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# E v o l D i r

May 1, 2007

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

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## Forward

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

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

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



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### Barcelona HumanGenomeVariation Sep6-8

#### 9th International Meeting On HUMAN GENOME VARIATION AND COMPLEX GENOME ANALYSIS

Dear Colleague,

The above meeting ('HGV2007') will be held from 6th (midday) - 8th (evening) September 2007 at the Hotel Dolce Sitges Conference Center, near Barcelona, Spain. This is a 5-star venue in a region of exceptional natural beauty.

Further details of the meeting and the venue are available at <http://hgv2007.nci.nih.gov/>. A flyer for the meeting can be downloaded from [http://hgv2007.nci.nih.gov/HGV2007\\_Flyer\\_2.pdf](http://hgv2007.nci.nih.gov/HGV2007_Flyer_2.pdf). The symposium will focus upon the latest breakthroughs and challenges concerned with genome variation, particularly aspects such as methods/strategies for effective utilization of SNPs and CNVs, functional genomics applications, bioinformatics, population genetics, ethics, and the study of human disease.

Confirmed Invited Speakers: John Armour, Ewan Birney, Esteban Burchard, Anne Cambon-Thomsen, Vivian Cheung, George Church, Don Conrad, Emmanouil Dermitzakis, Ivo Gut, Matthew Hurles, Iuliana Ionita, Heikki Lehvaslaiho, Debbie Nickerson, Jim Ostell, Chris Ponting, Lincoln Stein, Gilles Thomas, Barbara Trask, Joris Veltman.

Meeting Format: All sessions will be in plenum with 20-25 minute presentations by invited speakers and others selected from abstracts, with ample time for discussions. All applicants must submit an abstract. Delegates not giving an oral presentation are required to present a poster.

Attendance: The number of delegates at HGV2007 will be limited to 150. Applications to attend must include a relevant scientific abstract that will be competitively assessed and used as the basis for acceptance/rejection decisions. Accepted abstracts must be presented in poster or oral format, as allocated. To encourage attendance by students, postdoctoral fellows, and junior faculty member in under-represented groups, a number of meeting grants are available upon request to help defray costs for such individuals.

Applications: must be submitted via the meeting website by 15th May 2007.

On behalf of the HGV207 Organizers: Anthony Brookes, Stephen Chanock, Nancy Cox, Xavier Estivill, Pui-Yan Kwok, Steve Scherer

HGV200x mailing list HGV200x@lists.le.ac.uk <http://lists.le.ac.uk/mailman/listinfo/hgv200x> Institute of Genetics <adminig@sickkids.ca>

[nzerega@chicagobotanic.org](mailto:nzerega@chicagobotanic.org)

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## ChicagoBotanicGarden PlantCons Jul6

GREAT OPPORTUNITY FOR STUDENTS TO PRESENT AND LEARN ABOUT PLANT BIOLOGY AND CONSERVATION RESEARCH IN A COLLEGIAL LOW STRESS SETTING OR PRACTICE YOUR PRESENTATIONS FOR THE BOTANY 2007 MEETINGS

WHAT: PLANT BIOLOGY AND CONSERVATION STUDENT RESEARCH SYMPOSIUM WHERE: CHICAGO BOTANIC GARDEN WHEN: JULY 6, 2007 (IMMEDIATELY BEFORE BOTANY 2007 MEETING IN CHICAGO)

The Chicago Botanic Garden is pleased to host the first ever Student Research in Plant Biology and Conservation Symposium especially for graduate and undergraduate students and postdocs. It will be held on Friday July 6, 2007 immediately before the Botany 2007 meeting in Chicago.

This will be a day-long event that is focused on providing students with an early opportunity to present their research to colleagues. It is a wonderful chance for students with related interests and concerns to learn about the research of others, make contacts, and present their own work in a collegial and low stress environment. The event will close with our distinguished keynote speaker, Dr. Kent Holsinger, of the University of Connecticut.

We are accepting abstracts for either posters or 15-minute oral presentations. Registration is open to anyone interested in plant biology and conservation and related areas. For program updates and abstract submission guidelines, please visit:

<http://www.chicagobotanic.org/school/symposia> Or contact Beth Pinargote, Symposium Coordinator, at 847-835-8278.

