building SE-223 62 Lund

tel. +46 (0)46-222 3705 fax. +46 (0)46 222 4716 email. susanne.akesson@zooekol.lu.se <http://orn-lab.ekol.lu.se/birdmigration/>

Dear colleagues

The International Max Planck Research School (IMPRS) on 'The Exploration of Ecological Interactions with Molecular and Chemical Techniques' offers 5 PhD fellowships for graduate students in molecular biology, ecology, entomology or chemistry. Application deadline is 31st July 2004. The PhD program starts in January 2005 but earlier arrangements are possible. The Research School in Jena will be the first graduate school worldwide where modern chemical and molecular techniques will be systematically used to study ecological systems. Students will have the unique ability to combine the advances of the genomics revolution with the most advanced techniques in ecological analysis. For detailed information on the PhD school, application and admission procedures please see our homepage <http://www.ice.mpg.de/imprs> or contact the coordinator imprs@ice.mpg.de. I would appreciate it if you forwarded this message to interested students and colleagues.

Sincerely Karin Groten

MichiganStateU StatGenetics

Ph.D. Assistantship in Statistical Genetics and Genomics

Michigan State University (<http://www.msu.edu/>) Department of Fisheries and Wildlife (<http://www.fw.msu.edu/>)

We are currently seeking a highly qualified and motivated student with interest in statistics and bioinformatics applied to population/quantitative genetics and genomics.

Candidates should have a Masters degree in Genetics, Biology or related areas, with background in statistics and programming, or a Masters degree in Statistics/Mathematics or Computer Sciences, with a strong interest in genetics.

To apply, please mail/email a curriculum vitae and the names of three referees with a cover letter to:

Guilherme J. M. Rosa 1205-I Anthony Hall Michigan State University East Lansing, MI 48824-1225 USA
Email: rosag@msu.edu

–

Guilherme J. M. Rosa Assistant Professor Department

of Animal Science Department of Fisheries and Wildlife Michigan State University 1205-I Anthony Hall East Lansing, MI 48824-1225 USA

Phone: 1-517-353-5102 Fax: 1-517-432-9168 E-mail: rosag@msu.edu <http://www.msu.edu/~rosag/>

Newcastle MolEvol

Training Positions for EU PhD students available at Marie Curie Training Site

The European Union has awarded the University of Newcastle a Marie Curie training Site: "Molecular Tools in Evolutionary and Ecological Research" MOTIVE

Over a period of 4 years 10 positions will be available for PhD students from EU countries (but not the UK) to receive training for 6 -12 months in the area of the development and use of molecular tools and to perform part of their PhD studies in Newcastle.

The aim is to deliver training in the development of valuable multidisciplinary and transferable DNA techniques, such as RAPDs, microsatellites and DNA sequencing and their application as genetic tools in biodiversity, evolutionary and ecological research. We currently have 3 vacancies, to be filled between Sept 2004 and March 2005. We are particularly looking for students interested in plant population studies.

The scheme is for postgraduate students pursuing doctoral studies in a subject area similar to that of the Training Site. They should be affiliated to a University as PhD students both at the time of application and during the Marie Curie training fellowship.

The students will receive an allowance of 1200 Euro per month. Money for consumables and travel is available. The positions are now advertised and interested students are requested to apply directly to the organiser.

For information see the web site <http://www.staff.ncl.ac.uk/kirsten.wolff/MC.htm> or contact Kirsten Wolff, for example by sending an email to kirsten.wolff@ncl.ac.uk

Further information on Marie Curie Fellowships in general is available on: <http://www.cordis.lu/improving/-fellowships/home.htm> Kirsten Wolff

Dr. Kirsten Wolff Email:kirsten.wolff@ncl.ac.uk
Reader in Evolutionary Genetics University of New-

castle 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/>

PennStateU MammalianMolEvol

A graduate student position (leading to a PhD) is available beginning fall of 2004 in the group of Kateryna Makova at the Department of Biology, Penn State University. The focus of the group is in both computational and experimental molecular evolution of mammals. We explore available genomic and expression data and use the results to design and conduct wet lab experiments. We are particularly interested in two topics: variation in mutation rates in the genome (e.g., male mutation bias) and evolution of gene expression. For a background, please see several recent publications:

- Makova, K. D., and W.-H. Li. 2002. *Nature*, 416, 624-6. - Li, W.-H., S. Yi, and K. Makova. 2002. *Curr Opin Gen Dev* 12, 650-656. - Makova, K.D., and W.-H. Li. 2003. *Genome Research*, 13:1638-45.

I am seeking highly motivated applicants with strong interest in molecular evolution, bioinformatics, and/or population genetics. Prior experience is preferred, although not required. International students are encouraged to apply. The successful applicant will be guaranteed support for five years (a combination of research and teaching assistantships).

You have an opportunity to join a young dynamic group that enjoys interaction with the Center for Comparative Genomics and Bioinformatics (www.bx.psu.edu) and the Institute of Molecular Evolutionary Genetics (<http://www.bio.psu.edu/IMEG/>) at Penn State. The computational and experimental facilities at Penn State are outstanding and clearly suitable for state-of-the-art large-scale evolutionary analysis. The Makova Lab has been participating in the analysis of the Rat Genome and is currently a member of the Chicken Genome Analysis Group.

Penn State is situated in State College. It is a college town located in beautiful hilly central Pennsylvania within the driving distance to New York City and Washington, D.C. The town of State College is famous for its affordable living, excellent public schools, and lowest crime rates in the country.

Inquiries should be addressed to Kateryna Makova (kdm16@psu.edu). Applications should be sent electronically to kdm16@psu and should include a CV, statement of research interests, copies of relevant publications, GRE scores (and TOEFL scores for international students), and names and e-mail addresses of three recommenders. For more information on the group, see the website: <http://www.bx.psu.edu/-makova.lab/>. All applications received before April 15 will be given consideration. The actual starting date for the position is negotiable (an earlier start is possible).

Kateryna Makova Assistant Professor Department of Biology Penn State University 208 Mueller Laboratory University Park, PA 16802 Tel:(814)863-1619 Fax:(814)865-9131 E-mail:kdm16@psu.edu

Kateryna MAKOVA <kdm16@psu.edu>

RoslinInst ComplexTraits

Please pass onto UK RESIDENTS who might be interested....

BBSRC-funded Ph.D. studentship: Genome analysis of the interaction between production and fitness traits. AVAILABLE FOR UK RESIDENTS

A PhD studentship is currently available at the Roslin Institute (starting October 2004). The objective of this project is to identify Quantitative Trait Loci (QTL) affecting production and fitness-related traits in cattle and to explore whether QTL affecting one trait have an effect on others. Phenotypic and genotypic data that has already been collected on an experimental resource herd of cattle created at the Roslin Institute will be used to test the hypothesis that there is a trade-off between production and fitness traits. Quantitative genetics and QTL detection methodologies will be used to search for genetic regions contributing to variation in performance and fitness traits. QTL that map to similar locations will be investigated further using multi-trait analyses to test whether they contain genes with pleiotropic effects. Results from this study will provide valuable information on the genetic interactions between complex traits and may also be applied to the development of selection strategies in livestock production. Further details available by emailing Dr. Pam Wiener (pam.wiener@bbsrc.ac.uk) or Dr. John Williams (john.williams@bbsrc.ac.uk).

Applicants should have or expect to obtain a first

or upper second class degree in statistics or quantitative/population genetics and be resident in the UK (residents of EU Member States are eligible for fees only). Applications including a full CV and the names and addresses (including email addresses) of two academic referees should be sent to: Jane Anderson, Human Resources, Roslin Institute (Edinburgh), Roslin, Midlothian, EH25 9PS or by email to jane.anderson@bbsrc.ac.uk by 11 March 2004.

Dr. Pamela Wiener Roslin Institute Roslin, Midlothian EH25 9PS +44 (0) 131 527 4460 (phone) +44 (0) 131 440 0434 (fax)

“pam wiener (RI)” <Pam.Wiener@bbsrc.ac.uk>

SimonFraserU PlantEvol

GRADUATE STUDENTSHIP(S) Graduate student positions in Plant Evolutionary Ecology are available in the lab of Dr. Elizabeth Elle, in the Department of Biological Sciences (<http://www.sfu.ca/biology/>) at Simon Fraser University starting summer, 2004. Possible research projects include 1) Mating system evolution and inbreeding in fragmented landscapes; 2) Relative contribution of mating system and demographic parameters to rarity; and 3) Hybrid origin and phylogeography of a highly variable species. Students in my laboratory utilize a variety of techniques including genetic methodologies (allozymes, DNA sequencing and microsatellites), field surveys focused on both plant and insect (especially bee) diversity, and controlled experiments both in the field and in the growth chamber.

Support will include stipends for a combination of teaching and research assistantships, contingent annually upon progress towards a degree. Internal fellowships are also available at SFU, and individuals competitive for NSERC awards will be given priority. SFU is located in the greater Vancouver area of British Columbia, Canada. Opportunities for intellectual interaction occur both within SFU (the Behavioural Ecology Research Group, <http://www.sfu.ca/biology/-berg/>, and FAB-lab, <http://www.sfu.ca/~rvosa/FAB/>) and between SFU and UBC (the Vancouver Evolution Group, <http://www.zoology.ubc.ca/veg/>). For more information about my research group please visit <http://www.sfu.ca/biology/faculty/elle/> or contact me directly (elizabeth_elle@sfu.ca)

Dr. Elizabeth Elle Assistant Professor Dept. of Biological Sciences Simon Fraser University Burnaby,

B.C. V5A 1S6 CANADA 604-291-4592 (office) or -3304 (lab) FAX: 604-291-3496 <http://www.sfu.ca/biology/-faculty/elle/>

TexasTechU TropicalTreeEvol

Graduate Research Assistantship

A PhD graduate student position is available in the lab of Dr. Chuck Cannon, Dept. of Biological Sciences, Texas Tech University (www.biology.ttu.edu), starting Sept. 2004. The research pursued in Dr. Cannon's lab addresses a wide variety of topics from SE Asia wide surveys of genetic diversity in several groups of trees to the development of DNA fingerprinting techniques to detect illegal logging practises. Students will learn advanced molecular DNA techniques (PCR, sequencing, microsats, subtractive hybridization) and also be expected to develop more traditional taxonomic/phenotypic skills. Opportunities will also be available for participation in various conservation projects.

This position will involve a combination of teaching and research, with two to three years of full research possible, given adequate progress and self-motivation. Texas Tech University will be opening a new Experimental Sciences Building by late 2004 and the Dept. of Biological Sciences will be hiring several new faculty over the next few years. The USDA also maintains an active program in the gene expression and engineering of crop plants.

Interested students should send an email (to: chuck.cannon@ttu.edu), stating your interest and contact info, along with a brief resume. Please visit my website (<http://www.biol.ttu.edu/biol2003/-faculty-details.asp?name=Chuck.Cannon>) for details about my current research and publications.

Chuck Cannon Dept. of Biological Sciences Texas Tech University Box 43131 (Flint and Main St) Lubbock, TX 79409-3131 USA 806.742.2715 806.742.3993 fax: 806.742.2963

chuck.cannon@ttu.edu

UBern 2 ConsBiol

Two PhD positions available

An important concept in species protection and population management is to breed some individuals in a protected environment (e.g. in a zoo or a fish hatchery) and to release the progeny into the wild. We study the consequences of different management options for the long-term survival of vertebrate populations.

Start: summer 2004 or earlier Duration: 3 years Salary: according to the guidelines of the Swiss National Science Foundation

We are seeking a person with a degree in biology and strong interests in conservation genetics, life-history, evolution and behaviour.

For further information please contact Prof. Claus Wedekind, Dept. of Conservation Biology, University of Bern, Erlachstrasse 9a, 3012 Bern (claus.wedekind@eawag.ch). Please send your application with your Curriculum vitae and a list of references not later than March 15th to the same address (preferentially by email).

–

Claus Wedekind <claus.wedekind@eawag.ch>

UGroningen EvolEcol

The Centre for Ecological and Evolutionary Studies at the University of Groningen (Netherlands) offers a new Master's programme in ecology and evolution. This "Top Master's Programme Evolutionary Biology" provides an intense training in modern research techniques and is therefore an optimal preparation for a subsequent PhD programme. In order to guarantee an excellent teacher-student ratio, the number of positions is limited to 15. The programme is highly selective and aimed at the brightest and most ambitious students from all over the world. All students admitted will receive a scholarship for the two-year Top Master's programme and potentially an additional four-year scholarship for a subsequent Ph.D. programme. The deadline for application is 15 April 2003. For more information visit www.rug.nl/biologie/cees or contact

Franz J. Weissing Professor of Theoretical Biology Centre for Ecological and Evolutionary Studies University of Groningen Kerklaan 30 9751 NN Haren The Netherlands tel: +31-50-363-2131 fax: +31-50-363-3400 email: weissing@biol.rug.nl

URL: www.rug.nl/biologie/theobio Franjo Weissing <F.J.Weissing@biol.rug.nl>

UGroningen EvolEcol correction

Graduate: New Top Master's Programme in Ecology and Evolution

Sorry for posting this twice, but there was an error in the earlier version of this message.

The Centre for Ecological and Evolutionary Studies at the University of Groningen (Netherlands) offers a new Master's programme in ecology and evolution. This "Top Master's Programme Evolutionary Biology" provides an intense training in modern research techniques and is therefore an optimal preparation for a subsequent PhD programme. In order to guarantee an excellent teacher-student ratio, the number of positions is limited to 15. The programme is highly selective and aimed at the brightest and most ambitious students from all over the world. All students admitted will receive a scholarship for the two-year Top Master's programme and potentially an additional four-year scholarship for a subsequent Ph.D. programme. The deadline for application is 15 April 2004. For more information visit www.rug.nl/biologie/cees or contact

Franz J. Weissing Professor of Theoretical Biology Centre for Ecological and Evolutionary Studies University of Groningen Kerklaan 30 9751 NN Haren The Netherlands tel: +31-50-363-2131 fax: +31-50-363-3400 email: weissing@biol.rug.nl URL: www.rug.nl/biologie/theobio Franjo Weissing <F.J.Weissing@biol.rug.nl>

ULaval SalmonidEvol

POSTDOCTORATE or Ph.D. POSITION IN SALMONID EVOLUTIONARY FUNCTIONAL GENOMICS

We are currently looking for either a postdoctorate or Ph.D. candidate to be involved in our ongoing research project regarding the elucidation of functional genomic bases of growth and anadromy in salmonid fishes. This multidisciplinary project is funded by

FQRNT (Quebec) and NSERC (Canada) and is also part of the research program of the Canadian Research Chair in conservation genetics of aquatic organisms.

The originality and interest of this project is based upon a multidisciplinary approach integrating genomics, physiology and immunology. The use of charr species (*Salvelinus*) as a model system offers particular interest for investigating the functional genomic bases of growth and anadromy. Namely, some of these species are well differentiated in terms of growth potential and physiological adaptations to seawater. Yet, such species can interbreed in laboratory and natural conditions, which offers a unique opportunity to investigate the basis of heterosis and outbreeding depression at the functional genomics level.

The specific objective of the proposed research will be to apply microarray technology for quantifying gene expression profiles in pure brook and arctic charr, as well as in their hybrid crosses in order to determine and compare the nature and number of genes potentially involved in differential growth in both freshwater and saltwater. A 16000 gene microarray recently developed in salmonids is already available to achieve this work.

We are primarily looking for a candidate with strong laboratory expertise in functional genomics, a solid theoretical background in evolutionary biology, quantitative genetics or comparative physiology, as well as expertise in management and analysis of large data bases.

The position is available now.

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

To learn more about ...

Quebec city : <http://www.quebecweb.com/tourisme/-quebec/villequebec/introang.html> Laval University : <http://www.ulaval.ca/> The Biology department and our research programs: <http://www.bio.ulaval.ca/-index-alt.html>

ULeicester L1 Evol

Dear EvolDir,

MRC CAPACITY BUILDING* STUDENTSHIP Department of Genetics, University of Leicester Applications are invited for a three-year PhD studentship avail-

able from 1st October 2004 within the Department of Genetics, a 5-star rated research department. *These prestigious awards aim to support provision of multidisciplinary training that will help to build the research workforce in areas of new or expanding research opportunity.

The successful candidate will study the impact of L1 retrotransposons (our most active transposable element) on human genetic variation, particularly in gene expression, using complementary bioinformatic and molecular genomic approaches. In addition the dissemination of this genomic variation data through novel informatic approaches is also of primary interest.

Enthusiastic science graduates with a background in evolutionary genetics and/or bioinformatics, looking for a challenge at the interface between these disciplines, are encouraged to apply.

Please note full studentships are available to UK citizens only (see the MRC website (<http://www.mrc.ac.uk>) for eligibility details). Informal enquiries (as soon as possible) to Richard Badge by email: rmb19@leicester.ac.uk To apply send your CV and the names and addresses of two referees to the academic secretary Sarah Laband, either by email at: sll6@leicester.ac.uk , or mail to: Department of Genetics, Adrian Bldg Rm G6, University of Leicester, University Road, Leicester, LE1 7RH.

Thank you for your attention,

Dr Richard M. Badge, Lecturer Department of Genetics, University of Leicester, University Road, Leicester LE1 7RH UK Email: rmb19@leicester.ac.uk Office phone: 0116 2525042 Lab phone: 0116 2522843

UNeuchatel 2 PlantInsect interactions

2 PhD Positions

at the Laboratory of Animal Ecology and Entomology University of Neuchâtel, Switzerland

The Laboratory of Animal Ecology and Entomology invites applications for 2 PhD positions in the field of Ecology of plant-insect interactions

We study the ecology and evolution of tri-trophic interactions between plants and insects in natural and agricultural systems. Current projects combine lab and fieldwork to investigate: * the ecology of an alpine

leaf beetle * the attraction of parasitoids by herbivore-damaged plants * the consequences of plant domestication for tri-trophic interactions (for details see: <http://www.unine.ch/zool/leae/index.html>).=20

We are looking for highly motivated graduate students with some background in any of the following fields of research: insect-plant interactions, three trophic level interactions, chemical ecology, animal behaviour, population genetics or evolutionary biology. Students with experience in molecular biology or analytical chemistry are highly encouraged to apply. The research topics will be defined in consultation, but should complement our on-going research. A contribution to lab courses (Entomology or Ecology) for second and third year Biology students is expected. Teaching is done mostly in French but the lab is international. The positions are for a minimum of 3 years (maximally 4). Starting dates are June 1 and October 1, 2004.

Apply by sending an email describing your experience and research interests. Send applications and requests for further information to Martine Rahier (Martine.Rahier@unine.ch), Betty Benrey (Betty.Benrey@unine.ch) or Ted Turlings (Ted.Turlings@unine.ch)

as polyploids can be found. This makes the genus very interesting from an evolutionary genetics point of view. The *Plantago* species that are most common in the UK have been studied for their variation at allozyme loci, minisatellite DNA fingerprinting and cp RFLP variation. Studies describing variation at microsatellite loci are underway. Many aspects of the genetics of *Plantago* have already been studied, but even more questions have not been answered, such as the discrepancy between sequence evolution of the different genomes, microsatellite variation in relation to the mating system or QTL analysis of ecological genes in two sister taxa. Therefore, there are opportunities for developing the project in a number of directions depending on the interests of the student appointed.

Please contact me if you are interested in the opportunity and would like to know more.

How to apply? see the webpage.

Kirsten Wolff

Dr. Kirsten Wolff Email:kirsten.wolff@ncl.ac.uk
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/>

UNewcastle EvolBiol

PhD studentships in the School of Biology at the University of Newcastle, UK.

We are an enthusiastic and growing research community which provides a stimulating and exciting research environment. This year we are offering a number of studentships funded by Research Councils and School Divisions.