The deadline for receipt of abstracts is MAY 15, 2007. Registration is \$29 and includes morning coffee, lunch, parking and all symposium handouts.

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## ChicagoBotanicGarden StudentPlantEvol Jul6

GREAT OPPORTUNITY FOR STUDENTS TO PRESENT AND LEARN ABOUT PLANT BIOLOGY AND CONSERVATION RESEARCH IN A COLLEGIAL LOW STRESS SETTING

WHAT: PLANT BIOLOGY AND CONSERVATION STUDENT RESEARCH SYMPOSIUM WHERE: CHICAGO BOTANIC GARDEN WHEN: JULY 6, 2007 (IMMEDIATELY BEFORE BOTANY 2007 MEETING IN CHICAGO)

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[nzerega@chicagobotanic.org](mailto:nzerega@chicagobotanic.org)

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## Christchurch Evolution2007 Jun16-20 RegistrationExtended

The Allan Wilson Centre for Molecular Ecology and Evolution in New Zealand is pleased to be hosting "Evolution 2007", the joint annual meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN). The meeting is being held June 16-20, 2007 at the Christchurch Convention Centre, Christchurch, New Zealand.

Please note that the early bird registration period has been extended until 15th April.

Please see the website for details: [www.evolution2007.com](http://www.evolution2007.com) – Prof David Lambert Distinguished Professor Allan Wilson Centre for Molecular Ecology and Evolution Institute of Molecular BioSciences Te Kura Putaiao Koiara-a-Ngota Massey University Private Bag 102 904 North Shore Mail Centre Auckland New Zealand

Phone: +64-9-414 0800 extension 41110 Fax: +64-9-441 8142

Email: [D.M.Lambert@massey.ac.nz](mailto:D.M.Lambert@massey.ac.nz) Website: <http://imbs.massey.ac.nz/Staff/Lambert.html> Evolution Conference in 2007 <http://www.evolution2007.com/>  
 Courier Address: Building 11, Massey University, Oteha Rohe Precinct Gate 4, Albany Highway Post code 1311 Albany, Auckland

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

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## ChristchurchNZ ASNSSBSSE2007 Jun16-20 RegistrationDeadline

Early Registration (reduced rate) for Evolution 2007 Ends April 15th....

The annual meetings of The American Society of Naturalists (ASN) <http://www.amnat.org/>, Society of Systematic Biologists (SSB) <http://systbiol.org/>, and the Society for the Study of Evolution (SSE) <http://www.evolutionsociety.org> are scheduled to be held June 16-20, 2007 at the Christchurch Convention Centre,

Christchurch, New Zealand. Saturday June 16 is the arrival day (pre-conference tours, council meetings and opening reception), Sunday June 17 through Wednesday June 20 (scientific sessions) with closing awards banquet scheduled for the evening of Wednesday, June 20. Thursday June 21 is departure day.

Full details on this combined meeting and registration details are available at the Evolution 2007 web site, [www.evolution2007.com](http://www.evolution2007.com) – Chris Simon Professor, Ecology & Evolutionary Biology 75 North Eagleville Road, University of Connecticut Storrs, CT 06269-3043 [chris.simon@uconn.edu](mailto:chris.simon@uconn.edu) (Please note that my old uconnvm address no longer works) Office (860) 486-4640; Lab (860) 486-3947; Fax (860) 486-6364, Biopharm 305D, 323,325

June-August: Victoria University of Wellington, School of Biological Sciences, Wellington, New Zealand Office: Kirk 611; Office phone: +64-4-463-5026; Fax: +64 4 463 5331; email: as above Home phone 64-4-970-0265

Home page: <http://hydrodictyon.eeb.uconn.edu/-people/simon/Simon.htm> Reprints: <<http://hydrodictyon.eeb.uconn.edu/projects/cicada/-Resources/reprints.html>> [chris.simon@uconn.edu](mailto:chris.simon@uconn.edu)  
[chris.simon@uconn.edu](mailto:chris.simon@uconn.edu)