Research falls into the following broad groupings:

* Visual Neuroecology * Molecular Ecology & Technology * Biological Complexity & Modelling

There are a large number of possible projects about which you can find more information on <http://www.ncl.ac.uk/biol/postgrad/funding.htm> One of the opportunities is:

Molecular evolution in the genus *Plantago*

The genus *Plantago* has been studied for a wide range of questions, from ecology, via genetics to physiology. The species in the genus have mating systems from obligate outcrossing to highly selfing, and also diploids as well

UVictoria EvolEcol

GRADUATE STUDENT POSITIONS Dr. Brad Anholt, in the Department of Biology, University of Victoria seeks two students at the MSc or PhD level with interests in Evolutionary Ecology. Two model systems are established in the laboratory: 1) The evolution and ecological consequences of inducible defenses in the hypotrich ciliate *Euplotes*. 2) Environmental sex determination and its dynamic consequences in the supratidal copepod *Tigriopus californicus*. Research approaches combine modeling, molecular, experimental and statistical methods.

The department guarantees a minimum support level of \$17K for 2yr of MSc and \$18K for 3yr of PhD. Support sources include a combination of teaching and research assistantships, and competitive scholarships.

Victoria is on Vancouver Island with easy access to the outer coast and diverse marine habitats. We are connected to the mainland by a scenic 95 minute ferry ride.

Initial expressions of interest can be sent by email to banholt@uvic.ca

Bradley R. Anholt, Professor and Canada Research Chair Dept Biology University of Victoria

banholt@uvic.ca voice: 250-721-7106 FAX : 250-721-7120

“Bradley R. Anholt” <banholt@uvic.ca>

VirginiaTechU EvolFishImmuno

Ph.D. Assistantship in Ecology, Evolution and Fisheries Science, Virginia Tech University and USDA-ARS Center for Cool and Coldwater Aquaculture.

Responsibilities: Conduct research and coursework towards the doctorate degree. Research will address characterization of genetic variation in immune response genes of rainbow trout and its association with disease resistance. Coursework will be taken at Virginia

Polytechnic Institute and State University. Research will be conducted at the USDA - Agricultural Research Service (ARS) Center for Cool and Cold Water Aquaculture (as an ARS Federal Government student employee). Qualifications: Highly-motivated self-starter with M.S. in fisheries science, immunology, genetics or related field, experience in molecular genetics, interest in fish immunology and/or genetics. Salary: Graduate teaching assistantship and graduate tuition while at Virginia Tech and a student salary while at USDA. Closing date: Until filled. Anticipated start date, Fall 2004. Contacts: Inquiries may be addressed to either: Eric Hallerman, Professor, Department of Fisheries and Wildlife Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA 20461-0321. Tel: 540-231-3257, Email: ehallerm@vt.edu. Yniv Palti, Research Scientist, U.S. Department of Agriculture Agricultural Research Service, Center for Cool and Cold Water Aquaculture, 11861 Leetown Road, Leetown WV 25430, Tel: 304-724-8340 ext.2134, Email: ypalti@ncccwa.ars.usda.gov. Online applications may be downloaded at <http://www.grads.vt.edu/-homeapply.html>. For general information on the NCCCWA-ARS-USDA research program go to <http://ncccwa.ars.usda.gov/>. ypalti@yahoo.com

Jobs

ATCC ProtistEvolution	17	Sweden FieldworkAssist	21
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Denver MolEvol	19	UArizona GenomicsLabManager	22
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Lisbon FishPopGenet	20	ULyon 2 PopGenetics	24
Paris EvolGenomics	21		
SUNY Fredonia PlantBiologist	21		

This email is to notify you of a position currently available at the ATCC for a Research Scientist.

We are seeking an individual with strong molecular biology capability interested in molecular taxonomy or evolutionary biology of free-living protists. This indi-

ATCC ProtistEvolution

vidual must be interested in pursuing research by publication in peer-reviewed journals and seeking funding to support his/her research program.

This is the web address [http://www.atcc.org/Employment/jobdetail.cfm?job_id7] for the protistology research scientist position. If you have additional questions regarding this position please feel free to contact me.

Donald E. Burgess, Ph.D. Collection Scientist, Protistology ATCC 10801 University Blvd. Manassas, VA 20110 U.S.A.

phone: 703-365-2700 fax: 703-365-2730

"Burgess, Donald" <DBurgess@atcc.org>

BarnardCollege ArabidopsisGenetics

Please post the following job to the EvolDir site. It is for a fulltime BA/BS/MS level research assistant position, available immediately or with a start-date no later than Summer 2004.

Thank you. Hilary Callahan

Barnard College, Columbia University, seeks FULL-TIME RESEARCH ASSISTANT to conduct large-scale field and growth-chamber experiments with the model plant species *Arabidopsis thaliana*. The research addresses the quantitative genetic architecture and fitness consequences of variation in flowering habit (i.e., phenotypic plasticity) induced by normal and milder winter temperature regimes and regulated by FRI, FLC and other flowering time genes.

STARTING DATE AND DURATION: Available immediately, this NSF-funded position requires a minimum 2-year commitment. A 3-year commitment is desirable and longer-term employment is possible, contingent on funding renewal.

RESPONSIBILITIES:

Implement and maintain growth chamber and field experiments Phenotype plants: quantify flowering behavior and plant fitness. Input, organize, manage, and archive large data sets. Use Columbia U. libraries and e-bibliographic databases. Assist with preparing figures and text for publication. Supervise some aspects of undergraduate projects and provide some training. Participate in other lab projects and perform basic duties (e.g., order supplies, care for plants and maintain

seed stocks, maintain equipment, backup and maintain computers)

QUALIFICATIONS:

Minimum B.A. or B.S., preferring major in biology or botany. Basic computer use and experience with MS-Excel essential. Must be able to work independently and be meticulous in data handling and plant care. Prior research experience and courses in evolution, genetics, population genetics, ecology, or biostatistics desirable. Exposure to Powerpoint, EndNote, SigmaPlot, SAS or SPSS, ImagePro, or QTL Cartographer desirable. Training will be provided. Some weekend work.

SALARY:

\$33,000/yr, plus health benefits, partial tuition support, travel expenses to field site.

LOCATION:

Barnard College, affiliated with Columbia University in the City of New York. Field work will be conducted at nearby Lamont-Doherty Earth Observatory campus in Palisades, NY.

Barnard College is an Equal Opportunity Employer and encourages applications from women and members of underrepresented groups.

TO APPLY:

Provide: (1) a letter stating why you are interested in the position and summarizing relevant academic and work experience, (2) a resume, and (3) name, phone number, e-mail, and address of three references, including at least one academic and one employment reference.

Send materials to:

Human Resources

Attn: Plant Biology Research Assistant

3009 Broadway

New York, NY 10027

fax: 212-854-2454

email: hr@barnard.edu

DEADLINE: Applications accepted until position is filled. Must start no later than Summer 2004.

hcallaha@barnard.edu

RESEARCH ASSISTANT (RA1B)

Department of Genetics

Salary: £18,265 - £20,311 pa

Limit of tenure: 31 January 2007*

We wish to appoint a full time Research Assistant to work on the research projects of Dr. José M. Ranz in Prof. Michael Ashburner's laboratory. The focus of the research is the study of evolution at a regulatory level in the model organism *Drosophila* using microarray technology.

You will be expected to conduct experiments involving molecular biology and genetic techniques including, but not restricted to, PCR, DNA and RNA extraction, DNA and RNA hybridisation with microarrays, DNA sequencing and data analysis. You should have a degree in the biological or life sciences and at least one year's practical experience in a molecular biology laboratory.

The position, which is funded by the BBSRC, is available until 31 January 2007 in the first instance and may, subject to the availability of funding, be renewed for a further period or periods.

Informal enquiries can be addressed to Dr. José M. Ranz (jmr68@mole.bio.cam.ac.uk) or Prof. Michael Ashburner (ma11@gen.cam.ac.uk).

For an application cover sheet please ring 01223 - 333980 or visit <http://www.admin.cam.ac.uk/offices/personnel/forms/-pd18> Full applications in the form of the cover sheet, a letter stating research interests and a CV, with the names of two referees who may be contacted prior to interview, should be sent to Mrs Tracy Oakley, Departmental Secretary, Department of Genetics, Downing St, Cambridge CB2 3EH UK; email t.oakley@gen.cam.ac.uk FAX: 44 (0) 1223 333992.

Closing date: 31st March 2004.

"Jose M. Ranz" <jmr68@mole.bio.cam.ac.uk>

Denver MolEvol

Molecular Evolution - Scientist/Post-doc

Evolutionary Genomics, a genomics company based near Denver, Colorado, is recruiting Post-docs and/or Scientists (Level 1 and 2) with broad experience in

molecular evolution/comparative genomics, as well as general molecular biology expertise. We use strategies derived from molecular evolution to identify yield genes in domesticated plants. Familiarity with Ka/Ks (Dn/Ds) techniques is especially desirable. Expertise in database design and maintenance is desirable, as is coding experience. We encourage publication and original thought. While we are currently primarily looking for persons with experience in plant molecular biology, we will also consider mammalian biologists with a thorough knowledge of molecular evolution. (www.evolgen.com). Salary commensurate with skill set and experience. Please send CV by email ONLY to Dr. Walter Messier, Chief Technology Officer.

Walter Messier, Ph.D. Chief Technology Officer Evolutionary Genomics, L.L.C. 12635 East Montview Boulevard Aurora, CO 80010 Phone: (720) 859-4084 FAX: (720) 859-4076 Email: wmessier@evolgen.com

HighlandsBioStation AssocDirector

Associate Director Highlands Biological Station

Position Information

The Highlands Biological Station, an interinstitutional center of the University of North Carolina, seeks a full-time associate director whose duties will be split between academic teaching and student coordination and administrative duties. Salary is \$30,000 per year plus full state benefits.

Position Description

Duties include teaching an advanced undergraduate-level course, coordinating research internships and a group project, and helping to build infrastructure to benefit students in the Carolina Environmental Program (UNC-Chapel Hill), who spend the fall semester in residence at HBS. Other duties include helping to maintain and upgrade databases, websites, and accounting systems. The individual will also help to coordinate an annual native plant conference and a summer conservation lecture series. Some help with grant writing and other efforts to build infrastructure will be required.

Knowledge, Skills, and Abilities Required

The person should have experience and a strong interest in teaching undergraduates. The person should be willing to take on responsibilities related to database

management and program coordination.

Education and Training Requirements

The successful candidate should have a Ph.D. in biological sciences, environmental sciences, or a related field with interest and experience in teaching undergraduates. The person must have the capacity to learn new computer skills, including database management and web page construction. Experience writing grant proposals and coordinating conferences/lectures is desirable.

How to Apply

Submit a curriculum vitae, statement of teaching interests and experience, and at least three letters of recommendation to Dr. Robert Wyatt, Executive Director, Highlands Biological Station, Highlands, NC 28741; 828-526-2602; e-mail: wyatt@email.wcu.edu; www.wcu.edu/hbs. Also submit a state employment application, which can be downloaded at <http://admfina.wcu.edu/hr/formspage.htm>.

**** Robert Edward Wyatt, Ph.D. Executive Director Highlands Biological Station 265 Sixth Street, P.O. Box 580 Highlands, NC 28741 USA tel: 828-526-2602 fax: 828-526-2797 e-mail: wyatt@email.wcu.edu <http://www.wcu.edu/hbs> Robert Wyatt <wyatt@email.wcu.edu>

It also provides international Reference Laboratories for foot-and-mouth disease (FMD) and eight other diseases. An important mission of the WRL-FMD is to perform primary or referral FMD diagnosis and to characterise FMDV isolates from countries around the world. This characterisation (genetic and antigenic) is necessary to determine the origin of ongoing and future epidemics and to select appropriate strain(s) to include in vaccine antigen banks. Nucleotide sequencing of the viral genome is a powerful tool used in the tracing of FMDV and is helpful for the selection of vaccine strains.

The Molecular Epidemiology Group within the World Reference Laboratory for FMD at Pirbright is seeking a freelance professional in computing (i) to set up a database to store sequencing data and epidemiological information on FMD virus isolates and (ii) to link a combination of software to process genetic sequences and perform phylogenetic analysis on these sequence data.

For any information, please contact: Jean-Francois Valarcher, Institute for Animal Health, Pirbright Laboratory, Ash Road, Woking, Surrey, GU24 0NF;

By Email : jean-francois.valarcher@bbsrc.ac.uk or by Tel: 01483 23 11 32 or 01483 23 10 23

Eddie Holmes <edward.holmes@zoology.oxford.ac.uk>

InstituteAnimalHealthUK Bioinformatics

Short-term Bioinformatics Position

The Institute for Animal Health (IAH) is one of eight research institutes of the Biotechnology and Biological Sciences Research Council (BBSRC) and is at the forefront of research into animal diseases.

It is based on three sites: Compton (near Newbury); Pirbright (near Woking); and Edinburgh. In total, the Institute employs some 500 staff and, at any one time, is host to up to 100 students and visiting scientists. Additionally, the Institute provides services for the Edward Jenner Institute which has around 50 staff, co-located on the Compton site.

The Pirbright site deals with exotic viral diseases of livestock. With 170 staff and postgraduate students, the Pirbright laboratory is the principal UK centre carrying out basic and applied research to underpin UK policies for safeguarding livestock against virus infec-

Lisbon FishPopGenet

Dear EvolDir, The Department of Animal Biology (Faculty of Sciences - University of Lisbon) has a 1 to 3 years Research Grant, immediately available in the frame of a National Project on Phylogeography and Population Genetics of Southern Iberian Freshwater fish. The successful candidate will have a Graduation in Biology, with research interests in phylogeography, population genetic structure or related topics. Furthermore a very good English background and a strong commitment to timely publication of results, will be essential. Informal inquiries may be made to Prof Manuela Coelho at the email address: mmcoelho@fc.ul.pt. Application is by CV with details of one referee to the same address. The deadline for applications is the 31st March 2004. Please note this grant is available only to Portuguese citizens. Thank you for your attention,

Manuela Coelho (Associate Professor) mmcoelho@fc.ul.pt Faculdade de Ciências da Universidade de Lisboa 1749-016 Lisboa tel. 217500000 ext. 24319

fax. 217500028.

Maria Manuela Coelho <mmcoelho@fc.ul.pt>

Paris EvolGenomics

ASSISTANT PROFESSOR IN EVOLUTIONARY GENOMICS

An assistant professor position in evolutionary genomics will be opened soon at the Institut National Agronomique Paris-Grignon (INAP-G) in Paris, France.

INAPG (<http://inapg.fr>) is an institution for advanced education whose 2nd and 3rd years are comparable to a Master in the University system. Students are accepted into the Institute after a two-year preparation and a competitive exam. The teaching curriculum covers a wide spectrum of fields : statistics, biology, agronomy, animal sciences, biotechnology, food sciences, environmental sciences, ecology, economics, etc...

We are looking for a candidate with a strong background in biology, evolutionary and population genetics, molecular evolution, and interested in the study of the evolution of complex traits. Research will concern the relationship between molecular and phenotypic evolution. It will be held at the UMR de Genetique Vegetale du Moulon (<http://moulon.inra.fr/>), near Paris, France.

Working language is french. More details about the position can be found at (<http://moulon.inra.fr/SGV/-jobs>).

Contacts : Philippe Brabant (brabant@moulon.inra.fr) or Christine Dillmann (dillmann@moulon.inra.fr)

dillmann@moulon.inra.fr

SUNY Fredonia PlantBiologist

The Department of Biology at the State University of New York (SUNY), Fredonia invites applications for a tenure-track ASSISTANT PROFESSOR position in botany/plant biology, beginning August 2004. We seek a broadly trained person with a commitment to excellence in teaching. Teaching responsibilities will in-

clude an introductory majors course in plant diversity, upper-level courses in plant biology, and a nonmajors biology course. The successful candidate will be expected to maintain a scholarly research program that involves undergraduate and Master's degree students. Ph.D. and postdoctoral experience are required. Send curriculum vitae, statement of teaching philosophy, research interests, unofficial copies of undergraduate and graduate transcripts, and three letters of reference by March 26, 2004, to: Chair, Plant Biologist Search Committee, Department of Biology, State University of New York, Fredonia, Fredonia, NY 14063. E-mail: biology@fredonia.edu ; fax: 716-673-3493. SUNY, Fredonia is an Affirmative Action Employer. We actively seek and encourage applications from minorities, women, and people with disabilities.

William Brown <William.Brown@fredonia.edu>

Sweden FieldworkAssist

We are looking for a field assistant for this spring's lapwing (*Vanellus vanellus*) breeding season. The study site is at Öland Island, just off = the south-east coast of Sweden.

The field project will run from approximately 27 March to 18 June.

The salary is 1500 euro/month, lodging included.

Responsibilities include: * behavioral observations * monitoring of breeding parameters * trapping, ringing and taking blood samples of lapwings

Qualifications: * keen observational skills * experience in trapping and handling birds * an interest in behavioral ecology * a tolerance for cold weather * a willingness to work long and odd hours when needed

Applicants are encouraged to send an e-mail stating experience, background, interests along with two recommendations as soon as possible to:

Dr. Richard Wagner E-mail: R.Wagner@klivv.oeaw.ac.at
Konrad Lorenz Institute, Austrian Academy of Sciences, Savoyenstrasse 1a, A-1160 Vienna, Austria

with a copy (Cc) to:

Dr. Gaute Grönstöl E-mail: g.gronstol@klivv.oeaw.ac.at
Konrad Lorenz Institute, Austrian Academy of Sciences, Savoyenstrasse 1a, A-1160 Vienna, Austria

wli@midway.uchicago.edu

Taipei Director Biodiversity

Dear All, Attached below please find an ad for Director for a new Biodiversity Center at Academia Sinica, Taipei, Taiwan. The research support and salary are both good.

Wen-Hsiung ———

Research Center for Biodiversity, Academia Sinica, Taipei, Taiwan DIRECTOR Academia Sinica, Taipei, Taiwan is seeking a distinguished scientist to be the Director of the newly established Research Center for Biodiversity (RCBAS).

The RCBAS is located on the Academia Sinica campus in Nankang, Taipei. Its mission is to promote basic biodiversity research in Taiwan and to advance domestic and international research collaboration in the conservation, education, and sustainable use of biodiversity. RCBAS currently has 19 principal investigators engaged in various disciplines of biodiversity research and will recruit several new members. For details about Academia Sinica and its current biodiversity research, please visit the websites: <http://www.sinica.edu.tw/>, <http://www.sinica.edu.tw/zool/english/eindex.htm>, and <http://botany.sinica.edu.tw/>. To learn about the Plan for the RCBAS, please visit the website: <http://biodiv.sinica.edu.tw/>. Qualifications for the new Director include a Ph.D. degree or equivalent, a record of distinguished research accomplishments, and evidence of strong leadership. The initial appointment is for a period of three years (renewable for a second term). The Director will also carry the title of Research Fellow. The salary is competitive.

Academia Sinica encourages applications and nominations from all sources by the closing date of May 31, 2004, but will continue to accept late applications until the position is filled. Applications or nominations should include a full curriculum vitae, together with a publication list, five representative reprints, as well as a list of five references (including names, postal and/or e-mail addresses, and phone and/or fax numbers) who are knowledge of the applicants or nominees qualifications for the position. These items should be submitted to Dr. Michael Lai, Office of the Vice President, Academia Sinica, Nankang, Taipei 11529, Taiwan. Nominations should have the consent of the nominee. For any additional questions, please contact Dr. Kwang-Tsao Shao at zoskt@gate.sinica.edu.tw.

U dEvry MathGenomics

A position of Professeur of Mathematics applied to Genomics will be open next year at the Universite d'Evry (near Paris - Trance). The research will be done in the Lab' Statistique et Genome (CNRS-INRA-University)

To get more details, please contact Bernard Prum prum@genopole.cnrs.fr

– Bernard PRUM Laboratoire “Statistique et Génome” (UMR CNRS 8071) La genopole Tour Evry 2 - 523 place des Terrasses - 91000 Evry, France tél (33) 1 60 87 38 06 - fax (33) 1 60 87 38 09

Bernard Prum <prum@genopole.cnrs.fr>

UArizona Genomics Lab Manager

Evolutionary Genomics Assistant Staff Scientist/Lab Manager The University of Arizona Tucson, Arizona

Position Type: Appointed Benefits Eligible: Yes Salary: DOE Opening: 2/24/04 Hours: Full-time Closing: Open Until Filled

Position Summary: An Assistant Staff Scientist and Manager of the Genomic Analysis and Technology Core (GATC) (formerly the Laboratory of Molecular Systematics and Evolution) is being recruited at the University of Arizona. The GATC is a university-wide core facility providing a wide range of molecular biology services and instruction in current molecular genetic methods including DNA Sequencing, Fragment Analysis, Affymetrix GeneChip, Custom Spotted Microarray, DNA Purification and Quantification, and Real-time PCR. This position requires the professional and intellectual ability to provide services on the cutting edge of today's technology in molecular genetic methods, and to provide leadership in the application of molecular genetic methods to research and teaching.

Duties & Responsibilities: - Provide leadership in the application and development of molecular biology services. - Maintain a high quality technical output. -

Oversee daily operation of the facility. Supervise and train technical operators of the facility. Assure that facility instrumentation is properly maintained. Monitor facility budget, schedule, and prioritize instrumentation use. - Assure that GATC instrumentation and services are continually upgraded with advancing technology so that the facility maintains its status as a "state-of-the-art" facility. - Develop, coordinate, and deliver workshops, classes, and seminars on emerging and fundamental techniques in the application of molecular genetic methods. - Work with Director and faculty committee to establish facility priorities and to develop strategic plans.

Minimum Qualifications: - Bachelor's degree in Molecular & Cellular Biology, Genetics, Biochemistry or related field and six years of related experience with increasing responsibility in a research and/or educational setting including at least two years of experience in a leadership/manager position. - Expertise in automated DNA Sequencing technologies - Advanced knowledge in other molecular biology techniques including genomic DNA isolation, plasmid and phage isolation, PCR product purification, DNA quantification, RNA isolation/quantification, DNA/RNA purity verification, southern/northern blotting, and PCR. - Thorough knowledge of related instrumentation and equipment. - Excellent interpersonal and communication skills. - Demonstrated supervisory skills.

Preferred Qualifications: - Advanced degree in Molecular & Cellular Biology, Genetics, Biochemistry or related field and four years of related experience with increasing responsibility in a research and/or educational setting including at least two years of experience in a leadership/manager position. - Related work experience in a Core Facility. - Experience in spotted microarray techniques, Affymetrix system, quantitative PCR, and fluorescent fragment analysis. - Good experimental design skills. - Conversant with molecular biology computer software and analysis tools.

For more detailed information and instruction on how to apply, please visit our website: <https://www.uacareertrack.com> (job #30181). Consideration of completed applications will begin on March 22nd, 2004. Questions regarding the application process may be directed to Karen Batcheller at kbatcheller@arl.arizona.edu.

The University of Arizona is an EEO/AA - M/W/D/V Employer .

- Michael Hammer Dept. EEB Biosciences West University of Arizona Tucson AZ 85721 mfh@u.arizona.edu (520) 621-9828

Michael Hammer <mfh@u.arizona.edu>

UGeorgia ResearchTech 2

The University of Georgia, Savannah River Ecology Laboratory seeks a term appointment Research Technician. This position will be in association with Travis Glenn's molecular ecology lab involving conservation genetics and genotoxicology. Primary duties for this position consist of laboratory work including DNA extraction, setting up PCR reactions, gel electrophoresis, genotyping microsatellite loci, and automated sequencing. Small amounts of field work may be required. Candidates should have a BS degree in biology, ecology, molecular biology, genetics or a related field and have some experience with genotyping. The successful applicant must meet badging requirements for the Savannah River Site. Interested candidates should submit a letter of application, resume, copy of transcripts (unofficial is OK), and a list of three references including current contact information to Mandy Schable, Savannah River Ecology Laboratory, Drawer E, Aiken, SC 29802 or schable@srel.edu <<mailto:schable@srel.edu>>. Further information about the SREL DNA Lab is available at our website: http://www.uga.edu/srel/DNA_Lab/index.htm. Review of applications will begin immediately and will continue until the position is filled. The University of Georgia is an Equal Opportunity and Affirmative Action Institution.

sushaus@biol.sc.edu

UHull 2 Cichlids

Two jobs: Genetic basis of speciation traits in African cichlid fish

We invite applications for two BBSRC-funded positions: a 3 year Postdoctoral Research Associate and a 3 year Research Technician. We are looking for enthusiastic and competent individuals to investigate the genetic basis of reproductive isolation in closely related species of cichlid fish from Lakes Malawi and Victoria. Specifically, we will investigate the genetic basis of male courtship colour and female mate preference in sister species and their hybrids bred in

our experimental aquarium systems. The project will be located in the Department of Biological Sciences, University of Hull (lead PIs George F. Turner and Ole Seehausen (U Hull and Institute of Zoology, U Bern). Further details of the project can be found on the web at <http://www.hull.ac.uk/cichlids/BBSRC.html> General details on the PIs and their research groups can be found at <http://www.hull.ac.uk/cichlids>, <http://www.hull.ac.uk/biosci/staff/turner.html>, <http://www.hull.ac.uk/biosci/staff/seehausen.html>

(1) Postdoctoral Research Associate: Salary will be according to UK academic grade RA1A point 6 (GBP 20,311pa). Duties include designing and carrying out experimental crosses, designing and carrying out experimental tests of mate preference, assaying male colour phenotypes, molecular paternity analysis, data analysis and writing publications, dissemination of results through conference presentations and papers published in international journals, supervision of a research technician, assistance with supervision of undergraduate and masters student projects, participation in general duties within the research group, such as maintenance of aquarium fish stocks, molecular lab duties, group publicity (e.g. web site) etc.

We are looking for someone with a PhD in Evolutionary Biology or a related field, a record of published research in international journals, strength in molecular genetic laboratory and analytical techniques, some experience in handling live fish and aquaria, good interpersonal skills and the ability to work regular hours and to deadlines, and sometimes non-standard hours. The work will involve thorough participation in team-centred research activities in collaboration with other researchers and research students.

(2) Research Technician Salary for the Research Technician will be according to UK University technical staff Grade D point 15 (GBP 15,053pa). Duties include general maintenance of aquaria including cleaning, replacing of basic components, basic servicing of life support systems, maintaining fish stocks and experimental cross breeding of fish, tagging fish and collecting tissue samples for DNA analysis, keeping stock records, application of basic molecular genetic techniques, digital photography including computer analysis of photographs.

We are looking for a computer-literate person with Level 2 qualifications and ideally experience in handling live fish and the servicing of aquaria and/or some experience of molecular techniques and/or digital photography. The person appointed will work in collaboration with a postdoctoral researcher but will be expected to carry out some work unsupervised and may have to work non-standard hours. An appropriately qualified candidate may have the opportunity to register for a

part-time PhD.

Applicants should submit an application letter, CV, and contacts of two academic referees. Applicants for the Postdoctoral Research Assistant should send their application directly to George Turner (g.f.turner@hull.ac.uk) or Ole Seehausen (o.seehausen@hull.ac.uk). Applicants for the Research Technician should submit their application to George Turner (g.f.turner@hull.ac.uk) or Margaret Huffee (M.Huffee@hull.ac.uk) (Departmental superintendent).

The closing date for applications is 12th March 2004, though applications after that deadline may be considered. We expect to interview shortlisted candidates for both positions shortly after that. Starting date will be as soon as possible after 1 April 2004.

— Ole Seehausen Molecular & Evolutionary Ecology Group, Dept. of Biological Sciences, University of Hull, Hull HU6 7RX, U.K. Phone +44 (0)1482 465962 Fax +44 (0) 1482 465458 O.Seehausen@hull.ac.uk

ULyon 2 PopGenetics

Two assistant professor positions are open in “Laboratoire de Biometrie et Biologie Evolutive” of the University of Lyon (France) :

- 1) Theoretical population genetics and comparative genomics.
- 2) Theory and modelling of parasitic and symbiotic systems.

The application procedure is described at: http://www.education.gouv.fr/personnel/-enseignant_superieur/enseignant_chercheur/-antares.htm The dead line for applications is April 5, 2004.

Further information can be obtained by contacting the host laboratory’s director: Prof. C. Gautier (cgautier@biomserv.univ-lyon1.fr). The host laboratory’s web site is : <http://biomserv.univ-lyon1.fr> –

| Manolo Gouy | | Laboratoire de biometrie et biologie evolutive - UMR CNRS 5558 | | Universite C. Bernard - Lyon 1 | E-MAIL : mgouy@biomserv.univ-lyon1.fr | | 43 Bd du 11 Novembre 1918 | Tel : +33 4-72-43-12-87 | | 69622 Villeurbanne, France | Fax : +33 4-72-43-13-88 |

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BioRad microarrays

Dear Colleagues

I would like to contact people working with microarrays (expression/snp screening) but using Bio-Rad equipment.

Thank you in advance for your attention.

Sincerely,

Cristiane

Cristiane Bastos-Silveira Centro de Biologia Ambiental Faculdade de Ciências-UL Edifício ICAT Campo Grande 1749-016 Lisboa Portugal Tel: (+351) 21 750 00 00 Ext. 24404 (office) ou 20115 (lab) Fax: (+351) 21 750 01 72 e-mail: <mailto:cbasilveira@fc.ul.pt> cbasilveira@fc.ul.pt or <mailto:cbasilveira@netcabo.pt> cbasilveira@netcabo.pt

CV comparison

Dear Evoldir members, does anyone know if the only way to perform statistical comparisons among coefficients of variation (CVs) of different traits is with the "c" value. Ive only found the "c" value cited in Markow et al., 1996 (Anim. Behav. 52:759-766), but Im struggling to find the book where this calculation is described (Woolf, C. M. 1968. Principles of Biometry. Toronto: Van Nostrand). Is there any other test that can be successfully employed? If there is not, could someone tell me any reference where this calculation (c value) is explained.

Thanks in advance,

Aurelio F. Malo E-mail: malo@mncn.csic.es

Cattle samples

Dear Evoldir members,

I am after some samples... I am a PhD student investigating genetic variation within and between species of cattle. I am having trouble sourcing wild relatives of the domestic European cow (*Bos taurus*). I would be grateful if anyone would be able to provide me with DNA, blood, semen and/or tissue from any of the following species: Banteng (*Bos javanicus*), Gaur (*Bos gaurus*), Yak (*Bos grunniens*), African Buffalo (*Syncerus caffer*), Asian Buffalo (*Bubalus bubalis*). 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.

Kind Regards,

Sean

Sean MacEachern Department of Genetics Department of Primary Industries 475 Mickleham Rd. Attwood, Victoria Australia, 3049. phone (03) 9217 4200 fax (03) 9217 4299 email Sean.Maceachern@dpi.vic.gov.au

Collinsia seeds

Folks,

I am undertaking a phylogeography study to investigate the putative hybrid origin of a tetraploid *Collinsia* species in British Columbia, potentially a hybrid of

diploid *C. parviflora* and *C. grandiflora*. I am hoping some of you are willing to collect seeds of *C. parviflora* for me. This widespread species is found throughout most of western and central North America, and as far east as Pennsylvania and Ontario. I will be collecting in CA, OR, WA, and BC; if anyone on evoldir lives or works in other states/provinces, knows this diminutive plant, and would be willing to collect seeds for me, please send me an e-mail (elle@sfu.ca) and I'll suggest a methodology. I'll also be eternally grateful :)

Thanks, Elizabeth Elle

Dr. Elizabeth Elle Assistant Professor Dept. of Biological Sciences Simon Fraser University Burnaby, B.C. V5A 1S6 CANADA

604-291-4592 (office) or -3304 (lab) FAX: 604-291-3496

<http://www.sfu.ca/biology/faculty/elle/>

ColoradoStateU Evol2004 BookDonations

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

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

Crustacean micros

Dear all,

Does anyone know if microsatellite primers exist for the following families: Trochidae (Gastropoda), Palaeomonidae and Grapsidae (Crustacea)?

Thanks for the help

Judite

Maria Judite Alves Museu Bocage, Museu Nacional de História Natural Rua da Escola Politécnica 58 1269-102 Lisboa, Portugal Tel.: 351 213921886, Fax: 351 213969784 E-mail: mjalves@fc.ul.pt

DNasequence analysis

Hi,

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

Thanks a lot for your suggestions.

Regards, Jens –

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

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

DataMonkey

DataMonkey Update

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

Encouraged by the positive feedback we received from the launch of DataMonkey, we have added two new methods to detect selection on single amino acid sites. The first method involves estimating the ratio of non-synonymous to synonymous substitutions at a site using an approximate maximum likelihood method, which involves fixing nuisance parameters such as branch lengths to speed up computations. The second method is a full maximum likelihood approach, a generalization of the models implemented in Ziheng Yang's PAML software, which allow for variation in both nonsynonymous and synonymous rates, more general nucleotide bias models, and the use of Bayes factors for empirical Bayes result processing of rate classes at individual sites.

Both 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. Likelihood based methods tend to have more power (lower type 2 error) but also produce more false positives (higher type 1 error) than counting-based methods (which are already implemented in DataMonkey), especially for small datasets. Those that were discouraged by not finding any selection in their datasets using counting-based methods may wish to try again!

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>. Enjoy! Sergei L. Kosakovsky Pond and Simon D.W. Frost UCSD Antiviral Research Center San Diego, CA, USA

Distance calculations

Hello,

I have a couple of large data sets for which I would love to get average pairwise distances. I know that PAUP will give you all the pairwise distances for each combination of taxa, but averaging those numbers has proved enormously difficult (even in Excel owing to formatting issues).

Does anyone know of any software that will calculate this value for me (and give me a std. dev.)? Our lab is all Macs so I'd prefer Mac based (OSX or OS9) software hints but if all else fails, I can find a PC and go that route. Thanks in advance,

Greger greger.larson@zoo.ox.ac.uk

Distance calculations answers

Hello,

a few people emailed me and asked if i would share the responses i got (and there were many) from my initial query re: calculating average pairwise distances.

my initial query was this:

I have a couple of large data sets for which I would love to get average pairwise distances. I know that PAUP will give you all the pairwise distances for each combination of taxa, but averaging those numbers has proved enormously difficult (even in Excel owing to formatting issues).

Does anyone know of any software that will calculate this value for me (and give me a std. dev.)? Our lab is all Macs so I'd prefer Mac based (OSX or OS9) software hints but if all else fails, I can find a PC and go that route. Thanks in advance, Greger

By far the most common answer was to download MEGA2 which is free, easily downloadable, and easy to use. The best aspect of this software is that it understands that computing std. error from a list of pairwise distance values must take into account the non-independent nature of those values. And it gives you several options (bootstrapping, etc.) to better estimate the standard deviations around the derived mean.

Unfortunately, MEGA2 is only available as Windows software and thus, for people like me stuck in an all Mac lab, it's not ideal. I have located a PC and will switch computers when I need to.

Other recommended software packages included:

genetic software package: Peakall and Smouse (2001) GenAlEx. Genetic Analysis in Excel, <http://www.anu.edu.au/BoZo/GenAlEx/> The serious statisticians use R (a free, open source version of S+). I've used it on my Mac as well as my linux boxes. You can get it from <http://www.r-project.org/> <http://www.tree-puzzle.de> - which is coming out with a MAC version soon

and

MVSP is a great statistical software package from Kovach Computing Systems that does the calculations you are looking for. They still may have a downloadable version online. I have been using CalcDist for all kinds of distance calculations. It is (was) a DOS-executable freeware, but I don't know whether it is still available (I could sent you the program + documentation if you are interested). You find descriptions and links of a whole bunch of distance software programs on Phylip's website: <http://evolution.genetics.washington.edu/-phylip/software.html> Alternatively i was given lots of tips for writing my own code in Mathematica or any other language (C, pascal, etc.)

Lastly, as it turns out, you can get just the average using PAUP. after asking PAUP to compute pairwise differences, under the file menu there is an option to 'save distances to file' with a box that allows you to save the output in a single column thus eliminating the formatting issue of the big triangles.

Thanks everyone for the multitude of useful and timely responses.

Greger

Greger.Larson@zoology.oxford.ac.uk

Drosophila lines

New Drosophila isofemale lines and stocks from the Tucson Stock Center:

The Tucson Drosophila Species Stock Center has new isofemale lines of the species listed below: a) D. simulans 54 isofemale lines from El Tuito, Jalisco, Mexico (1/19/2004) Collected by M. Mateos in banana bait. 34 isofemale lines from San Antonio de Guadalupe, Zumpahuacan, Edo. Mexico, Mexico (1/04/2004) Collected by M. Mateos in banana 20 isofemale lines from San Pablo Etla, Oaxaca, Mexico (12/2003) Collected by T. Markow in banana bait. 15 isofemale lines from

San Blas, Nayarit, Mexico (1/15/2004) Collected by M. Mateos in banana bait . b) *D. melanogaster* 17 isofemale lines from San Blas, Nayarit, Mexico (1/15/2004) Collected by M. Mateos in banana bait 4 isofemale lines from El Tuito, Jalisco, Mexico (1/19/2004) Collected by M. Mateos in banana bait 4 isofemale lines from San Pablo Etla, Oaxaca, Mexico (12/2003) Collected by T. Markow in banana bait.

c) *D. pseudoobscura* 17 isofemale lines from Santa Cruz Island, Channel Islands, California (1/2004) Collected by L. Matzkin in banana bait 7 isofemale lines from San Pablo Etla, Oaxaca, Mexico (12/2003) Collected by T. Markow in banana bait. 1 isofemale line from San Antonio de Guadalupe, Zumpahuacan, Edo. Mexico, Mexico (1/04/2004) Collected by M. Mateos in banana bait

d) *D. busckii* 3 isofemale lines from San Antonio de Guadalupe, Zumpahuacan, Edo. Mexico, Mexico (1/04/2004) Collected by M. Mateos in banana bait

e) *D. malerkotliana* 2 isofemale lines from San Blas, Nayarit, Mexico (1/15/2004) Collected by M. Mateos in banana bait f) *D. willistoni* 2 isofemale lines from El Tuito, Jalisco, Mexico (1/19/2004) Collected by M. Mateos in banana bait Isolines are \$20 each. For orders more than 20 isofemale lines the price is \$10 each. Isofemale lines will be available until the end of May. Isofemale lines can be ordered by contacting Sergio Castrezana, at castreza@email.arizona.edu New *Drosophila* stocks: The Tucson *Drosophila* Species Stock Center has incorporate in the collection the stocks listed below (check website for collection info): *D. ananassae* 14024-0371.12 (Marathon, Florida) *D. melanogaster* 14021-0231.27 (Kisangani, Congo) *D. pseudoobscura* 14011-0121.95 (Sonora, Mexico) *D. simulans* 14021-0251.184 (Kisangani, Congo) *D. simulans* 14021-0251.185 (Rosario, Baja, Mexico) *D. simulans* 14021-0251.186 (Sonora, Mexico) *D. sturtevanti* 14043-0871.10 (Veracruz, Mexico) *D. sturtevanti* 14043-0871.11 (Turner's Hall Woods, Barbados) *D. sturtevanti* 14043-0871.12 (Panama) *D. wassermani* 15090-1697.12 (Oaxaca, Mexico) *D. willistoni* 14030-0814.11 (Tena, Equator) *D. willistoni* 14030-0814.12 (Toro Negro, Puerto Rico) *D. willistoni* 14030-0814.13 (St. Vincent & Grenadines) *D. willistoni* 14030-0814.14 (Grand Etang, Grenedines) *D. willistoni* 14030-0814.15 (Veracruz, Mexico) *D. willistoni* 14030-0814.16 (Laguna Negra, Uruguay)

Therese Ann Markow
<tmarkow@public.arl.arizona.edu>

Drosophila species

Dear All, We are currently trying to obtain fresh stocks of the *D. robusta* group, *D. pseudosordidula* Kaneko, Tokumitsu, & Takada, *D. okadai* Takada, and *D. neokadai* Kaneko & Takada, *D. cheda* Tan, Hsu, & Sheng, *D. pullata* Tan, Hsu, & Sheng, *D. gani* Watabe, Liang, & Zhang, *D. yunnanensis* Watabe, Liang, & Zhang, *D. bai* Watabe, Liang, & Zhang, *D. fluvialis* Beppu, Peng, & Xie, and *D. medioconstricta* Watabe, Liang, & Zhang) from Japan, Korea and China. The Tucson stock center has only a few very old species stocks. We currently have *D. robusta*, *D. sordidula* Kikkawa & Peng and *D. lacertosa* Okada. Thank you very much. Bill

William J. Etges Department of Biological Sciences
SCEN 632 University of Arkansas Fayetteville, AR
72701 USA wetges@uark.edu <http://comp.uark.edu/~wetges/wetges.html> office: (479) 575-6358 lab: (479) 575-7437 FAX (479) 575-4010

Drosophila stocks

Dear Colleagues,

The Coyne Lab is discarding a number of its *Drosophila* stocks listed below. If you would like a vial of these flies, please contact me, Susannah Elwyn (elwyn@uchicago.edu) by March 14, 2004. We are willing to send vials if you provide us with a FedEx or UPS number, covering the cost of shipping.