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## Halifax SMBE Jun24-28 Info

2007 Annual meeting of the society for molecular biology and evolution

JUNE 24-28?Dalhousie University, Halifax, Nova Scotia, Canada

<http://www.smbe.org/> IMPORTANT INFORMATION:

-As of January 2007, all United States citizens will be required to show United States passports in order to re-enter the US from Canada. This has resulted in delays in processing passport applications. If you need to renew or obtain a US passport in order to attend the conference, we recommend that you apply as soon as possible. Please refer to the conference registration page (and links contained therein) for more information on traveling to Canada from the US and other countries:

<https://smbe2007.dal.ca/Registration/> -Halifax is a busy tourist destination in summertime. We strongly advise you to reserve your hotel or dorm rooms early:

<https://smbe2007.dal.ca/Accommodation/>  
Archibald <jmarchib@dal.ca>

John

complex models of evolution. We invite papers that present and evaluate in some detail new models and methods for these two problems and that go beyond the current limitations for handling indels and site substitutions, e.g., by (1) including location- or neighbor-dependencies, (2) modeling larger scale events (duplication and loss, rearrangements, etc.), or (3) targeting noncoding regions.

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## Hangzhou QuantGenetics Aug18-24 TravelScholarships

Applications are invited for travel scholarships to the 3rd International Conference on Quantitative Genetics, to be held in Hangzhou, China August 18-24, 2007. Details about the conference may be found at <http://ibi.zju.edu.cn/ICQG>. Preference will be given to junior faculty members at US Universities who have submitted an abstract for a contributed paper to the conference and who list potential future collaborators in China. The Conference Organizers will try to facilitate meetings with these collaborators. Women and under-represented minority faculty members are especially encouraged to apply.

Applicants should send a CV, a letter of reference from a senior colleague, a statement of purpose in attending the conference, and a copy of their submitted abstract to Dr B.S. Weir, Department of Biostatistics, University of Washington, Seattle WA 98195-7232, USA preferably by email attachment to [bsweir@u.washington.edu](mailto:bsweir@u.washington.edu)

Applications are due by 5 pm Pacific Daylight Time on Tuesday, May 1.

Bruce Weir

Bruce Weir <[bsweir@u.washington.edu](mailto:bsweir@u.washington.edu)>

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## Hawaii PacificSympBiocomputing Jan4-8 CallPapers

Call for Papers and Participants

Next January 4-8 at the 2008 Pacific Symposium for Biocomputing (PSB 2008) in Hawaii <<http://psb.stanford.edu/>>, there will be a session entitled, "Beyond Gap Models: Reconstructing Alignments and Phylogenies Under Genomic-Scale Events," chaired by Michael Brudno, Randy Linder, Bernard Moret, and Tandy Warnow. The session will focus on multiple sequence alignment and phylogeny estimation under

The full "Call for Papers and Posters" can be viewed at: <<http://psb.stanford.edu/cfp-gap.html>>. Please note that PSB is a bit different than most standard biological conferences. Papers that are submitted for presentation will be peer reviewed and published. The core of the conference consists of rigorously peer-reviewed full-length papers reporting on original work. Accepted papers will be published in a hard-bound archival proceedings (equivalent to a peer-reviewed journal publication), and the best of these will be presented orally to the entire conference. You can view previous publications at <<http://psb.stanford.edu/psb-online/>>. The final submission date for papers is July 17, 2007.

Researchers wishing to present their research without official publication are encouraged to submit a one page abstract by November 9, 2007 to present their work in the poster sessions.

If you are interested in participating in the session, but are not sure whether your work would be appropriate, please feel free to contact one of the session chairs. We are very interested in having both computational and biological perspectives presented at the session and in generating interactions between the biological and computational fields. We very much want to encourage the biological evolution community to participate.

Session chair contact information:

Michael Brudno [brudno@cs.toronto.edu](mailto:brudno@cs.toronto.edu)

Randy Linder [rlinder@mail.utexas.edu](mailto:rlinder@mail.utexas.edu)

Bernard Moret [bernard.moret@epfl.ch](mailto:bernard.moret@epfl.ch)

Tandy Warnow [tandy@cs.utexas.edu](mailto:tandy@cs.utexas.edu)

[rlinder@mail.utexas.edu](mailto:rlinder@mail.utexas.edu) [rlinder@mail.utexas.edu](mailto:rlinder@mail.utexas.edu)

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## IndianaU MechanismsOfGenomeEvol Jul11-13

SYMPOSIUM: MECHANISMS OF GENOME EVOLUTION

## AMERICAN GENETIC ASSOCIATION ANNUAL MEETING

11-13 July, 2007 Indiana University, Bloomington, IN

<http://www.theaga.org/agasymposium/index.html>

Conference organized by Michael Lynch and Eva Allen.

The availability of genome-sequence data has forever transformed our ability to understand the molecular basis of the evolutionary process, but it also remains true that the mechanisms of evolutionary change ultimately reside at the population-genetic level. Thus, the goal of this conference is to help bring about a synthesis of our understanding of genomic evolution from the standpoint of both population genetics and molecular biology, and to outline the major challenges to the transformation of the descriptive field of comparative genomics into an explanatory field of evolutionary genomics. The meeting will consist of talks and poster and discussion sessions to encourage broad participation. Funds will be made available, on a competitive basis, to defray the costs of student registration.

### Featured Speakers

Wilhelmine Key Lecturer: Sally Otto: The Causes of Evolution...in the Era of Genomics.

John Archibald: Genome reduction in eukaryotes: nucleomorph genomes as a case study.

Chris Burge: Determinants of microRNA targeting.

Francesco Catania, X. Gao, & D. Scofield: Origins and evolution of spliceosomal introns.

Brian Charlesworth: Mutation, selection and genome evolution.

Andrew Clark: 12 Drosophila genomes: Some lessons in evolutionary genomics.

Adam Eyre-Walker: The relationship between gene expression evolution and sequence evolution - exploring the hidden content of the genome.

Matthew Hahn: Natural selection on gene duplication and loss.

Eugene Koonin: Origins and evolution of eukaryotic gene structure.

Harmit Malik: Causes and consequences of centromere complexity in plants and animals.

Eric Meyer: Recognition of intervening sequences with weak consensus signals: RNA and DNA splicing in the ciliate Paramecium.

Jeffrey Palmer: Horizontal gene transfer gone wild in plant mitochondrial genomes.

David Penny: The RNA infrastructure of the ancestral eukaryote.

Victoria Prince: The role of gene and genome duplications in evolution: insights from the ray-finned fishes.

Ellen Pritham: Transposable elements and the dynamic genome.

Scott Roy: Unraveling the mysteries of transcript splicing in eukaryotes.

Arlin Stoltzfus: Mutation as a cause of non-randomness in evolution.

Soojin Yi: Molecular mechanisms of mutations and genome evolution.

Michael Lynch [milynch@indiana.edu](mailto:milynch@indiana.edu)

Distinguished Professor Dept. of Biology Phone: 812-855-7384 Indiana University FAX: 812-855-6705 Bloomington, IN 47405

Lab: [www.bio.indiana.edu/facultyresearch/faculty/Lynch.html](http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html) <<http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html>>

2007 AGA Genome Evolution Symposium:

[www.theaga.org/agasymposium/index.html](http://www.theaga.org/agasymposium/index.html) <<http://www.theaga.org/agasymposium/index.html>>

IU Biology: [www.bio.indiana.edu](http://www.bio.indiana.edu) <<http://www.bio.indiana.edu/>> Daphnia Genomics Consortium: [daphnia.cgb.indiana.edu](http://daphnia.cgb.indiana.edu) <<http://daphnia.cgb.indiana.edu/>> NSF Training Grant: Evolution, Development, & Genomics: [evodevo.uoregon.edu](http://evodevo.uoregon.edu)

[milynch@indiana.edu](mailto:milynch@indiana.edu) [milynch@indiana.edu](mailto:milynch@indiana.edu)

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## MNHN Luxembourg Phylogeography Conservation of Postglacial Relicts Oct18-20