Cheers, Susannah

D. simulans

e ebony (chromosome 3) ro rough eyes (chromosome 3)
Sim line #2 wild type stock, collected in Winters, CA
1992

D. mauritiana

w, f white, forked (X chromosome) j; irr jaunty, irregular (chromosome 2,3) sn; irr singed; irregular (chromosome 1,3) Maur B/S line B wild type stock MS 34 wild type from Bill Ballard

D.sechellia w, f white, forked (X chromosome) (1-4, 56 [D. simulans locations] cn, pur cinnabar, purple (chromosome 2) SY 034 isofemale line collected on Avocado fruit 4/98 by B. Ballard

D. melanogaster St. Croix Cave Bay (line A rep B)

–

Susannah Elwyn Senior Research Technician Laboratory of Jerry Coyne Dept. of Ecology and Evolution University of Chicago 1101 E. 57th St. Chicago, IL 60637 phone: (773)702-1106 FAX: (773)702-9740 elwyn@uchicago.edu

Susannah Elwyn <elwyn@uchicago.edu>

presented in the video are bogus (two of the teachers believe that the evidence in this video proves evolution to be false), and I am wondering if anyone out there has already put together a response to this particular video.

Thanks, Jeff

– Jeff Conner Professor Kellogg Biological Station and Department of Plant Biology Michigan State University 3700 East Gull Lake Drive, Hickory Corners, MI 49060 e-mail: connerj@msu.edu <http://www.kbs.msu.edu/Faculty/Conner/Index.htm> Phone: 269-671-2269 FAX: 269-671-2104

Jeff Conner <connerj@kbs.msu.edu>

Eagle micros

Dear All I am a doctoral student at the University of Nottingham studying the population genetics of the golden eagle in the British Isles and the phylogeography of the species in Europe. This study will use a combination of microsatellite and mitochondrial markers. I am currently in search of microsatellites to test in golden eagles. Apart from Begona Martinez-Cruz and Sandy Talbot, is there anybody currently developing Aquila microsats and who is willing to collaborate in this study? I am also looking to screen other Falconiforme microsats but have yet to come across any published data for the genus Buteo, Accipiter or Hieraaetus. Is anybody aware of the existence of these or other unpublished falconiforme microsats? Could you please send replies directly to me at lgxbpb@nottingham.ac.uk.

Thanks for your help, Brian Bourke.

Brian Bourke <lgxbpb@nottingham.ac.uk>

Evolution video

Folks:

My daughter's 7th grade science teacher showed the class a creationist video entitled "Evolution...Fact or Belief?". My daughter was particularly offended by the statement in it that evolutionary biologists aren't scientists! Some of us are working with the school district to help educate the teachers about why the facts

Fst statistics

Dear evoldir member,

I am trying to calculate Fst statistics (Fst, Fis, Fit) in a tetraploid specie. But, at the moment, I have not found any software able to estimate these statistics. Know somebody a software able to do it?

Thank in advance

Miguel Angel

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

Phone:+34.928.45.45.43 Fax: +34.928.45.29.22

e-mail: mgonzalez@becarios.ulpgc.es

Fst statistics answers

Dear Evoldir members,

Thank you very much for your answers to my question about software able to calculate F-statistics in tetraploid specie. Because a lot of people were interested in the answers, also, I summarized them.

QUESTION:

Dear Evoldir members, I am trying to calculate Fst statistics (Fst, Fis, Fit) in a tetraploid specie. But, at

the moment, I have not found any software able to estimate these statistics. Know somebody a software able to do it?

Thank in advance

Miguel Angel

RESPONSES:

1) If its autotetraploid (polysomic inheritance) and you can score genotypes (i.e. tell the difference between and aabb and an aabb) then Spagedi by Hardy and Vekemans will do it.

Hardy OJ, Vekemans X (2002) SPAGEDi: a versatile computer program to analyse spatial genetic structure at the individual or population levels. *Molecular Ecology Notes* 2, 618-620.

If its disomic (allotetraploid inheritance) and you have to score aabb and abbb both as "ab" then I have written a program that might help - please email me

Darren – Darren Obbard Department of Plant Sciences Oxford darren.obbard@plants.ox.ac.uk Office: (01865) 275075 Lab: (01865) 275013 Mobile: 07968 838 635 Home: 0870 276 0911

2) Hi Miguel Angel,

The software "populations" downloadable at <http://www.cnrs-gif.fr/pge/bioinfo/populations/-index.php?lang=en&doc=populations> calculates Fst statistics from haploid, diploid and polyploid species. It is a DOS program but very easy to use, you only have to take care to save your input data in text (MS-DOS) format.

Good luck,

Iris

Dear Miguel, If the species you are studying is an autotetraploid species, you can have a look at the paper I am attaching with this Email and contact Joelle Ronfort (ronfort@ensam.inra.fr) to obtain the software she developed to estimate F statistics in autotetraploid species. Best Thomas

3) Dear Miguel, If the species you are studying is an autotetraploid species, you can have a look at the paper I am attaching with this Email and contact Joelle Ronfort (ronfort@ensam.inra.fr) to obtain the software she developed to estimate F statistics in autotetraploid species. Best Thomas

4) Dear Miguel,

I have calculated F statistics with Gene4x, a software written by Joelle RONFORT, at INRA of Montpellier in France. The method is explained in a paper: Ronfort et al (1998): analysis of population structure in

autotetraploid species. *Genetics*, 150, 921-930.

The software is free, you can ask a copy directly to J. Ronfort: ronfort@ensam.inra.fr I have used it to analyse genetic diversity among and between alfalfa populations, with microsatellite markers. It cannot take into account the null alleles, and you need to read the dose of each allele. From my preliminary results, it works very well.

Good luck

Bernadette Julier

mgonzalez@becarios.ulpgc.es

Halimolobus samples

Dear evoldir members

I am looking for samples of *Halimolobus berlandieri* (Brassicaceae) for a phylogenetic study. I prefer seeds but any kind of tissue that contains DNA would be fine. If there is anyone that can help me, please contact me directly via alf.ceplitis@cob.lu.se

Many thanks,

Alf Ceplitis

Alf Ceplitis, PhD Department of Cell and Organism Biology (Genetics) Lund University Sweden

Postal address: Solvegatan 29, SE-22362 Lund Phone: +46 46 2227857 Fax: +46 46 147874

Haplotype tables

Dear Evoldir Members:

I'm searching for a Windows program that collapses a DNA sequence alignment to a table of haplotypes and variable sites. (For instance, for analysis or publication purposes). Both 'MacClade' and David Posada's free programme 'Collapse' carry out the 'collapse characters' and 'collapse taxa' functions for Macintosh users. Are there any Windows programmes with equivalent functions? ('MEGA' and 'Mesquite', for instance, don't appear to have a 'collapse taxa' function). Alternately, has anybody out there ported David Posada's pro-

gramme 'Collapse' to Windows? I'd love to hear any further suggestions.

Many thanks.

Murray Cox murray_c@sanger.otago.ac.nz

Human gene flow

Dear all, When I was a population genetics student I was told of this study which found a correlation between the invention and widespread use of the bicycle at the end of the 19th century and the increase in distance between the place one was born and the place one married (I seem to remember the study was made in Italy). I am after the original reference, and although I have made various searches (Google, Web of Science, etc) I got nowhere trying to track it down. The only hint I found was that Sewall Wright seem to have commented on it. Any help will be welcome, Best,

Africa

Africa Gómez Postdoctoral Research Assistant Department of Biological Sciences University of Hull Hull, HU6 7RX U.K.

Tel: +44 (0)1482 465505 Fax: +44 (0)1482 465458
<http://www.hull.ac.uk/molecol/Africa.html> -----

Inferring Phylogenies typos

My book "Inferring Phylogenies" will very soon have another printing, and we want to correct as many of the typographical and algebraic errors as we can. I have posted a web site with the (too many) that we have found so far: <http://evolution.gs.washington.edu/-book/typos.html> I would like to request that people knowing of further errors let me know, if possible within the next few days. The publisher (Sinauer) and I promise to send one copy of the reprinting to each person who tells me of 20 new errors. They have to be ones that I agree really are errors, and that are not on our errors list and have not previously been reported to me. That means that of two people who report the same new error, the first to do so gets credited with the

report. If you can respond, a response in the next week would be most helpful. Thanks for your help.

(note the anti-spam-modified email address from below from which you should remove the "removethispart.") – Joe Felsenstein joe@removethispart.gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 357730, Seattle, WA 98195-7730 USA

Irregular micros

Hello Everyone,

I've developed a panel of AAAG-repeat microsatellite loci for my PhD and I have a question regarding the analysis of irregular allele size distributions. For example, at one locus most of the alleles conform to the 4 bp size distribution expected for the repeat motif, while also containing alleles of irregular size, i.e., differing by 1, 2, and 3 bp. In some instances the allele distributions seem to have shifted, still conforming to the 4 bp distribution. The microsatellite loci all contain perfect repeat arrays and the allele peaks are very clean with no signs of 'stuttering'. The genotyping of 900 individuals from 23 different populations has revealed, for some loci, a large proportion of irregular size variants. There appears to be little information in the literature on how such non-conforming size variants should be handled, and I would appreciate any suggestions on how to proceed.

Thanks Paul

Mr Paul Bloor School of Biological & Earth Sciences James Parson Building Liverpool John Moores University Liverpool L3 3AF UK

Tel. 0151 2312181 Fax 0151 2073224
p_bloor@hotmail.com

Lasergene DNASTar usage

– Dear Evoldir members,

I would be very grateful if anyone that has used the software lasergene from DNASTAR could give me feedback about it.

Many thanks

France Dufresne, Ph.D. Département de biologie Université du Québec à Rimouski 300 allée des ursulines Rimouski, Québec, Canada G5L 3A1 tel (418) 723-1986 ext. 1223 fax (418) 724-1849 rbduffra@jafar.uqar.qc.ca

please? Cheers, Mark

Mark de Bruyn, PhD Candidate School of Natural Resource Sciences Queensland University of Technology GPO Box 2434, Brisbane, Qld, 4001, Australia Ph: +61-7-3864-5051; Fax: +61-7-3864-1535 E-mail: m.debruyn@qut.edu.au Web: <http://www.sci.qut.edu.au/nrs/research/popgen.htm>

Lepidopteran phylogeny

Dear all, Could anybody please refer me to a paper/textbook/website with a Lepidoptera phylogeny with some sort of time calibration. It would be especially interesting to have an estimate of the time of divergence (in MY) among our different putative Lep models (e.g. Bombyx, Manduca, Heliothis, Heliconius, Papilio, Bicyclus) and between them and other classical model systems (e.g. Drosophila, Apis, Anopheles). Estimates of divergence times between different Lepidopteran groups would be good too. Does anybody know where I can find this type of information in some organized/useful manner? Many thanks, Patricia Beldade

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

pbeldade@uci.edu

Long branches

Dear All, I am working on giant freshwater prawns using COI mtDNA. Within the Australasian region, I have sampled approx 40 ind's from each of 11 sites. This has resulted in the id. of 30-40 haplotypes. One Australian 'population' is characterised by 4 haplotypes (out of 8) having much longer branch lengths than any of the other haplotypes from this dataset. My question is: is this telling me something important about the evolutionary history of this site/population? (Are these haplotypes older/ different effective pop size, etc? Some people have even suggested this could mean pseudogenes?) There doesn't appear to be a consensus in the literature. Any advice, or any literature out there

Matrilines

Dear Evoldir members,

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

Any advice is appreciated

Monika

—

Monika Zavodna, PhD student Netherlands Institute of Ecology Centre for Terrestrial Ecology P.O.Box 40 6666 ZG Heteren The Netherlands phone: +31 26 4791259 fax: +31 26 4723227 email: m.zavodna@nioo.knaw.nl <http://www.nioo.knaw.nl/CTE/index.htm> <http://www.nioo.knaw.nl/CTE/index.htm>

Micro Null alleles

Dear Evoldir-members,

I am looking for a program/possibility to check my microsatellite data for null alleles, where calculations are not based on the heterozygosities. If anyone has an idea, I will be happy to hear about it.

Thank you very much for your help,

Martina Zeller

Martina Zeller <zeller@mpil-ploen.mpg.de>

Micro Null alleles answers

Dear Evoldir members,

thank you very much for your answers to my question about null alleles. Because a lot of people were interested in the answers, also, I summarized them.

Martina Zeller Max-Planck Institute for Limnology, Plön, Germany zeller@mpil-ploen.mpg.de

Initial query: I am looking for a program/possibility to check my microsatellite data for null alleles, where calculations are not based on the heterozygosities. If anyone has an idea, I will be happy to hear about it.

Responses:

1 Dear Martina, Try Micro-checker from Hull University. All the best Ana Elisabete Pires

Ana Elisabete Pires Cardiff University School of Biosciences Main Building Park Place PO Box 915 Cardiff CF10 3TL

2 Martina,

the best way to check for null-alleles is to examine the inheritance of alleles in known pedigrees. The only non-pedigree-based methods that I know of are based on heterozygote deficiencies. If you hear of any other ways, I would love to hear about them.

All the best

Craig

Craig Primmer Academy Fellow Department of Biological and Environmental Sciences P.O. Box 65 (Biocentre 3, Viikinkaari 1) FIN-00014 University of Helsinki FINLAND

tel. +358 9 191 57685 fax. +358 9 191 57694 email: craig.primmer@helsinki.fi <http://www.helsinki.fi/~primmer> —

3 Hi Martina

Sorry to reduce time I cut and pasted An equation to detect null alleles has been given by Chakraborty (Chakraborty et al., 1992), subsequently modified by Brookfield (Brookfield, 1996) to take account of double null alleles. This method determines 'r' the frequency of null alleles within a sample, using the observed and expected heterozygosities in relation to Hardy-Weinberg expectations (Brookfield, 1996; Chakraborty et al., 1992). Similar estimates are obtained with both mod-

els when the observed and expected heterozygosity is high, however, larger differences in the estimates for 'r' are observed when heterozygosity is low (Brookfield, 1996). The two equations are: $r = (He - Ho) / (He + Ho)$ (Chakraborty et al., 1992) $r = (He - Ho) / (1 + He)$ Brookfield's modification (Brookfield, 1996)

I think that Marshall 1998 also provides a null allele detection option in his computer program examining parentage (sorry can't remember the name offhand and don't have the details here, nor the full references - if you can't find them I can look - he is at Edinburgh Uni UK). Hope this helps Tee

— Dr Tiawanna Taylor Centre for the Environment and Development (CEAD) University of KwaZulu Natal Pietermaritzburg Private Bag X01 Scottsville 3209 KwaZulu Natal South Africa Tel: +27 (0) 33 260 5872 Fax: +27 (0) 33 260 6157

Wales, UK

4 In outbreeding populations, heterozygosity based estimators will be quite reliable for estimating null allele freqs. Unless pedigree data or other special situations (e.g., pine megagametophytes or clever molecular techniques) let you get to the haplotypes, I cannot see other ways of estimating null alleles. In inbreeding populations, my colleagues and I have developed a technique to estimate null alleles (High resolution analysis of mating systems: inbreeding in natural populations of *Pinus radiata*, C Vogl, A Karhu, G Moran, O Savolainen, Journal of Evolutionary Biology, Volume 15, Issue 3, Page 433-439, May 2002). It is similar to the procedure Holsinger uses for dominant markers (really the same situation, since null alleles are recessive). But of course, this technique is also related to heterozygosity. Furthermore, it is confounded with the inbreeding level, such that it is in principle very difficult to estimate both the frequency of null alleles and the inbreeding coefficient. (This is also true for the Holsinger method.)

The method is available, in case it suits your data.

Baba

Claus

5 Dear Martina Zeller,

We recently finished a software programme called Micro-Checker that will probably do the things you require doing. The programme is freeware and can be downloaded from <http://www.microchecker.hull.ac.uk/> The help pages can be accessed from the net and may give you an idea what the programme is exactly doing. You may be particularly interested in the link to 'null alleles', which explains the various algorithms for estimating

the null allele frequency, and tells you under which circumstances those are appropriate.

If you have any queries, please contact me!

Best wishes, Cock – Dr. Cock van Oosterhout
NERC Research Fellow University of Hull Hull
HU6 7RX, UK Tel.: +44(0)1482 465505 Tel.:
+44(0)1482 466434 Fax.: +44(0)1482 465456 <http://www.hull.ac.uk/biosci/staff/vanoosterhout.html>

<http://www.microchecker.hull.ac.uk> 6 Dr. Zeller,
cervus is what I use; but I don't know how Tristan
derived 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/evoldir.html>

Micro staining

Dear, colleague I am trying to do microsatellite by silver staining method. at the moment I have some problems:
- Difficult separation long and short glass plates - Gel stick on two glass plates - Can not remove bind silane It is appropriate if anyone have some advice? Best regards

Binh Thai Master Student School of Ecology and Environment Deakin University Warrnambool VIC 3280 AUSTRALIA Tel: 61.3.55633569, 61.3.55615831 Mob: 0408038242 http://www.deakin.edu.au/sch_ecol_env/-research/mol_ecol_bio/home.htm

Binh Thai <tbt@deakin.edu.au>

MississippiStateU REU Conservation

Applications are now being accepted for an NSF-funded Research Experience for Undergraduates program in “Conservation Biology in the Southeastern United States” at Mississippi State University. The program will take place during the summer of 2004. Undergraduate students will conduct independent research projects with faculty mentors and participate in group activities that complement individual efforts.

This program focuses on building confidence and skills in conservation biology research and targets students who would not otherwise have the opportunity to participate in research activities at their home institution or are from typically underrepresented groups in the sciences. The application deadline is March 15. For more information, please visit the program website: <http://csmt.msstate.edu/html/REU/> Mark Fishbein Assistant Professor Director, Miss. St. Univ. Herbarium (MISSA) Department of Biological Sciences Mississippi State University P.O. Box GY Mississippi State, MS 39762 USA ph: (662) 325-7577, -7570 fax: (662)325-7939 email: fish@biology.msstate.edu

Multidistribute MacOSX

I am looking for compiled versions of Dr. Jeffrey Thorne's divergence time estimation package of programs named Multidistribute (containing programs “estbranches”, “multidivtime” and “paml2modelinf”) for Mac OS X. As provided by Dr. Thorne, the programs need a C compiler, but Apple does not provide one for use in their “terminal” shell. I would greatly appreciate it if someone could provide those programs or suggest someone who might have them.