Dear EvolDir-Team,

in October 2007 we are organising a very interesting meeting about the "Phylogeography and Conservation of Postglacial Relicts". Could you put the following text on your website:

Phylogeography and Conservation of Postglacial Relicts, 18.-20. October 2007, MNHN Luxembourg, Keynote lecturer: J. Avise, M. Veith, Z. Varga, G. Nève, J. Mallet and others

Website: [www.symposium.lu/relicts](http://www.symposium.lu/relicts) Dear Sir and Madams,

The Natural History Museum Luxemburg invite you to participate the international symposium "Phylogeography and Conservation of Postglacial Relicts" in October 2007 (18.-20. 10. 2007). Population biology and phylogeography are crucial for the conservation of relict species and their genetic diversity. The meeting provides an unique opportunity in bringing together representatives from natural sciences and applied conservation management. This combination will enable participants to develop new ideas on how to manage these endangered species of major importance. Please notice that the conference capacity is limited to 110 persons. Deadline for registration is 1st August 2007.

You find more details on our website: [www.symposium.lu/relicts/](http://www.symposium.lu/relicts/) Sincerely Jan Habel & Marc Meyer

– Dr. Jan Christian Habel

Musée national d'histoire naturelle Luxembourg 25, rue Münster L-2160 Luxembourg

Tel.: ++352 (0) 46 22 33 405 Fax: ++352 (0) 47 51 52

<http://www.symposium.lu/relicts> <http://www.univ-trier.de/~biogeo/Personal/Name/Habel.htm#>  
<http://www.mnhn.lu/recherche/zoologie/phyloge/default.asp> "Feel free" - 10 GB Mailbox, 100 FreeSMS/Monat ... Jetzt GMX TopMail testen: <http://www.gmx.net/de/go/topmail> Jan Christian Habel <janchristianhabel@gmx.de>

Unique population resources

HGM2007 CONFIRMED SPEAKERS AND CHAIRS  
 Hiroyuki Aburtani, Clement Adebamowo, David Altshuler, Brenda Andrews, Stephan Beck, Emelia Benjamin, David Bentley, John Bergeron, Samir Brahmachari, Alexandre Bureau, Wylie Burke, Howard Cann, Ruth Chadwick, Susan Clark, Ellen Clayton, Rory Collins, David Cox, Mark Daly, Manolis Dermitzakis, Jamie Engert, Ian Frazer, Kelly Frazer, Jan Friedman, Josef Gecz, Michel Georges, Daniel Geschwind, Richard Gibbs, Chris Goodnow, Seth Grant, Philippe Gros, Annick Harel-Bellan, Michael Hayden, Helen Hobbs, Tom Hudson, Matthew Hurles, Li Jin, Steven Jones, Kazuto Kato, Nico Katsanis, Bartha Knoppers, Damian Labuda, Lawrence Lesko, Klaus Lindpaintner, Marco Marra, John Mattick, Peter McGuffin, Michael Meaney, Mark McCarthy, Roderick McInnes, Andres Metspalu, Joe Nadeau, Yusuke Nakamura, Debbie Nickerson, Stephen O'Brien, Sava Paabo, Lyle Palmer, Aarno Palotie, Nancy Pedersen, Leena Peltonen, Michael Phillips, David Porteous, Jane Rogers, Hans Hilger Ropers, Guy Rouleau, Steve Scherer, Erwin Schurr, Jacques Simard, Mike Stratton, Sarah Tishkoff, Cornelia van Duijn, Veronica van Heyningen, Gert-Jan van Ommen, Sylvia Vidal, Claes Wahlestedt, Michel Weber, Emma Whitelaw, Roland Wolf, Orsetta Zuffardi

HGM2007 Secretariat HUGO, 144 Harley Street, London, W1G 7LD, UK Tel: +44 (0)20 7935 8085, Fax: +44 (0)20 7935 8341, Email: [secretariat@hugo-international.org](mailto:secretariat@hugo-international.org)

HUGO - Human Genome Meeting  
 <[hugo@lifescience.tv](mailto:hugo@lifescience.tv)>