Sincerely, Ron Adkins – Ronald M. Adkins radkins1@utmem.edu Assistant Professor Office: 901-572-5357 50 North Dunlap Lab: 901-572-4583 Children's Foundation Research Center FAX: 901-572-5036 and Center of Genomics and Bioinformatics Room 308, West Tower Le Bonheur Children's Medical Center University of Tennessee - Memphis Memphis, TN 38103

Ron Adkins <radkins1@utmem.edu>

Myotis samples

Dear all,

I am a PhD student working on the phylogenetic evolution of the cosmopolitan bat genus Myotis (Chiroptera, Vespertilionidae). Myotis is one of the few worldwide naturally distributed mammalian genus, with about 100 species. Thank to many collaborations I have now samples of a great number of species and I wish to

reconstruct the entire historical biogeography of that genus. Unfortunately, some very important and interesting species are still missing in my tissue collection. Therefore, I am sending this message to the Evoldir community to see if anyone can help me to find two species:

Myotis chiloensis which is present in the Chiloe Islands, Chile and Islets on eastern side. *Myotis aelleni*, present in Argentina.

Please if you have one of them (small piece of tissues is sufficient) in your collection that could be use for molecular use, or if you have any idea about how obtain them, or any contacts who are likely to have or capture them, please contact me. I will be very grateful to any answer!

Thanks

Benoît

***** Benoît Stadelmann PhD student, University of Geneva Department of Zoology and Animal Biology Molecular Systematics Group Science III 30, quai Ernest-Ansermet CH-1211 Genève 4 Geneva, Switzerland

Phone: +41 (0)22/379.30.77 Fax: +41 (0)22/379.67.95
e-mail: Benoit.Stadelmann@zoo.unige.ch <http://www.unige.ch/sciences/biologie/biani/msg/>

Nematode micros

Request for nematodes for cross-species microsatellite testing

We've cloned several microsatellites in the grouse parasitic nematode *Trichostrongylus tenuis*, and we'd like to test them on other species of nematode. We'd be very grateful to receive donations of nematode tissue from other species, mainly those closely related to *T. tenuis*. There's a 'want' list at the foot of this email, but if your species isn't on it and you think our microsatellites might work, please get in touch anyway.

To arrange to send samples, please email me at p.johnson@bio.gla.ac.uk, or just send them to me at the address below.

For each species we would like at least 8 adult worms. They should be male (females might be contaminated with male sperm), from as wide a geographical range as possible, and preferably preserved in 70-100% ethanol. Alternatively, DNA samples would be welcome.

Preliminary results show that our microsatellites can work in other *Trichostrongyloid* genera, so we have high hopes of getting a few loci working well in congenetics.

Many thanks, Paul Johnson

————— We would like:

Any *Trichostrongylus* spp.: *Trichostrongylus axei* *Trichostrongylus capricola* *Trichostrongylus colubriformis* *Trichostrongylus probolurus* *Trichostrongylus retortaeformis* *Trichostrongylus rugatus* *Trichostrongylus tenuis* (from outside the UK) *Trichostrongylus vitrinus*

Any other *Trichostrongyloid* genera, e.g. *Haemonchus*, *Ostertagia*, *Teladorsagia*

Some *Strongylids* outside the *Trichostrongyloidea* (although this is probably a long shot). —————

Paul Johnson Division of Environmental and Evolutionary Biology (DEEB), Graham Kerr Building, Glasgow University, Glasgow, UK, G12 8QQ Tel +44 (0)141 330 6625, Fax +44 (0)141 330 5971, p.johnson@bio.gla.ac.uk

Paul Johnson <p.johnson@bio.gla.ac.uk>

Onagraceae micros answers

For those interested here are the answers I received in response to my Micro library problem/question (satellite/repetitive elements showing up prior enrichment): I, by the way, have not yet decided how to proceed. Thanks to all of those who replied.

ORIGINAL POSTING: Our lab is currently trying to develop a microsatellite library for *Camissonia cheiranthifolia* (Onagraceae), but we are having some problems. Before the enrichment phase, but after the digestion (with *RsaI* and *BstUI* each) and linker ligation several highly concentrated bands appear within the smear on a gel (6-10 bands in the 500-1000bp region). The problem seems to be that the genome has several highly repetitive elements present, which obviously also contain enzyme cut sites. Since these elements are appearing even prior to enrichment we are concerned that this species might not be a good candidate for microsatellite library development as it would likely become heavily biased for these repetitive elements. Has anyone ever experienced this problem before? If so, how did you handle it? More specifically, has anyone had success (or not) with an Onagraceae species or had a similar result?

RESPONSES: I've used a microsatellite enrichment method to successfully isolate microsatellites in numerous reptiles species. In one species I encountered problems similar to those that you have described. After running the restriction digest products on a gel I noticed several concentrated bands. When I sequenced the resulting clones I discovered that I had isolated many AAAG repeats that were part of a larger minisatellite that contained the AAAG microsatellite. To produce a more diffuse population of fragment sizes I experimented with different combinations of REs until I found the combination that produced the most appropriate size range of fragments. This resolved my problem. I'm no molecular biologist by trade, but experience has shown me that even within closely related taxa one may have to try different combinations of REs to produce the same range of digest products.

I haven't had this problem with microsatellite libraries before, but I think you would be able to at least try to get around it by avoiding sequencing too many bands in the size classes you mentioned, while still sequencing bands in the background smear. In the microsatellite library protocol I use, you ligate the SSR enriched DNA into pGEM, then PCR to screen the inserts before sequencing. When you check your library screening PCR on a gel, you could try to select inserts for sequencing that are of a variety of lengths to avoid repetition. Sequence a few (I usually start with 20) to check for repetition before sequencing many more. From the gel you talked about in your email, you might know which size inserts to look out for and avoid (taking into account where the primer site in the vector is - using my M13 primers I usually find the PCR product is ~250bp bigger than the insert). If you do a large enough transformation, and PCR screen a large number of colonies, you should be able to choose enough to sequence for microsatellites.

I'd suggest mechanical shearing of the genomic DNA rather than enzymatic digestion. Fill in the blunt ends, and then do a blunt end ligation to your linkers. Mechanical shearing is used to randomly fragment genomes prior to shotgun cloning and full genome sequencing.

I used an enrichment protocol to develop microsatellites in red-billed gull (*Larus novaehollandiae scopulinus*) and appear to have had a similar experience during the digestion stage. There were three distinct bands after digestion of total genomic DNA with HaeIII and RsaI. I proceeded with the isolation protocol (on the advice of several others who had used the protocol) and had no problems isolating a good number of microsatellite loci. My advice would be to continue with the procedure. If you get a high proportion of identical

inserts in your clones then these bands would appear to be a problem. However, from my experience it appears that this may not be the case.

I've seen the same thing in microsatellite library development for other some other organisms. As long as the 6-10 bands that probably represent repetitive elements have no long repeats that you are interested in (the di-, tri- or tetranucleotides that you will be using for the capture and probe phase), they will be selected against and "lost" from the library in the forthcoming steps.

In *Physalis*, we have encountered the same problem with some restriction enzymes, but have found that other enzymes give perfectly usable smears in the right size range. My advice is to do a few digestions with different enzymes and see which ones give the best fragments before ordering any linkers.

Some species are more difficult than others. We have done many species and most haven't had the problem you describe, but those species that have those strong bands at that stage cause a problem indeed.

— / —

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>

PUC18 source

We recently learned that Amersham no longer sells puc18 plasmid vector that has been pre-cut with BamHI and treated with BAP. We cannot located another source for this product - does anyone have any suggestions?

Thanks,

Lisle Gibbs Department of Evolution, Ecology and Organismal Biology Ohio State University Columbus, OH 43210-1293 email: gibbs.128@osu.edu – H. Lisle Gibbs Associate Professor Department of Evolution, Ecology and Organismal Biology Ohio State University 300 Aronoff Laboratory 318 W. 12th Ave. Columbus, OH 43210-1293

Tel: 614-688-3861, Fax: 614-292-2030 email: gibbs.128@osu.edu <http://www.biosci.ohio-state.edu/~eeob/gibbs/index.html> Lisle Gibbs <gibbs.128@osu.edu>

Polyploid software answers

Hi,

Here are the replies that I received for my question at the forum a couple of days ago. It seems like there are really not too much options of software to study polyploid species. I have worked with potato: diploid, triploid and pentaploid species, and used the software Freetree to construct dendrograms from similarity values. But this program isn't useful to calculate Goldstein genetic distance (dmu2) or to perform other population genetics analysis. Now I'm working with quinoa (allotetraploid) and I was trying the program populations. It accepts more than two alleles per locus, but there has to be the same number of alleles for all the loci, that means that the program assumes that I can distinguish allele dosage, but with microsatellites I can't. I'll just keep looking for until the data for my results are complete. Thanks to everybody who wrote to me.

Iris

My original question: Hi everyone,

I need a software to perform analyses using molecular marker data (microsatellites) from polyploid species. All the software that I have proved until now seems to be made specially for diploid data. If someone knows about some software that could be useful to me (especially if it can calculate Golstein genetic distance) please let me know.

Thanks for any advice,

Iris irisxkx@yahoo.com

Responses:

Hi, this is a bit of an issue all round at the moment.

The questions you need to answer before doing the analysis are:

- (1) Is inheritance disomic, or polysomic?
- (2) Can you score genotypes, or only identify allele presence/absence? (ie, can you distinguish an aabb tetraploid individual from an abbb individual or aabb individual)

If inheritance is polysomic (as in most autopolyploids) and you can score genotypes then there is some good software:

Hardy OJ, Vekemans X (2002) SPAGEDi: a versatile computer program to analyse spatial genetic structure at the individual or population levels. *Molecular Ecology Notes* 2, 618-620.

for F-stats etc, and also

Thrall PH, Young A (2000) AUTOTET: A program for analysis of autotetraploid genotypic data. *Journal of Heredity* 91, 348-349.

If inheritance is disomic (most allopolyploids) or you cannot score genotypes then there is a big gap in the literature.

I have written a program which makes the best of a bad job for disomic allopolyploids, and I am halfway through writing a brief review of some of the approaches that can be used in polyploids.

Please let me know if you get any good answers to your question from other people.

Thanks,

Darren

– Darren Obbard Plant Sciences, Oxford darren.obbard@plants.ox.ac.uk

I don't have any software, but you may enjoy reading our paper about studying population genetics in a polyploid:

Espinoza and Noor, Population genetics of a polyploid: is there hybridization between lineages of *Hyla versicolor*? 2002. *Journal of Heredity* 93(2):81-85.

Good luck. –Mohamed Noor

Hi Iris,

Recently a evoldir member threw the same question, and these are the reply that he received. Anyway, I am very interesting in a software for microsatellite analysis in tetraploid species, so if you receive any new reply could you send me, please.

good luck

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

Phone: +34.928.45.45.43 Fax: +34.928.45.29.22

e-mail: mgonzalez@becarios.ulpgc.es

De: <evoldir@evol.biology.mcmaster.ca> Para: <canariensis750@hotmail.com> Asunto: Other: re-

sponses to microsatellite diversity in triploids Fecha: viernes, 27 de febrero de 2004 7:24

Hi everyone-

A lot of people requested that I post responses to my question regarding microsatellite diversity in triploids. The responses are listed below in the order in which they were received. Thanks so much for all your suggestions! They were very helpful.

cheers, Maurine

Original question: Hello- I would like to use microsatellite data to calculate allelic and genotypic diversity (including richness and evenness) for populations with both diploid and triploid individuals. I was wondering if there was a program designed to calculate these values that can accomodate polyploid data (the ones that I am familiar with seem to be limited to diploid data).

Thanks, Maurine Neiman mneiman@bio.indiana.edu

Responses:

Hi,

It depends how you want to define diversity, and what your data looks like.

If you can score genotypes: i.e. you can tell that the difference between individuals carrying alleles (a,a,b) and individuals carrying (a,b,b) then you should try looking at

Hardy OJ, Vekemans X (2002) SPAGEDi: a versatile computer program to analyse spatial genetic structure at the individual or population levels.

— / —

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>

Primer ConsGenetics

'A Primer of Conservation Genetics' by Frankham, Balou & Briscoe is now published by Cambridge University Press [pb & hb].

This has similar content to 'Introduction to Conservation Genetics', but is a shorter [221 pages], simpler version for an audience with less background in genetics, or those wanting a quick overview.

Regards Dick

Professor Richard Frankham Feb-July 2004 Program for Evolutionary Dynamics Faculty of Arts and Sciences, Harvard University One Brattle Square - room 637 Cambridge, MA 02138, USA Phone [1] 617 496 5544 Normally Department of Biological Sciences Macquarie University, NSW 2109 Australia Phone [612] 9850-8186 Fax [612] 9850-8245 email rfrankha@els.mq.edu.au

Richard Frankham <rfrankha@rna.bio.mq.edu.au>

SeqAlignment Editor answers

Dear all, One week ago I post on Evoldir website a question which sequence editors and alignment softwares use for teaching. I received many good advices, below I wrote a quick reader digest :

- MEGA3 (www.megasoftware.net/mega3) : very good software for editing sequence, alignment, phylogenetic analysis and others. It is a good "all in one". It allows exports of data to PAUP or phyllip with just some small editing, very good.

- DAMBE (<http://aix1.uottawa.ca/~xxia/software/software.htm>), as the former a good "all in one", both Mega and Dambe are able to work together, and complete for molecular evolution.

- BioEdit <http://www.mbio.ncsu.edu/BioEdit/bioedit.html> : editing, alignment, easy to use, a good choice, most of the replies vote for BioEdit. Personally I encounter some troubles to run clustal from Bioedit on Windows XP.

- I received a lot of replies about Seal, Sea view, multalin, or Qalign (<http://www.ridom.de/qalign/index.html>), but sorry I had no time to try them.

I hope that may help u !

Best regards

A. Baumel

Alex Baumel Institut Méditerranéen d'Ecologie et de Paléocécologie UMR-CNRS 6116 - Université Aix-Marseille III

IMEP - Bat. Villemin Europeole de l'Arbois BP80 - 13545 Aix en Provence Cedex 04

Tel. : (33) 04 42 90 84 53 Please, visit our web site : <http://www.imep-cnrs.com> Alex Baumel <alex.baumel@univ.u-3mrs.fr>

Franz Manni <manni@mnhn.fr>

Software Barrier 2 2

A new software called "BARRIER VS. 2.2" for MS Windows is available. It computes genetic barriers from X/Y coordinates and a corresponding distance matrix. LINK: <http://www.mnhn.fr/mnhn/ecoanthropologie/software/barrier.html> The scientific interest of the software is discussed in the following article to be published next April: F. Manni, E. Guérard & E. Heyer (2004). Geographic patterns of (genetic, morphologic, linguistic) variation: how barriers can be detected by Monmonier's algorithm. *Human Biology*, 76(2): 173-190 (in press).

ABSTRACT OF THE ARTICLE: When sampling locations are known, the association between genetic and geographic distances can be tested by spatial autocorrelation or regression methods. These tests give some clues to the possible shape of the genetic landscape. Nevertheless, correlation analyses fail when attempting to identify where genetic barriers may exist, namely the areas where a given variable shows an abrupt rate of change. To this end, a computational geometry approach is more suitable since it provides the locations and the directions of barriers and it can show where geographic patterns of two or more variables are similar. In this frame we have implemented the Monmonier's (1973) maximum difference algorithm in a new software in order to identify genetic barriers. To provide a more realistic representation of the barriers in a genetic landscape, a significance test was implemented in the software by means of bootstrap matrices analysis. As a result, i) the noise associated in genetic markers can be visualized on a geographic map and ii) the areas, where genetic barriers are more robust, can be identified. Moreover, this multiple matrices approach can visualize iii) the patterns of variation associated to different markers in a same overall picture. This improved Monmonier's method is highly reliable and it can be applied to a wider range of data than genetic: whenever sampling locations and a distance matrix between corresponding data are available.

 Dr. Franz Manni Maître de conférences / Assistant professor UMR 5145 - Eco- Anthropology Group National Museum of Natural History MNHN - Musée de l'Homme 17, Place du Trocadéro 75016 Paris - France Tel. 0033 1 44 05 72 84 Fax. 0033 1 44 05 72 41 Telex Musethno -----

Software ClockTreefinder

A new TREEFINDER version is ready to download!

TREEFINDER can now optimize trees under a molecular clock. It searches for optimal roots of clocklike trees, and thereby for the the most recent common ancestor of a set of sequences. The new feature is also available in bootstrap analysis, rate profiling and in all other utilities that involve maximum likelihood tree reconstruction.

The other major improvement is a paired-sites test to estimate the confidence of inferred branches, which is much faster than bootstrapping. The so-called Local Rearrangement Paired-sites method (LRP) is following the work of Kishino and Hasegawa (*J. Mol. Evol.* 29:170-179). By applying their famous KH test to all local rearrangements in a tree, the LRP method is assigning to every edge the probability that the local topology around the edge has a higher likelihood than all near rearrangements.

The tree viewer has now a midpoint rooting utility and inferred trees come midpoint-rooted by default. A codon position filter has been added to switch on and off the codon positions in a sequence alignment. The frontend does accept files by drag & drop, dialogs have been simplified. A help menu is available.

Not new, but still worth mentioning is the fact that TREEFINDER is able to compute trees from partially overlapping sequences.

Last but not least I managed to fix some problems with the Macintosh frontend. The installing procedure for Windows was simplified.

As usual, the new TREEFINDER version can be downloaded free of charge from www.treefinder.de . There are packages for Windows, Linux and MacOS X.

I wish everybody a Happy New Year 2004!

Gangolf Jobb

jobb@stat.uni-muenchen.de

Software Network 4-1

Dear EvolDir Readers,

Some months ago, advice was sought on graphical presentation of phylogenetic networks within the free program package Network 3.1.

The new version Network 4.1 is now available and offers improved graphical features including user-defined pie charts for nodes, and publication-quality pdf diagrams. A new parsimony processing allows the user to clean up complex networks considerably by eliminating non-optimal links.

Furthermore, the process of manual data entry is now simplified for nucleotide sequences, STRs (microsatellites), amino acids, RFLPs, and combinations of these data types. Other acceptable formats now include NEXUS and PHYLIP formats.

Calculation times within the Reduced Median algorithm have now been accelerated by a factor of more than 100 according to initial trials.

Free download at: <http://www.fluxus-engineering.com>
Good luck, Peter Forster

Dr. Peter Forster Molecular Genetics Laboratory The McDonald Institute for Archaeological Research University of Cambridge Downing Street Cambridge CB2 3ER England

tel. +44-(0)1223-339-330 fax. +44-(0)1223-339-285
email: pf223@cam.ac.uk

Squat lobster samples

Dear colleagues, My name is Patricia Pérez Barros and I am a PhD student at CADIC, Ushuaia (Argentina) under the supervision of Dr. Gustavo Lovrich. Part of the aim of my project is to study the phylogeography of the squat lobsters *Munida gregaria* and *M. subrugosa*. I am writing to you in the hope that you may be able to help me obtaining samples. I would only require a small amount of specimens of each species stored in ethanol (96%). If this would not be possible, could you provide me with any contacts that may be able to help

me? Thanking you in advance for your cooperation in this matter. Any help you could provide me with would be greatly appreciated.

Kindest Regards,

Patricia.

Lic. Patricia Pérez Barros Centro Austral de Investigaciones Científicas (CADIC-CONICET) CC 92 - V9410BFD Ushuaia Tierra del Fuego Argentina

Tel: +54-2901-422310 // 422314 // 422278 FAX: +54-2901-430644 <http://www.cadicush.org.ar>
patopb@yahoo.com

Teaching Plant Evolution

Hi All, Does anyone know of software for teaching about Evolution/Population Genetics at the undergraduate level that features plants instead of animals? Thanks for your help, Shanna

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

Teaching WebSite

This looks like a really lovely basic teaching resource, of potential interest to everyone.

Cheers, - Jason

From: DR Lindberg
<drl@UCLINK.BERKELEY.EDU> Subject: A new web site in support of the teaching of Evolution

Colleagues:

Introducing UNDERSTANDING EVOLUTION

<http://evolution.berkeley.edu>

<<http://evolution.berkeley.edu>>

The University of California Museum of Paleontology, in partnership with the National Center for Science

Education, is pleased to announce a new comprehensive website on evolution developed especially for teachers. Its purpose is to provide content and resources for teachers at all grade and experience levels in order to facilitate the teaching of evolution. The site was funded by the National Science Foundation and the Howard Hughes Medical Institute and was developed by a team of scientists, graduate students, and teachers.

We hope you will find it useful in your teaching, especially introductory classes, as well as in your local communities.

Best, David

David R. Lindberg Professor & Chair, Dept. of Integrative Biology Curator, UC Museum of Paleontology <http://www.ucmp.Berkeley.Edu/people/davidl/>
----- A.P. Jason de Koning, Doctoral candidate
Email: apjdk@albany.edu Department of Biological Sciences Lab: (518) 442-4347 University at Albany, SUNY FAX: (518) 442-4767 1400 Washington Ave., Albany NY 12222, USA Mobil: (518) 210-4504 -----

Testing Linkage Equilibrium

Dear Members of Evoldir,

A few years ago Richard Hudson and I developed a web program for detecting linkage disequilibrium in multilocus data (Bioinformatics, 16:847-848.). This program has had a somewhat chequered history on the web, but it can now be found again at

<http://adenine.biz.fh-weihenstephan.de/lian/>

The web page provides an interface for testing linkage equilibrium in multilocus data. In addition, a stand-alone version of the software for Intel-Linux can be downloaded from there.

Best regards, Bernhard Haubold.

Department of Biotechnology & Bioinformatics University of Applied Sciences Weihenstephan 85350 Freising Germany Ph ++49-8161-715274 Fax ++49-8161-715116 Email: bernhard.haubold@fh-weihenstephan.de
Web: <http://www.fh-weihenstephan.de/bt/-haubold.html>

Bernhard Haubold <bernhard.haubold@fh-weihenstephan.de>

Topology Newick to Nexus

Dear Colleagues,

I am wondering if anyone is aware of any program that could detect the frequency of different topologies +given a group of trees for same taxa. PAUP has a very similar option in calculating consensus trees, but +it gives a table of partition or group frequencies, not the overall tree topology frequencies.

Also, I am trying to convert tree files from Newick to Nexus format. Does anybody know the programs to do this?

Your information is highly appreciated!

Tuo Shi

Institute of Marine and Coastal Sciences Rutgers University 71 Dudley Road, New Brunswick, NJ 08901 Phone: (732)-932-6555 ext. 332 Fax: (732)-932-4083 Email: tuoshi@imcs.rutgers.edu <http://www.marine.rutgers.edu/ebme/index.html>

Tree correlations

Hi there

could anyone recommend me a reference/method/software to infer/test correlation between intraespecies trees / genealogies?

thanks a lot

Santos Alonso

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

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

TreeFile publication answers 2

Hello,

I've received several more suggestions on manipulating tree figures, and one question, so I'm forwarding another summary message. Thanks again for such helpful responses.

Connie Mulligan

Initial query: Does anyone know how to take tree files from PAUP, MrBayes, or TreeView and import them into Adobe Illustrator or Photoshop so that they can be manipulated and eventually inserted into a Word file for publication? TreeView only allows you to save files as .emf or .wmf and Adobe doesn't recognize those files.

Follow-up question: I appreciated receiving copies of the responses you got, but did anyone else mention how to transfer the tree PICT file, created through PAUP (Mac version), to a PC for either Photoshop or Illustrator to manipulate? I do my analyses and tree constructions on a Mac, but create my Powerpoint presentations on a PC. Knowing how to do this would be a great help. Cheers, Bill Chapco.

Reponses: >One potentially important comment that didn't come through in your recent email that took me a while to figure out is that when importing trees with branch lengths into PAUP from MrBayes or other programs (the .con file for example in MrBayes) for the purpose of making a file to print it is important to click the "store branch lengths" box from the options window inside the "get trees from file" window. Then when printing (or previewing) you just click the "use user provided branch lengths" box. Otherwise, PAUP will attempt to reestimate branch lengths under whatever optimality criterion you have set.

Dave

>I was editing the trees created by Treeview directly in MS Word and it had worked very good (simply insert the file, click on it and you can start edition). Besides I suppose you could open it in Corel Draw but I'd never needed it. Regards Maciek Konopinski

– Connie J. Mulligan, PhD Assistant professor Department of Anthropology PO Box 117305 University of Florida Gainesville, FL 32611 Tele: (352) 392-2253, ext 248 Fax: (352) 392-6929 email: mulligan@anthro.ufl.edu website: <http://www.clas.ufl.edu/users/mulligan/Webpage/index.html>

Connie Mulligan <mulligan@anthro.ufl.edu>

TsTv estimates

EvolDir, I would like to estimate the % transition and Transversion values per site from mean pairwise comparisons of sequences. Does anyone know of a program that does this? Thank-you, Peter.

pjmschofield@hotmail.com

UWisconsinMadison ChapmanLecture

WITH APOLOGIES FOR MULTIPLE POSTINGS:

The University of Wisconsin-Madison (Animal Breeding and Genetics area) is pleased to announce that the year 2004 A.B. Chapman Lecturer in Animal Breeding and Genetics will be Prof. L. Dale Van Vleck, Department of Animal Science, University of Nebraska-Lincoln, and Research Geneticist at the U. S. Meat Animal Research Center, ARS, USDA.

Dr. Van Vleck has written extensively in animal breeding and genetics. His bibliography includes over 300 refereed papers and many books. He has taught courses in quantitative genetics, variance component estimation and mixed model methodology.

Dale Van Vleck has degrees from the University of Nebraska (BS, 1954, Technical Science in Agriculture; MS, 1955, Animal Science) and Cornell University (Ph.D., 1960, Animal Breeding, Statistics and Physiology). His many distinctions and honors include the Animal Breeding and Genetics Award (1972, American Society of Animal Science); the J. L Lush Award in Animal Breeding and Genetics (1983; American Dairy Science Association), and an Honorary Doctorate conferred by the University of Nebraska (1986)

The titles and venues for his lectures are:

Modeling competition effects as an embedded trait
Tuesday, May 4, 12:05, 236 Animal Sciences Building

On the paths of Gordon E. Dickerson: From Madison to Lincoln
Tuesday, May 4 4:00, 236 Animal Sciences Building

A history of genetic evaluation of sires and cows for the dairy and beef cattle industries Wednesday, May 5 8:50, 209 Animal Sciences Building

A.B. Chapman Lecturers in previous years have been: Prof. Brian W. Kennedy (Canada, 1994); Dr. Jean-Louis Foulley (France, 1995); Prof. William G. Hill (United Kingdom, 1996); Prof. Brian P. Kinghorn (Australia, 1997); Dr. R. Leyden Baker (Kenya, 1998); Dr. Louis Ollivier (France, 1999); Prof. Morris Soller (Israel, 2000); Dr. Laurie Piper (Australia, 2001); Prof. Max. F. Rothschild (Iowa State University, 2002), and Prof. James F. Crow (University of Wisconsin, 2003).

For additional information, please write to: gianola@calshp.cals.wisc.edu

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

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

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

<http://www.ansci.wisc.edu/facstaff/Faculty/pages/-gianola/index.html>

Unknown ploidy

Dear All, I have studied the isozymes of a red alga, which present a large variety of morfologies. I collected the samples at four localities, but at all localities one of the morfological variants was always sterile. Since the sporophytes and the gametophytes are morphologically identical in this species, I couldn't find out the ploidy of the sterile individuals. I usually found more sporophytes than gametophytes for the other morfologies. How can I analyze my data? Does someone know any program that is able to analyze data of samples which ploidy is unknown? Thanks in advance

Milena

Milena Polifrone Dr. in Biology of Algae Departamento de Biología Universidad de Las Palmas de Gran Canaria Campus Universitario de Tafira 35017 Las Palmas Canary Island, Spain – mpolifrone@becarios.ulpgc.es

PostDocs

Barcelona L1 Evol	45	UCambridge PrimateCoatColour	49
Barcelona Speciation	45	UHelsinki InsectDispersal	50
CornellU EvolGenomics	46	UIllinois Bioinformatics	50
MichiganStateU StatGenetics	46	UIowa Genetics	50
Montpellier MultiGenePhylo	47	ULyon HostParasitoid	51
Montpellier Phyloinformatics	47	UOregon CelegansEvol	51
RutgersU ShellfishGenetics	48	UParisOrsay MicrobialGenomes	52
SUNYStonyBrook PhenotypicPlasticity	48	UParisOrsay PlantSpeciesInvasion	52
UCIrvine InfluenzaEvol	48	UPierreMarieCurie EvolNeuralCells	53
UCIrvine PlantPopGenetics	49		
UCSantaCruz EvolGenetics	49		

Barcelona L1 Evol

Postdoc job: Retrotransposon evolutionary dynamics in species hybrids

General description A postdoctoral position is available to study Osvaldo retrotransposon expression in *Drosophila buzzatii*, *D.koepferae* and their hybrids. Work in our lab has shown that Osvaldo transposes at higher rate in hybrids than in parental species (Labrador et al. 1999, *Mol.Biol.Evol.* 16: 931-937) and that hybrids generate genetic instability (Naveira and Fontdevila 1985, *Chromosoma* 91: 87-94). Other similar results have been obtained in different organisms, such as mammals and plants. The putative evolutionary implications of hybrid genetic instability, mainly in introgression and hybrid speciation, is going to be investigated in relation to hybrid retrotransposition increase. Combining genomic, molecular, cytogenetic, and population techniques we want to detect and interpret different expression levels of Osvaldo in species, populations, and hybrids and its relationship to structural changes in chromatin.

Applicant qualifications. The position is open to all nationalities, but in the case of nationals of Spain they must be residents in a foreign country and they must be working regularly out of Spain at the moment of application. Applicants must have completed their PhD degree before March 30, 2004 and after January 1st, 1998. They must have either a strong background in *Drosophila* molecular evolutionary genetics of transposable elements or a strong background in

molecular genetics with a high interest in evolution and transposable elements. Applicants are expected to provide innovative views and new technical skills to improve the research qualifications of the host group.

Procedure Applicants must contact immediately Dr. Antonio Fontdevila at antonio.fontdevila@uab.es sending a cover letter, a CV, one or two representative publications (in PDF) and the names, affiliation, address, e-mail address, and telephone number of two persons of reference. Deadline for submission is March 20, but immediate notice is encouraged. Salary range is 1270-2325 euros (before taxes) and duration is 18 months. The successful applicant is expected to start working on September 1, 2004, but, if justified, his/her incorporation can be delayed until March 1, 2005.

Antonio Fontdevila Grup de Biologia Evolutiva Departament de Genetica i Microbiologia Edifici C Univer-

sitat Autònoma de Barcelona 08193 Bellaterra, Spain
Phone: 34-93-5811083 Fax. 34-93-5812726 e-mail: antonio.fontdevila@uab.es

Barcelona Speciation

Postdoc job: Two three year postdoc positions on speciation in Barcelona

General description

First position A postdoctoral position is available to study Osvaldo retrotransposon expression in *Drosophila buzzatii*, *D.koepferae* and their hybrids. Work in our lab has shown that Osvaldo transposes at higher rate in hybrids than in parental species (Labrador et al. 1999, *Mol.Biol.Evol.* 16: 931-937) and that hybrids generate genetic instability (Naveira and Fontdevila 1985, *Chromosoma* 91: 87-94). Other similar results have been obtained in different organisms, such as mammals and plants. The putative evolutionary implications of hybrid genetic instability, mainly in introgression and hybrid speciation, is going to be investigated in relation to hybrid retrotransposition increase. Combining genomic, molecular, cytogenetic, and population techniques we want to detect and interpret different expression levels of Osvaldo in species, populations, and hybrids and its relationship to structural changes in chromatin.

Second position Another position is open to study speciation genes in *Drosophila*. Using hybrids of *D.buzzatii* and *D.koepferae*, and backcrosses one can introgress genomic fragments in the background *buzzatii* genome. These introgressed hybrids can be scored cytogenetically for introgressed chromosomal segments and studied for molecular markers to map genetic markers in the introgressed fragments associated with male sterility and inviability. The first work performed (Naveira and Fontdevila 1986. *Genetics* 114: 841-857) showed that these fragments act additively, but a recent theoretical reassessment of these data (Marín 1996. *Genetics* 142: 1169-1180) suggested that a few fragments could act epistatically. The present project tries to combine small fragments, using molecular markers, to test this epistatic hypothesis. This project combines a series of cytogenetic, molecular, physiological and genomic techniques.

Applicant qualifications. The position is open to all nationalities. Applicants must have completed their PhD degree after March 22, 2001. Except for those who have

obtained their PhD less than 12 months ago, applicants must have spent at least 12 months working in a University or Research Institute different from that where they have obtained their PhD. They must have either a strong background in *Drosophila* molecular, evolutionary genetics of transposable elements or a strong background in

molecular genetics with a high interest in evolution, transposable elements and speciation. Applicants are expected to provide innovative views and new technical skills to improve the research qualifications of the host group.

Procedure Applicants must contact immediately Dr. Antonio Fontdevila at antonio.fontdevila@uab.es sending a cover letter, a CV, one or two representative publications (in PDF) and the names, affiliation, address, e-mail address, and telephone number of two persons of reference. Deadline for submission is March 17, but immediate notice is encouraged. Salary per year is 23.000euros (before taxes) and duration is three years. The successful applicant is expected

to start working on October 2004, but, if justified, his/her incorporation can be delayed until December, 2004.

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CornellU EvolGenomics

POSTDOCTORAL POSITION AT THE MATH/BIOLOGY INTERFACE IN EVOLUTIONARY GENOMICS at Cornell with Rick Durrett, Chip Aquadro and Rasmus Nielsen

A postdoctoral position is available to work at the interface of computational, statistical and empirical evolutionary genomics with Rick Durrett, Chip Aquadro and Rasmus Nielsen at Cornell. Support is available for two years, supported by grant from the joint NSF/NIGMS program for research at the interface of math and biology. We are looking for either (i) a person with a Ph.D. in the biological sciences with a strong background in the models of population genetics and the use of biological databases, or (ii) a person with a Ph.D. in mathematical, statistical or computational science

with an interest in studying biological problems arising from population and comparative genomics. Research opportunities include the analysis of patterns in DNA sequence and microsatellite variation particularly in *Drosophila* and mammals, the development, analysis, and application of methods to distinguish the effects of demography and population history from the effects of natural selection, the comparative analysis of the soon-to-be-available genome sequences of several additional *Drosophila* species, and the investigation of genome evolution by rearrangement and duplication. Cornell provides a stimulating environment in evolutionary genomics including the additional research groups of Andy Clark, Carlos Bustamante, Brian Lazzaro, Rick Harrison, Ed Buckler, Steve Kresovich, Steve Tanksley, Susan McCouch, Jeff Doyle, Bryan Danforth, and others, plus excellent mathematical, statistical and computational colleagues and resources (particularly the Cornell Theory Center). Applications or inquiries should be emailed to Rick Durrett (RTD1@CORNELL.EDU) or Chip Aquadro (CFA@CORNELL.EDU). Send a full CV that includes educational background, publications, and a statement of research interests, and arrange for two people to send letters of recommendation. The position can start in the summer or fall of 2004.

Rick Durrett Department of Mathematics 523 Malott Hall Cornell University Ithaca NY 14853 RTD1@CORNELL.EDU Phone: 607-255-8282 FAX: 607-255-7149 <http://www.math.cornell.edu/~durrett>

Chip Aquadro Department of Molecular Biology and Genetics 235 Biotechnology Building Cornell University Ithaca, NY 14853 CFA1@CORNELL.EDU Phone: 607-254-4838 FAX: 607-255-6249 <http://www.mbg.cornell.edu/aquadro/aquadro.html>

MichiganStateU StatGenetics

Michigan State University Postdoctoral Position in Statistical Genetics

A postdoctoral position in the area of Statistical Genetics is available at the Department of Animal Science and Department of Fisheries and Wildlife - Michigan State University, East Lansing, Michigan.

The successful candidate will work on a project related to the integration of genotyping errors in different applications of molecular marker information in animal breeding and wildlife studies, including (and depending on candidate's interests) genetic map construction,

QTL analysis, paternity uncertainty and pedigree reconstruction, and mark-recapture models for studying natural populations.

Candidates with a PhD degree in Genetics or Animal Breeding (or similar areas) with a strong background in statistics and programming; or a PhD degree in Statistics or Computer Sciences (or similar areas), with some knowledge and strong interest on genetics are encouraged to apply.

Interested candidates should contact (preferably by email):

Guilherme J. M. Rosa Department of Animal Science
1205-I Anthony Hall Michigan State University East
lansing - MI 48824-1225 Phone: (517) 353-5102 Email:
rosag@msu.edu

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Guilherme J. M. Rosa Assistant Professor Department
of Animal Science Department of Fisheries and Wildlife
Michigan State University 1205-I Anthony Hall East
Lansing, MI 48824-1225 USA

Phone: 1-517-353-5102 Fax: 1-517-432-9168 E-mail:
rosag@msu.edu <http://www.msu.edu/~rosag/>

Montpellier MultiGenePhylo

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

“Maximum likelihood methods and algorithms for phylogenetic reconstruction based on multiple gene data sets”

The goal is to pursue the work on PHYML (Guindon and Gascuel 2003, Syst. Biol. 52:696), to allow for simultaneous analysis of multiple genes, as encountered in several recent phylogenetic studies. As different genes often have different substitution patterns (Delsuc, alii, and Douzery, 2002, Mol Biol. Evol. 19:1656), it is required to take this heterogeneity into account, which involves works on substitution models and likelihood optimization. The candidate will have an excellent level in computer science, with good knowledge in numerical optimization, Markovian modeling, and phyloinformatics.

Contacts:

Emmanuel J. P. DOUZERY - douzery@isem.univ-montp2.fr <http://www.isem.univ-montp2.fr/PPP/>-

PHYLMOL.php Olivier GASCUEL - gascuel@lirmm.fr
<http://www.lirmm.fr/~w3ifa/MAAS/> Application :
CNRS - S. T. I. C., offer N19. http://www.sg.cnrs.fr/-drhchercheurs/post_doc.2004/ -----

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

Olivier GASCUEL <gascuel@lirmm.fr>

Montpellier Phyloinformatics

Available post-doctoral position, starting September 2004, in Montpellier (France).

“Maximum likelihood methods and algorithms for phylogenetic reconstruction based on multiple gene data sets”

The goal is to pursue the work on PHYML (Guindon and Gascuel 2003, Syst. Biol. 52:696), to allow for simultaneous analysis of multiple genes, as encountered in several recent phylogenetic studies. As different genes often have different substitution patterns (Delsuc, , and Douzery, 2002, Mol Biol. Evol. 19:1656), it is required to take this heterogeneity into account, which involves works on substitution models and likelihood optimization. The candidate will have an excellent level in computer science, with good knowledge in numerical optimization, Markovian modeling, and phyloinformatics.

Contacts:

Emmanuel J. P. DOUZERY - douzery@isem.univ-montp2.fr

<http://www.isem.univ-montp2.fr/PPP/>-
PHYLMOL.php (Go to Research > Phyloinformatics
> Supertrees)

Olivier GASCUEL - gascuel@lirmm.fr

<http://www.lirmm.fr/~w3ifa/MAAS/> Application :
CNRS - S. T. I. C., offer N19.

http://www.sg.cnrs.fr/drhchercheurs/post_doc.2004/

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

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

RutgersU ShellfishGenetics

Postdoctoral Position In Shellfish Genetics

A postdoctoral associate position is available at the Haskin Shellfish Research Laboratory, Rutgers University. The position is funded by a grant from the New Jersey Commission on Science and Technology. Research will focus on the development of genetic tools needed for the mapping of economically important traits in the eastern oyster. Applicants should have a Ph.D. and background in genetics and molecular biology. Prior experience in cloning, sequencing and genotyping is preferred. The appointment starts on July 1, 2004 or soon after, and is for one year with possible renewal. Search will continue until the position is filled. Interested individuals should submit a CV, a brief statement of interest, and three letters of recommendation to: Dr. Ximing Guo, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349. Phone: (856) 785-0074 x124; Fax: (856) 785-1544; Email: xguo@hsrl.rutgers.edu. Web: <http://www.hsrl.rutgers.edu> . xguo@vertigo.hsrl.rutgers.edu

SUNYStonyBrook PhenotypicPlasticity

A two-year, NSF-funded post-doc position is available in Dr. Massimo Pigliucci's lab at SUNY-Stony Brook (Long Island, NY), beginning in August 2004.