## Montreal HGM2007

PLENARY SESSIONS ? Large-Scale Medical Resequencing ? Genome Wide Association Studies ? Structural Genomic Variation ? Genomic Medicine : Global Perspectives SYMPOSIA ? Public Population Project ? Genome Diversity ? Regulatory RNAs ? Epigenomics ? Neuropsychiatric Genetics ? Pharmacogenomics

WORKSHOPS 1 Functional Variation 2 Cancer Genomics 3 Ethical Issues Related to Genome-Wide Scans 4 Genes, chromosomes and diseases 5 Computational approach to QTL mapping 6 Neuromuscular genetics 7 Genetics of the heart

8 Animal models 9 Disease modifiers 10 Protein Function 11 Bioinformatics and Biostatistics 12 Large-Scale Genomics 13 High throughput genetic screens 14

## Montreal HGM2007 May21-24

GTGHGM2007 <http://hgm2007.hugo-international.org/>

REGISTER NOW FOR

HUGO'S TWELFTH INTERNATIONAL HUMAN GENOME MEETING

MONTRÉAL, CANADA MAY 21ST - MAY 24TH 2007

PLENARY SESSIONS SYMPOSIA

Large-Scale Medical Resequencing Public Population Project Genome Wide Association Studies Genome Di-

versity Structural Genomic Variation Regulatory RNAs  
Genomic Medicine : Global Perspectives Epigenomics  
Neuropsychiatric Genetics Pharmacogenomics

WORKSHOPS 1 Functional Variation 7 Unique population resource 2 Cancer Genomics 8 Animal models 3 Ethical Issues Related to Genome-Wide Scans 9 Disease modifiers 4 Genes, chromosomes and diseases 10 Genetics of the heart

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Stephan Beck, Emelia Benjamin, David Bentley, John Bergeron, Samir Brahmachari, Alexandre Bureau, Wylie Burke, Howard Cann, Ruth Chadwick, Susan Clark, Ellen Clayton, Rory Collins, David Cox, Mark Daly, Manolis Dermitzakis, Jamie Engert, Ian Frazer, Kelly Frazer, Jan Friedman, Josef Geetz, Michel Georges, Daniel Geschwind, Richard Gibbs, Chris Goodnow, Seth Grant, Philippe Gros, Annick Harel-Bellan, Michael Hayden, Helen Hobbs, Tom Hudson, Matthew Hurles, Li Jin, Steven Jones, Kazuto Kato, Nico Katsanis, Bartha Knoppers, Damian Labuda, Lawrence Lesko, Klaus Lindpaintner, Marco Marra, John Mattick, Peter McGuffin, Michael Meaney, Mark McCarthy, Roderick McInnes, Andres Metspalu, Joe Nadeau, Yusuke Nakamura, Debbie Nickerson, Stephen O'Brien, Savante Paabo, Lyle Palmer, Aarno Palotie, Nancy Pedersen, Leena Peltonen, Michael Phillips, David Porteous, Jane Rogers, Hans Hilger Ropers, Guy Rouleau, Steve Scherer, Erwin Schurr, Jacques Simard, Mike Stratton, Sarah Tishkoff, Cornelia van Duijn, Veronica van Heyningen, Gert-Jan van Ommen, Sylvia Vidal, Claes Wahlestedt, Michel Weber, Emma Whitelaw, Roland Wolf, Orsetta Zuffardi

For up-to-date information on the scientific programme, speakers and topics,

exhibitor information and hotel accommodation visit the HGM2007 website at

<http://hgm2007.hugo-international.org/>

HGM2007 Secretariat

Email: <mailto:hugo@hugo-international.org>

Address for HUGO International office, HUGO, 144 Harley St, London W1G 7LD, UK, Tel: [44] (20) 7935 8085 Fax: [44] (20) 7935 8341, email: [hugo@hugo-international.org](mailto:hugo@hugo-international.org) Website: <http://www.hugo-international.org> HUGO wishes to thank the following Companies, Governments and Organisa-

tions for their long term support: Academy of Finland MRC, F.Hoffmann-La Roche, Max-Planck Society, Australian Government, Irish Health Research Board,

Forthcoming HUGO meetings which may interest you: HUGO'S 12th ANNUAL GENOME MEETING, HGM2007, MONTREAL, CANADA, 21st -24TH MAY 2007 To register your interest visit the HGM website at : <http://hgm2007.hugo-international.org/>

HUGO'S 9th ANNUAL INTERNATIONAL SYMPOSIUM ON MUTATION DETECTION 23 - 27 SEPTEMBER 2007, XIAMEN CHINA 23 - 27 SEPTEMBER 2007 Detailed information will be available on the website soon [www.mutationdetection.org](http://www.mutationdetection.org)

The Human Genome Organisation <[hugo@hugo-international.org](mailto:hugo@hugo-international.org)>

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## New York AGA Conservation Genetics Sep27-29

ConGen3: The 3rd biannual International Symposium on Conservation Genetics

sponsored by the American Genetic Association

Date: 27-29 September, 2007

Location: American Museum of Natural History, New York, NY, USA

Website: <http://genomics.amnh.org/congen3> ConGen3 will be held at the AMNH Sackler Institute for Comparative Genomics in New York City.

Session topics:

- Genetic research for biodiversity surveys, characterization of unique microbial communities, and barcoding initiatives.
- Conservation Genetics in Time: conservation phylogenetics and tree reconstruction for identification of hidden biodiversity and examination of hybrid zones.
- Ex Situ Conservation Genetics: intensive metapopulation management in theory and practice.
- Genetics of Invasive Species: patterns and control.

More information regarding registration and poster abstract submission will be made available soon. Interested participants can exchange information on New York City-related travel and housing options on the online forum <http://groups.google.com/group/congen3>

On behalf of the organizers: George Amato (American Museum of Natural History) Gisella Caccone (Yale University) Rob DeSalle (American Museum of Natural



History)

— Sergios-Orestis Kolokotronis Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024 -USA- tel +1 212 313 7648 koloko@amnh.org <http://koloko.net> koloko@amnh.org

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## PurdueU Genomics Sep10-12

Convergence of Genomics and the Land Grant Mission: Emerging Trends in the Application of Genomics in Agricultural Research Purdue University, West Lafayette, Indiana September 10-12, 2007

You are invited to attend this national conference on agricultural genomics. The conference will feature invited presentations by recognized leaders in agricultural genomics from across the Land Grant University landscape and beyond. Topics focused on microbes, arthropods, plants, animals and ecological systems will be blended into sessions that address the following themes:

\* Transition from Model to Agricultural Species \* Integrating Information Across Databases \* Translational Challenges and Successes

Speakers will address emerging trends, opportunities for interactions with other genomics research groups, collaborations with applied researchers, and priorities for the future address. The meeting will conclude with a roundtable discussion and recommendations led by a distinguished panel. The conference is modeled after the Gordon Research conferences where all speakers are invited and the number of talks is limited to maximize interactions among participants. Poster presentations will be available to those interested.

This conference promises to be a rare opportunity to exchange scientific expertise and experiences among genomics researchers and stimulate new discussions with applied researchers, stakeholders, and decision makers who do not normally interact with the genomics community. The goal of the conference is to promote synergisms across disciplines, commodities, and species. A committee of recognized national leaders in molecular biology and genomics helped develop the program.

The final list of topics and speakers is now set (see the attachment or the website below for details). Registration and requests to submit poster presentations are now being accepted. To learn more about the program, the organizing committee and other meeting logistics,

go to the conference website at:

[www.entm.purdue.edu/conference](http://www.entm.purdue.edu/conference)

[dewoody@purdue.edu](mailto:dewoody@purdue.edu) [dewoody@purdue.edu](mailto:dewoody@purdue.edu)

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## Roscoff HostParasite Sep22-26

Jacques Monod Conference: Evolutionary genetics of host-parasite relationships

In Roscoff (Brittany), France, September 22-26, 2007

Deadline for application: May 15, 2007

More info under <http://www.cnrs.fr/sdv/cjm/-cjmebert.e.html> Organizers: Dieter EBERT, Universität Basel, Switzerland and Gabriele SORCI, Université de Bourgogne, Dijon, France

The Jacques Monod Conference “Evolutionary genetics of host-parasite relationships” aims to provide a state of the art assessment of what evolutionary thinking can contribute to an integrated understanding of the processes shaping host-parasite interactions. The conference is structured in three major topics, which are intimately linked with each other. Topic 1. Understanding the genetic interactions between hosts and parasites. Topic 2. Host and parasite evolution and the maintenance of sexual reproduction Topic 3. The evolutionary genetics of immune defence.