The project focuses on the molecular basis of and quantitative variation for plasticity to mechanical stimulation ("touch response"). The successful applicant will be expected to conduct greenhouse experiments as well as to contribute to the molecular component of the project. The research will be carried out in collaboration with two additional labs, Janet Braam's at Rice University, and Randy Small's at the University of Tennessee.

Stony Brook University is situated in the middle of

Long Island, on the north coast. It is connected by railroad and a major highway to New York City, and it affords a variety of cultural programs and other amenities.

More information about the Pigliucci lab can be found at www.genotypebyenvironment.org; for more about SUNY-Stony Brook's Ecology & Evolution department, go to <http://life.bio.sunysb.edu/ee/> If interested, please send an email cover letter, together with a c.v., list of publication, and general statement of research interest to Dr. Massimo Pigliucci at pigliucci@utk.edu; the search will continue until the position will be filled.

~~~ Massimo Pigliucci, Professor Exec. VP, Society for the Study of Evolution Depts. of Botany and of Ecology & Evol. Biology University of Tennessee, Knoxville, TN 37996-1100 phone 865-974-6221, fax 2258

[www.genotypebyenvironment.org](http://www.genotypebyenvironment.org) "All observation must be for or against some view if it is to be of any service." -Charles Darwin

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## UCIrvine InfluenzaEvol

The Department of Ecology & Evolutionary Biology on the UC Irvine campus is currently seeking a Postdoctoral Researcher/Postdoctoral Scholar to join the laboratory of Dr. Robin Bush:

We are seeking one or more Postdoctoral Researcher(s)/Scholar(s) to study the evolution of the influenza virus using computational techniques. Potential projects range from studying the molecular interactions between viral and host cell receptors using homology modeling to studying the interplay of epidemiology and evolution at the population level. A Ph.D. and experience in molecular evolution, epidemiological modeling, phylogenetics or protein homology modeling is required; knowledge of infectious diseases is desirable. Salary will be commensurate with experience.

Review of candidates and applications will commence on March 10, 2004 and continue through April 10, 2004. Applicants should submit a cover letter, a curriculum vitae and the name, address and phone number of two references by to the address listed below:

Contact information:

Dr. Robin Bush Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 e-mail: [rmbush@uci.edu](mailto:rmbush@uci.edu)



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

Robin Bush <rmbush@uci.edu>

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### **UCIrvine PlantPopGenetics**

#### **POSTDOCTORAL RESEARCHER/SCHOLAR POSITION(S)**

The Department of Ecology and Evolutionary Biology in the School of Biological Sciences at the University of California, Irvine seeks one or more Postdoctoral Scholar(s)/Researcher(s) in plant population genetics to join a project exploring the impact of phenological assortative mating on the genetic variance/covariance structure of flowering schedules. The successful applicant(s) will participate in planned field and greenhouse experiments and will develop related projects. The projected starting date is May 15, 2004. Review of candidates and applications will commence on March 8, 2004 and continue through April 8, 2004.

Postdoctoral positions start at a salary of \$31,044 per annum, plus benefits. The successful candidate(s) must have research experience with plant ecology and genetics, knowledge of quantitative genetic analysis and an understanding of artificial selection design. Excellent oral and verbal communication skills are also required.

To apply, send a letter of application, curriculum vitae, two reprints/preprints and the names and e-mail and postal addresses of three references by April 8, 2004 to:

Dr. Arthur E. Weis University of California-Irvine  
Department of Ecology and Evolutionary Biology 321  
Steinhaus Hall Irvine, CA 92697-2525

aeweis@uci.edu <http://ecoevo.bio.uci.edu/Faculty/-Weis/Weis.html>

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### **UCSantaCruz EvolGenetics**

NSF-Funded Postdoctoral Position in Evolutionary Genetics University of California, Santa Cruz

A three-year postdoctoral position is available to study the molecular population genetics of two NE Pacific marine taxa (the California sea mussel and purple sea urchin). The primary objective of the project is to investigate the impact of Pleistocene climatic oscillations on the historical ecology of mussels and urchins through the reconstruction of allelic genealogies from multiple nuclear genes. The successful applicant will have strong molecular (i.e., PCR, DNA sequencing, etc.) and analytical skills. Familiarity with coalescent theory and some experience in performing coalescent simulations would also be ideal.

The deadline for applications is March 31 and the starting date will be as soon as possible after April 15. Interested applicants should send a CV, a brief letter describing research interests and experience, and the contact information for three referees via email to Grant Pogson (pogson@biology.ucsc.edu).

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

Grant Pogson Department of Ecology and Evolutionary Biology University of California, Santa Cruz Santa Cruz, CA 95064 Phone: 831 459-5122 Fax: 831 459-5353 Email: pogson@biology.ucsc.edu

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### **UCambridge PrimateCoatColour**

Postdoctoral Research Associate, Department of Zoology, University of Cambridge

A Post-doctoral Research Associate is required to work on a BBSRC-funded project on the molecular genetic basis of coat colour evolution in primates. The project will investigate the role of candidate loci in the evolution of coloration in a variety of primate lineages. The research group occupies a newly refurbished lab and office space, and has diverse ongoing projects in adaptive evolutionary genetics. The Zoology Department achieved the highest research rating (5\*) and provides a stimulating and interactive environment.

Candidates should have a Ph.D. in evolutionary biology, molecular ecology, population genetics, developmental biology or a related field, and an interest in adaptive evolution. Salary will be on the RA1A scale (GBP18,265 - 27,339 pa). The appointment will be for up to two years subject to satisfactory completion of a six month probationary period, and will start after 1st June 2004.

Applicants will have to fill in an application form, including details of two professional referees. Forms are available from Anne Garlick, email: [ag318@hermes.cam.ac.uk](mailto:ag318@hermes.cam.ac.uk), tel: +44-(0)1223-336621

For further information please contact Nick Mundy at: [nim21@cam.ac.uk](mailto:nim21@cam.ac.uk) Website: <http://www.zoo.cam.ac.uk/zoostaff/egg>. The closing date for applications is 23rd March 2004.

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## UHelsinki Insect Dispersal

Postdoctoral Research Associate, Metapopulation Research Group, Dept of Biological and Environmental Sciences, University of Helsinki

A Postdoctoral Research Associate is required to work on molecular biology of flight performance of the Glanville fritillary butterfly. The project is closely linked with ongoing experimental and theoretical research on the evolution of dispersal behaviour in this butterfly, as a part of a large-scale project on metapopulation biology. The research group has much expertise in ecology, mathematical biology, and butterfly biology. The department is strong in behavioural and evolutionary ecology. We are located in the same campus with very large departments of molecular biology and biotechnology.

The project will attempt to integrate population biology with molecular mechanisms. Candidates should have a Ph.D. in molecular biology and preferably previous post doc experience. We look for a researcher who has the capacity to conduct independent molecular research, who is interested in supervising students, and who has an interest in integrated biology. Salary will be 2400-3200 euros per month depending on experience. Appointment will initially be until the end of 2005 but may be renewed. Appointment should be made August 1 the latest.

Send application with a statement of research interests and CV to Prof. Ilkka Hanski, and arrange two letters of recommendation to be sent to him independently. Email: [ilkka.hanski@helsinki.fi](mailto:ilkka.hanski@helsinki.fi). For further information contact Ilkka Hanski. The closing date for applications is 31st March 2004.

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## Ullinois Bioinformatics

Postdoctoral position in Statistical Genomics and Bioinformatics

A postdoctoral position in the areas of bioinformatics and statistical genomics is available at the Department of Animal Sciences, University of Illinois.

The successful candidate will work on models for gene expression (microarray), gene networks, DNA and protein sequences information in Bayesian and likelihood frameworks. The position is part of an NIH funded project on gene expression profiling of changes in social behavior and relies on interdisciplinary collaboration between faculty in the Neuroscience Program and in the departments of Statistics and Animal Sciences at the University of Illinois.

Applications from individuals holding a degree in Biology, Genetics, Neuroscience, Animal Sciences, Bioinformatics, Statistics, Computer Sciences or related areas are welcomed. Candidates should have a strong background in computational statistics and genetics with experience in programming.

Applicants should send a CV, a statement of research experience and interests, and names of two references with contact information to:

Sandra Rodriguez-Zas, Ph.D. Assistant Professor Department of Animal Sciences 1207 W. Gregory Dr. Urbana, IL 61801 Email: [rodrgrzs@uiuc.edu](mailto:rodrgrzs@uiuc.edu) <http://www.ansci.uiuc.edu/labs/bioinformatics/>

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## UIowa Genetics

Postdoctoral Associate / Assistant Research Scientist  
Center for Comparative Genomics Iowa City, Iowa

The University of Iowa Department of Biological Sciences is hiring an Postdoctoral Associate / Assistant Research Scientist for the position Geneticist / Biochemist. The position will perform genetic, biochemical, or bioinformatics research aimed at studying oxidative phosphorylation and mitochondrial efficiency (broadly defined) in *Drosophila*. This is a one year

appointment, with possible extension. Minimum requirement: M.A. in Biology, Genetics/ Biochemistry with 2 years research experience in molecular evolution, or equivalent combination of education and experience. Salary range \$37,608 to \$45,310. Send CV and letter of interest to Professor Bill Ballard, University of Iowa, 208 BB, Iowa City, IA, 52242. For more information visit <http://www.myweb.uiowa.edu/bballard>. Email [bill-ballard@uiowa.edu](mailto:bill-ballard@uiowa.edu)

– J. William O. Ballard 208 Biology Building Department of Biological Science The University of Iowa Iowa City Iowa, 52246 USA

<http://myweb.uiowa.edu/bballard/> <http://www.biology.uiowa.edu/ccg/> Bill Ballard <[bill-ballard@uiowa.edu](mailto:bill-ballard@uiowa.edu)>

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### ULyon HostParasitoid

Post-doctoral position, University Lyon, Influence of microorganisms on host-parasitoid association

The CNRS offers a one-year post-doctoral position starting September 1st to work on how symbiotic microorganisms can mediate host-parasitoid relationships in the University of Lyon.

Offer description: Many insects harbor vertically-transmitted symbiotic microorganisms. Most of these symbionts are neither mutualists, nor true pathogens, but they manipulate their hosts reproduction at their own advantage. These manipulations allow their spread in the host population, even though they induce a cost and reduce the mean fitness of their hosts. While the way these microorganisms spread is now well understood, their consequences on insect communities are still unknown, despite their potential to alter the population dynamics of their hosts. This is especially important in host-parasitoid associations where the host, the parasitoid or both may be infected, and sometimes with the same microorganisms. The project will focus on how the invasive dynamics of the microorganism can interfere with the demographic and evolutionary dynamics of the host-parasitoid system, and how this interaction may modulate the life histories of protagonists and their specificity. The project will focus on *Drosophila*, their parasitoid wasps and their symbionts consisting of both cytoplasmic incompatibility inducing *Wolbachia* and viruses that manipulate the parasitic behavior of insects. The experimental part of the project will study the effects of these microorganisms, their spread, and

their consequences on the functioning of host-parasitoid associations in microcosms. Mathematical models will be developed that include the demographic, genetic and evolutionary consequences of these microorganisms on the dynamics of insect populations and communities.

Candidate profile: Young researcher (less than 40) with good experience in concepts and methods in at least two of the following items: - Evolutionary biology and genetics of parasitic and symbiotic associations - Dynamics of host-parasite systems and epidemiology - Theory and modelling - Expertise in experimental evolution The successful candidate will work in a group that has much expertise at both the experimental and modelling level.

Candidature: Candidature must be sent before May 14th to F. Vavre (see contact). A candidature file and more information on the position (offer SDV 15) can be found on the following site: <http://www.sg.cnrs.fr/drhchercheurs/post.doc.2004/> Contact: F. Vavre ([vavre@biomserv.univ-lyon1.fr](mailto:vavre@biomserv.univ-lyon1.fr)) ou F. Fleury ([fleury@biomserv.univ-lyon1.fr](mailto:fleury@biomserv.univ-lyon1.fr)) UMR CNRS 5558, Biométrie et Biologie Evolutive Université Claude Bernard Lyon I 43 Boulevard du 11 Novembre 1918 69622 Villeurbanne Cedex France Tel: 00 33 4 72 43 19 21 Fax: 00 33 4 72 43 13 88

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### UOregon CelegansEvol

POSTDOCTORAL POSITION: EVOLUTIONARY GENETICS OF *C. ELEGANS*

A postdoctoral fellow is sought to contribute to an NSF funded project in the laboratory of Patrick Phillips, Center for Ecology and Evolutionary Biology, University of Oregon using the nematode, *Caenorhabditis elegans*, as a model system for studying the roles of mutation and outcrossing in adaptive evolution. The project involves utilizing genetic tools available for *C. elegans* to test specific hypotheses regarding the evolution of mating systems within an experimental evolution framework. See Stewart and Phillips (2002, *Genetics* 160:975-982) for background. See <http://www.uoregon.edu/~pphil> for other lab activities.

The University of Oregon is located in Eugene, OR, one of the most outstanding small cities in the US. The campus is one hour from the beautiful Oregon coast and one hour from mountain hiking and skiing. The initial appointment is for one year with likely extension for an additional year. The salary is US\$33,000

plus benefits. The start date is flexible, but ideally would be towards the beginning of the summer. Applications will be taken until the position is filled. Please send a statement of research interests, publications, CV, and letters from three references to Patrick Phillips at [pphil@uoregon.edu](mailto:pphil@uoregon.edu) or to Biology Department, University of Oregon, Eugene, OR 97403-1210. Review of applications will begin on April 19. The University of Oregon is an equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act.

Patrick C. Phillips, Associate Professor of Biology Center for Ecology and Evolutionary Biology  
 Email: [pphil@uoregon.edu](mailto:pphil@uoregon.edu) Phone: (541) 346-0916  
 | FAX (541) 346-2364 Address: 5289 University of Oregon Eugene, OR 97403-5289 USA Web: Lab  
<http://www.uoregon.edu/~pphil> EvoNet <http://www.EvoNet.org> CEEB <http://evolution.uoregon.edu>  
 IGERT <http://evodevo.uoregon.edu>

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## UParisOrsay MicrobialGenomes

A one year postdoctoral position is available in the group of Dr. Bernard Labedan "Molecular Evolution and Genomics", (see complete address below) on the following theme. Studying the fluidity of microbial genomes and reconstruction of minimal genomes. The advent of the complete sequence of numerous microbial genomes has underlined an unexpected variability in the panoply of genes between closely related species. We have compared exhaustively about one hundred genomes of various bacteria, archaea and fungi and we have built a suite of informatic tools to identify all orthologues and paralogues. The project will be to analyse these data in order to identify the genes which are omnipresent at different phylogenetic and taxonomic levels. This would allow to uncover the essential genes which were present in more and more distant ancestors and to reconstruct the corresponding minimal genomes. The candidate (under 35) must have a good experience in Microbiology and a solid knowledge of the informatic tools used for sequence analysis. Position is for 12 (minimum) - 18 (maximum) months and will start in september 2004. It is part of a special program provided by the French Ministry of Research and accordingly any visa procedure will be accelerated. The salary will be 1830 per month. A Social Security cover will be provided by the University of Paris-Sud. There will be no funding for travel expenses. Knowledge of the

French language is not required. Any people interested must contact me ASAP and before April 9.

Contact: Bernard Labedan, [labeledan@igmors.u-psud.fr](mailto:labeledan@igmors.u-psud.fr), 33 1 69 15 57 18 Institut de Génétique et Microbiologie, Université de Paris-Sud, Bâtiment 409, 91405 Orsay Cedex, France <http://www.igmors.u-psud.fr/-LABEDAN/LABEDAN-eng.htm> ———

Bernard Labedan <[labeledan@igmors.u-psud.fr](mailto:labeledan@igmors.u-psud.fr)>

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## UParisOrsay PlantSpeciesInvasion

A two year post doc position starting September 1 2004 on "Global change, plant species invasion and adaptation" is available in the Department Ecologie, Systématique et Evolution at the Université Paris-sud in Orsay, just south of Paris.

Project framework:

Global change, plant species invasion and adaptation.

Species invasions and range expansions expose organisms to new ecological conditions to which they must adapt. Several processes enable species to invade new communities, including their ability to adapt to new conditions and the characteristics of invaded communities, such as the presence of competitors and natural enemies. The adaptive process will be studied using transplantation and common garden experiments coupled with manipulation of environmental conditions that simulate predicted climate change. This adaptive process involves both phenotypic plasticity and genetic adaptation, and we will address both processes, the latter, using molecular markers that permit the assignment of organisms to their historical geographic ranges. In particular phenotypic plasticity for morphological and physiological traits will be studied since these should determine the success of invasions and range expansions. Interactions between invading species and their plant competitors and natural enemies such as herbivores and pathogens will also be investigated. In addition to studying the characteristics of invading species, we will also examine how competitive and trophic interactions will be altered by global change in invaded communities.

Profile sought: organismal biologist, plant ecologist, experimental ecologist, good statistical abilities, expertise in one or more of: plant physiological ecology, plant-pathogen or plant-herbivore interactions, plant population genetics

Interested candidates can download an application form at the following web-site

[http://www.sg.cnrs.fr/drhchercheurs/post\\_doc\\_2004/](http://www.sg.cnrs.fr/drhchercheurs/post_doc_2004/)

The project is number SDV 32 and can be found at this web site, in french, under "offres SDV". Candidates should fill out the (bilingual) form found on this web page with the link "Dossier de candidature" The completed application, including cv and a proposal for work to carry out over the two years that fits into the broad framework of the project outlined above should be sent, by the 14 May, 2004 at the latest to:

Jacqui Shykoff Laboratoire d'Ecologie, Systématique et Evolution CNRS UPRESA 8079 Université Paris-Sud Bâtiment 360 91405 Orsay Cedex France tel: ++33 1 69155666 fax: ++33 1 69154697 jacqui.shykoff@ese.u-psud.fr

– Jacqui Shykoff Laboratoire d'Ecologie, Systématique et Evolution CNRS UPRESA 8079 Université Paris-Sud Bâtiment 360 91405 Orsay Cedex France

tel: ++33 1 69155666 fax: ++33 1 69154697 jacqui.shykoff@ese.u-psud.fr

Shykoff Jacqui <jacqui.shykoff@ese.u-psud.fr>

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## UPierreMarieCurie EvolNeuralCells

Announcement :

Looking for a candidate to apply for a post-doctoral position. Our team is looking for a candidate to apply for a post-doctoral fellowship of the French Ministry of Research (simultaneous application for the team and the candidate). The deadline for candidatures is 5 April. The post-doctoral fellowship would be for one year, with possibility for a 6 months extension; the salary would be 1830 euros / month. We have recently initiated a research program on the origin and evolution of neural cells and the nervous system in non-bilaterians. We use as model species the ctenophoran Pleurobrachia

pileus and the hydrozoan cnidarian *Clytia hemisphaerica*. We are interested in several distinct but related aspects of neurogenesis: neuronal specification and differentiation, relationships between neural cells and ciliated epithelial cells, and molecular mechanisms involved in patterning the nervous system. The work will be done at the University Pierre et Marie Curie in Paris, with some stays at the Villefranche Marine Station. It will start with the analysis of a dataset consisting of 3000 EST from Pleurobrachia in a search for homologues of bilaterian developmental genes involved in neurogenesis, followed by the study of their expression patterns by in situ hybridization. By this mean the hypothesis of conservation of a neurogenetic function between Ctenophora and Bilateria will be tested for a number of genes randomly picked in the cDNA library and selected for their sequence homology with genes involved in neurogenesis (either neuronal determination / differentiation, or nervous system patterning). As a complementary approach, a random in situ hybridization screening from Pleurobrachia EST should permit the constitution of a collection of genes expressed in various aspects of nervous system development. Within this framework, the post-doc will have a large degree of initiative to finalize its own project in interaction with the remaining members of the team The candidate should have a strong background in developmental and molecular biology, and a real interest for comparative approaches. Preferably, but not necessarily, the candidate may have done his or her ph-D in the field of Evo-Devo, whatever the model and the problematic. Experience in phylogenetic and / or genomic analysis will be appreciated. Applicants should send quickly a CV to Michael.Manuel@snv.jussieu.fr

– Dr. Michael MANUEL

Maitre de Conférences (Assistant Professor) Université Pierre et Marie Curie (Paris 6) Equipe Evolution et Développement, UMR 7138 "Systematique, Adaptation, Evolution" Bat. B, 7eme etage, piece 705 9 quai St Bernard 75 005 Paris, FRANCE

tel. 33 (0) 1 44 27 34 69 33 (0) 6 14 65 48 05 fax 33 (0) 1 44 27 32 58 e-mail Michael.Manuel@snv.jussieu.fr

Michael MANUEL <mmanuel@snv.jussieu.fr>

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## Workshops Courses

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### Barcelona Genomics Jun1-15

International Postgraduate Course in Genomics

Universitat Autònoma de Barcelona (Barcelona, SPAIN) June 1-15, 2004

Invited Professors: Pieter de Jong Children's Hospital Oakland Research Institute (CHORI) Oakland (USA)

Mayuan Long Departament of Ecology and Evolution, University of Chicago Chicago (USA)

Content: Genome Projects. Size and anatomy of eukaryotic genomes. Repetitive DNA. Markers. Cloning vectors. Constructions and characteristics of genomic libraries. Uses and screening of genomic libraries. Linkage mapping. Physical mapping. Sequencing strategies. Shotgun sequencing. Bioinformatic tools and analysis of DNA sequences: ORF prediction, detection of regulatory sequences. Functional genomics. Molecular evolution. Rates and patterns of nucleotide substitution. Duplication and the origin of new genes. Gene traffic and genomic reorganization of sex-related genes. Detection of natural selection. Comparative genomics. Rates and patterns of chromosomal rearrangement. The human genome.

Dates: June 1-15, 2004, 10h - 13h30.

For registration and information, please contact:

Julia Provecho, Departament de Genética i de Microbiologia, Universitat Autònoma de Barcelona, 08193 Bellaterra (Barcelona), SPAIN. Tel. 34-93-581-2724, FAX 34-93-581-2387, E-mail: d.genetica@uab.es.

Alfredo Ruiz, Departament de Genética i de Microbiologia, Universitat Autònoma de Barcelona, 08193 Bellaterra (Barcelona), SPAIN. Tel. 34-93-581-2729, FAX 34-93-581-2387, E-mail: Alfredo.Ruiz@uab.es.

Alfredo Ruiz <Alfredo.Ruiz@uab.es>

### Barcelona Speciation May3-14

Two graduate courses in "Speciation" are offered at the Universitat Autònoma de Barcelona by international specialists in the field of Evolution.

GRADUATE COURSES IN SPECIATION

UNIVERSIDAD AUTÓNOMA DE BARCELONA

Title: Ecology and Genetics of Speciation

Professor: Dr. Lev Yampolsky, Department of Biological Sciences, East Tennessee University, USA

Synopsis: The purpose of this course is to overview current knowledge of causes and mechanisms of speciation. We will consider genetic and ecological factors of reproductive isolation, role of drift and selection in generating these mechanisms. We will utilize data from a variety of experimental systems, including *Drosophila*, *Rhagoletis*, birds, fishes and plants and will give special attention to speciation in species flocks.

Dates: May 3-14, 2004

Title: Controversial Topics in Speciation

Professor: Dr. Menno Schilthuizen, Institute for Tropical Biology and Conservation, University of Malaysia Sabah, Malaysia.

Synopsis: There are many ways to produce a new species, yet many of them, such as sympatric and hybrid speciation, to cite only a few of them, are still subject to great controversy. This course will analyze these controversial mechanisms in terms of their plausibility and frequency of occurrence using different case studies. The book by Dr. Schilthuizen entitled *Frogs, flies and dandelions* provides a guide to the course.

Dates: May 17-28, 2004

## REGISTRATION AND INFORMATION

Julia Provecho, tel. 93-5812724 d.genetica@uab.es

Dr. Antonio Fontdevila, tels. 93-5811083, 93-5812726;  
antonio.fontdevila@uab.es

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### Barcelona TEs May21-Jun11

Two courses on “Evolution of Transposable Elements” are offered at the Universidad Autònoma de Barcelona.

#### GRADUATE COURSES IN EVOLUTION OF TRANSPOSABLE ELEMENTS

##### UNIVERSIDAD AUTÒNOMA DE BARCELONA

Title: The contribution of retroelements to the evolution of genome structure and function

Professor: Dr. John F. McDonald, Department of Genetics, University of Georgia, Athens, USA

Synopsis: Retrotransposons are a significant component of all eukaryotic genomes. For many years retrotransposons and other transposable elements were considered “genomic junk” having no adaptive benefit to the host genomes in which they reside. The last ten years has witnessed a dramatic shift in our perception of the adaptive significance of retrotransposons. Retrotransposons are now perceived to have contributed to the evolution of genome structure and function both directly and indirectly. The direct effects include the contribution retrotransposons have made to the evolution of new genes and new regulatory patterns of gene expression. Indirect effects derive from the selective pressure retrotransposons impose on genomes to evolve new (largely epigenetic) regulatory systems that modulate retroelement replication and the co-opting of these systems for essential cellular functions.

Date: May 31 June 11, 2004

Title: Transposable elements: Their impact on population dynamics, biodiversity and evolution

Professor: Dr. Christian Biéumont, Laboratoire de Biométrie et Biologie Evolutive, CNRS, Université Claude Bernard, Lyon, France

Synopsis: Transposable elements appear now as major components of genomes. By their capacity of transposition along the genome they have the potentiality to outnumber genes, and they indeed exist in high pro-

portion in many genomes. In this course we will focus our attention to the forces of natural selection acting to contain their number. We will present models of their dynamics and the data used to test these models

Date: June 14 - 23, 2004

## REGISTRATION and INFORMATION

Julia Provecho, tel. 93-5812724 d.genetica@uab.es

Dr. Antonio Fontdevila, tels. 93-5811083, 93-5812726;  
antonio.fontdevila@uab.es

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### Helsinki SpatialEcol Nov5-9

## FIRST ANNOUNCEMENT

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A Spatial Ecology Workshop on

Spatial Ecology of Plant-Insect Interactions Department of Biological & Environmental Sciences, University of Helsinki, Finland, 5 - 9 November 2004

\*\*\*

Dear colleague,

Interactions between insects and their host plants has long been one of the most actively studied fields of ecology. In this general context, a new topic has recently been gaining increasing interest: how is the interplay between the plants and their herbivores affected by the spatial setting? With this workshop, we aim to bring together scientists working on diverse aspects of insect-plant interactions, all sharing an interest in spatially structured processes. The workshop is centred on six topics, as outlined on [http://www.helsinki.fi/ml/-ekol/se/w7\\_themes.html](http://www.helsinki.fi/ml/-ekol/se/w7_themes.html). We expect the event to result in vigorous and fruitful discussion, and to break new ground for collaboration among the participants. The following list of speakers will ensure some interesting moments:

Robert Denno (USA), Charles Godfray (UK), Ilkka Hanski (Finland), Erkki Haukioja (Finland), Susan Harrison (USA), Riitta Julkunen-Tiitto (Finland), Andrew Liebhold (USA), Eddy van der Meijden (The Netherlands), Susan Mopper (USA), Saskya van Nouhuys (USA), Vojtech Novotny (Czech Republic), Jens Roland (Canada), Tomas Roslin (Finland), Michael Singer (USA), Chris Thomas (UK), John Thompson (USA), Teja Tschardtke (Germany), Wolfgang Weisser (Germany)

IN ADDITION TO THE SPEAKERS, WE HAVE 18 SLOTS AVAILABLE FOR POSTER PRESENTATIONS. YOU ARE CORDIALLY INVITED TO PARTICIPATE!

Please send us a letter of interest, including a poster title and a short abstract of no more than 200 words by FRIDAY 16 APRIL 2004. We will make a decision on whether your poster has been accepted by MONDAY 3 MAY 2004.

Date: —

Friday 5 November to Tuesday 9 November 2004

Venue: —

Tvärminne Zoological Station (<http://www.helsinki.fi/ml/tvea>), Finland

Deadlines and Fees: —

Registration and submission of titles and preliminary abstracts are required by FRIDAY 16 April 2004.

The registration fee of 300 EUR includes: 1. Transport from the University of Helsinki to and from the Zoological Station 2. Accommodation at the Zoological Station 3. All meals 4. Workshop dinner 5. Workshop abstract book

Organisers: —

The Spatial Ecology programme, run by the Division of Population Biology, University of Helsinki ([http://www.helsinki.fi/ml/ekol/spatial\\_ecology](http://www.helsinki.fi/ml/ekol/spatial_ecology)).

Additional details and preliminary programme:

<http://www.helsinki.fi/ml/ekol/se/workshop7.html>

Contact person: —

Johan Kotze ([johan.kotze@helsinki.fi](mailto:johan.kotze@helsinki.fi))

– Johan Kotze Department of Biological and Environmental Sciences PO Box 65 (Biocenter 3, Viikinkaari 1) FIN-00014, University of Helsinki Helsinki, FINLAND  
Tel: +358 (0)9 191 57707 Fax: +358 (0)9 191 57694  
E-mail: [johan.kotze@helsinki.fi](mailto:johan.kotze@helsinki.fi)

Editor-in-Chief, Journal of Negative Results - EEB ([www.jnr-eeb.org](http://www.jnr-eeb.org)) [www.helsinki.fi/ml/ekol/spatial\\_ecology.html](http://www.helsinki.fi/ml/ekol/spatial_ecology.html) [www.helsinki.fi/science/globenet/](http://www.helsinki.fi/science/globenet/)

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## NCStateU SummerInstChanges

There have been some instructor changes for the Summer Institute in Statistical Genetics at NC State University:

Dr Pam Arroway of NC State has replaced Dr Jacqueline Hughes-Oliver in the first statistics module.

Dr Mike Denham (University of Reading) and Dr Eric Anderson (NOAA) have replaced Drs Sharon Browning and Beatrix Jones in the MCMC for Genetics module.

March 31 is the deadline for student scholarship applications. That is also the date to guarantee admission to any of the modules. The modules for Raleigh and Faro, Portugal are filling.

Full details at <http://statgen.ncsu.edu> Bruce Weir [weir@ncsu.edu](mailto:weir@ncsu.edu)

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## NatUIreland Phylogenomics Mar15

Hi folks,

Here is the agenda for the upcoming phylogenomics practical course.

<http://bioinf.may.ie/phylogenomics/> Deadline for applications is on March 15th.

James

++FACULTY

Dr. James McInerney, Maynooth, Ireland. Dr. Chris Creevey, Maynooth, Ireland. Prof. T. Martin Embley, Univ. Newcastle, UK. Dr. Mark Wilkinson, The Natural History Museum, London. Thomas Keane, Maynooth, Ireland.

++TOPICS+

Phylogenies - Maximum Parsimony. - Distance Matrix. - Maximum Likelihood. - Bayesian methods.

Setting up a phylogenomic infrastructure - Introduction to UNIX and shell scripting. - Installation of Fedora (linux). - Installation of ACNUC databases. - Installation of command-line BLAST and FastA software. - Installation of PHYLIP, PUZZLE, Mr. Bayes, ClustalW. - How to turn your desktop or laptop computer into a phylogenomics powerhouse.

Supertrees and Supermatrices - Introduction to Phylogenetic Supertrees. - The theory of putting phylogenetic trees with overlapping leaf-sets together into a single supertree. - Phylogenetic supertrees and phylogenetic supermatrices. - A comparison of the two most



commonly-used methods of using large datasets, with emphasis on the strengths and weaknesses of each approach.

Distributed computing - Introduction to distributed systems. - From MOSIX to MPI. - How to make an inexpensive supercomputer. - Using the NUI Maynooth beowulf cluster. - Parallel approaches to maximum likelihood tree reconstruction (DCPml). - Installation and use of parallel ML software. - How to get all the computers in your institution to work together as a single ML supercomputer.

Discussion and Student data

– Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@may.ie – Take a look at our website — <http://bioinf.may.ie/> –

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## NottinghamU TheoGenetics Aug23-27

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

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

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

Theme A: Genetic diversity within populations The neutral theory and the coalescent Mutation Human minisatellites Genomic context and molecular evolution Theme B: Genetic variability between populations. Theme C: Macroevolution and variation between species Alignment of sequences Reconstruction of Phylogenetic Trees, Detecting natural selection from gene genealogies Gene families, Gene duplications in evolu-

tion Genome alignment: Theme D: Evolution of development Theme E: Evolution in microorganisms

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

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

If, interested, please contact me at [john.brookfield@nottingham.ac.uk](mailto:john.brookfield@nottingham.ac.uk) for an application form, which should be returned to me. An application form can also be obtained from the BBSRC website at [http://www.bbsrc.ac.uk/news/-events/23\\_aug\\_04\\_tgess.html](http://www.bbsrc.ac.uk/news/-events/23_aug_04_tgess.html), but please note that the form should be returned to the email address [john.brookfield@nottingham.ac.uk](mailto:john.brookfield@nottingham.ac.uk), and not that included on the form.

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

John Brookfield Institute of Genetics University of Nottingham Queens Medical Centre Nottingham NG7 2UH  
John Brookfield <[John.Brookfield@nottingham.ac.uk](mailto:John.Brookfield@nottingham.ac.uk)>

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## PloenGermany InnateImmunity May6-9 2

WORKSHOP: REMINDER

We would like to remind you of the DEADLINE March 15, 2004 for application for the following workshop:

Innate immunity: bridging the gap between ecology and molecules. 6.-9. May 2004 Ploen (near Hamburg), Germany.

GRANTS: Thanks to funding by the VolkswagenStiftung, up to 30 GRANTS are now available for travel and accommodation for young researchers, preferentially at the level of PhD or young postdocs, to attend this workshop. You are invited to present your work in a POSTER and 1-2 slides advertising the main message in a special seminar.

TOPIC: The field of immunology is currently progressing rapidly with the study of innate immunity, often using the immune system of invertebrates as a model. In parallel, there is an intensifying focus of ecologists and evolutionary biologists on aspects of immunity. The goal of this workshop is to bring together people from these fields and to generate a discussion bridging the boundaries of the fields, in order to achieve a unified understanding of the evolution of innate immunity.

APPLICATION: Please send an E-MAIL with the subject header "VW" to "kurtz@mpil-ploen.mpg.de", containing the following information: your name and institutional address, a short CV (including a publication list, if available) and an ABSTRACT of the planned poster. Application DEADLINE is March 15, 2004.

TALKS: For your information, here is a list of the invited speakers: Shelly Adamo, Department of Psychology, Dalhousie University, Canada Aneil Agrawal, Indiana University, Bloomington, USA Nancy Beckage, University of California-Riverside, USA Michael Boots, University of Stirling, UK Thomas C.G Bosch, University of Kiel, Germany Michael Boutros, German Cancer Research Center Heidelberg, Germany Martin Brinkhoff, University of Bern, Switzerland George Dimopoulos, Johns Hopkins School of Public Health, Baltimore, USA Peter Hammerstein, Humboldt-Universität zu Berlin, Germany Dan Hultmark, Umea University, Sweden Hilary Hurd, Keele University, UK Gregory Hurst, University College London, UK Francis Jiggins, University of Edinburgh, UK Jacob C. Koella, Université Pierre et Marie Curie, France Lex Kraaijeveld, Imperial College at Silwood Park, UK Tom Little, University of Edinburgh, UK Yannick Moret, University of Sheffield, UK Matthias Noellenburg, VolkswagenStiftung, Hamburg, Germany Thomas Roeder, Zentrum für Infektionsforschung Wuerzburg, Germany Rebeca Rosengaus, Northeastern University, Boston, USA Paul Schmid-Hempel, ETH Zürich, Switzerland Hinrich Schulenburg, University of Muenster, Germany Mike T. Siva-Jothy, University of Sheffield, UK Valerie Smith, University of St Andrews, UK Kenneth Soederhall, Uppsala University, Sweden Carolyn Stenbak, CNRS, Gif-sur-Yvette, France Tina Trenzcek, University of Giessen, Germany Ken Wilson, University of Stirling, UK

We are looking forward to receive your applications.

Joachim Kurtz Department of Evolutionary Ecology, Max-Planck Institute of Limnology, Ploen, Germany

Jens Rolff University of Sheffield, Department of Animal and Plant Sciences, UK

–  
Dr. Joachim Kurtz

Max Planck Institute of Limnology Department of Evolutionary Ecology August-Thienemann Str. 2 24306 Ploen Germany

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### Smithsonian Conservation Genetics Aug16-27

American Genetic Association Laboratory of Genomic Diversity - National Cancer Institute The Smithsonian Institution's Conservation & Research Center announce a course

<sup>3</sup>RECENT ADVANCES IN CONSERVATION GENETICS<sup>2</sup>

August 16-27, 2004

At the Smithsonian Institution's Conservation & Research Center in Front Royal, Virginia, outside Washington, DC, the AGA and the LGD are presenting a 10-day intensive course in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species. This course will be taught by scientists with expertise and a variety of personal experiences in this important field. Participants will learn how to develop and interpret a wide range of genetic data.

COURSE DIRECTOR: Stephen J. O'Brien, Chief, Laboratory of Genomic Diversity, National Cancer Institute-Frederick, MD, USA

TOPICS include: Sample collection and processing PCR-based technologies for polymorphism detection Genetic analysis: bioinformatics and the use of molecular genetic databases estimating relative genetic diversity with gene markers phylogenetic algorithms: their use and interpretation phylogeography subspecies and population substructure demographic and genetic simulation modeling of small populations kinship and paternity assessment Host-pathogen interactions Conservation management applications

TUITION: US \$2,000 (includes housing, all meals, and

airport transfers) Deadline for receipt of applications: March 15, 2004. Admission is competitive; participants will be limited to 24. Limited financial aid is available.

The web page is:

[http://home.ncifcrf.gov/ccr/lgd/geneticcourse/-congen\\_2004/index\\_2004.asp](http://home.ncifcrf.gov/ccr/lgd/geneticcourse/-congen_2004/index_2004.asp)

or contact:

Ms. Jan Martenson, Course Coordinator, e-mail: noah-srcr@ncifcrf.gov NCI-Frederick, P.O. Box B Frederick, MD 21702-1201 Phone: 301/846-7513 FAX: 301/846-6327

Al Roca <roca@ncifcrf.gov>

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## UCalgary PlantBiodiversity

Dear All,

I am offering a one week course at the Kananaskis Field

Station through the Department of Biological Sciences at the University of Calgary this summer. Detailed ad below.

Thanks, Jana Vamosi [jvamosi@ucalgary.ca](mailto:jvamosi@ucalgary.ca)

Botany 507.91 (Plant Biodiversity Assessment) This course is an introduction to the rich diversity of plants in Kananaskis Country. Plant groups studied will include ferns, conifers and flowering plants. The course will focus mainly on plant identification, including sight recognition and use of taxonomic keys. Students will contribute to the development of a web-based Plant Biodiversity Monitoring Project. This course will be useful to those preparing for a career in environmental consulting, and will be of general interest to students in biology & environmental studies.

Suggested items to bring: comfortable clothing and footwear for hiking, hat, sunglasses, water bottle, sleeping bag, PDA/digital camera (optional), guide to local flora (optional)

Dates: July 19 - 25, 2004 Prerequisites: Introduction to Biology/Botany (suggested but not required) To register: please call (403) 220-5517 or visit [www.ucalgary.ca/infonet](http://www.ucalgary.ca/infonet)

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## Instructions

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

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

To send messages to the EvolDir direct them to the email [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains one of the keywords "Conference, Grad, Job, Other:, Postdoc, Workshop" and then the message stands a better chance of being correctly parsed.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. So please do not expect an instant

response.

## Afterward

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