More info under <http://www.cnrs.fr/sdv/-cjm/cjmebert.e.html> – Dieter Ebert [ [Mailto:dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch) ] <http://evolution.unibas.ch/> Universität Basel, Zoologisches Institut, Vesalgasse 1 4051 Basel, Switzerland Tel. +41-(0)61-267 03 60

[dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch) [dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch)

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## Seattle WEBS Oct14-17

Dear Colleagues,

We are writing to introduce you to WEBS (Women Evolving Biological Sciences), an annual three-day symposium aimed at addressing the retention of female scientists and issues related to the transition of women from early career stages to tenure track positions and

leadership roles in academic and research settings. We would appreciate your assistance in passing along this information to any of your colleagues who you think will be interested in our program.

WEBS will target early career women in the Biological Sciences with an emphasis on ecology and evolutionary biology. In particular, it will focus on women who have earned their doctoral degrees within the past two to eight years and who do not have tenure in order to address the critical transition period from graduate studies and post-doctoral positions to permanent research and teaching positions. The symposia will provide a forum for professional development, including awareness and improvement of academic leadership skills; opportunities to establish mentoring relationships; and resources for developing professional networks. \*The 2007 symposium will be held at Packforest Conference Center outside of Seattle, Washington from October 14-17, 2007.\*

Please visit our website (<http://www.webs.washington.edu>) for details and application materials. Feel free to contact us with any questions you might have ([websinfo@u.washington.edu](mailto:websinfo@u.washington.edu)). Applications will be due May 15, 2007.

Sincerely,

Claire Horner-Devine, Ph.D. University of Washington  
Samantha Forde, Ph.D. University of California Santa Cruz

Joyce Yen, Ph.D. University of Washington

Samantha Forde, PhD Assistant Research Biologist Department of Ecology and Evolutionary Biology Earth and Marine Sciences Building University of California Santa Cruz, CA 95064 (831)459-1541 [forde@biology.ucsc.edu](mailto:forde@biology.ucsc.edu)

Samantha Forde <[forde@biology.ucsc.edu](mailto:forde@biology.ucsc.edu)>

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### StAndrews ArcticAlpineFlora Jun25-27

Dear Colleagues

The programme for the international symposium on the HISTORY, EVOLUTION AND FUTURE OF ARCTIC AND ALPINE FLORA

to be held in St Andrews, Scotland, June 25-27, 2007, is available at

<http://biology.st-andrews.ac.uk/aafcon> Deadline for Registration: 25 May 2007

Sincerely, Richard Abbott (Symposium organizer)

– Professor Richard Abbott School of Biology University of St Andrews St Andrews, Fife KY16 9TH UK Tel. 01334 463350 Fax. 01334 463366 Email. [rja@st-and.ac.uk](mailto:rja@st-and.ac.uk) Website: <http://biology.st-and.ac.uk/staff/abbott.html> [rja@st-andrews.ac.uk](mailto:rja@st-andrews.ac.uk)

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### Sydney AustralasianEvolSoc Jun12-15

Early bird registration for the 5th Australasian Evolution Society meeting ends on 30th April. Participants registering before this deadline who wish to give spoken papers or posters are guaranteed of a space. Participants who register after this date will be allocated spoken paper or poster slots subject to availability.

There are no abstracts for this conference, you need only submit a paper or poster title. We have participants registered from all over the world, many of whom are heading on to evolution2007 in Christchurch after our meeting. There are talks on all aspects of evolutionary biology from functional genomics to palaeontology.

More details on the conference can be found at the following website: <http://aes.eriophora.com.au/events/-2ndannouncement.htm> Australasian Evolution Society <http://www.evolutionau.org> [rob.brooks@unsw.edu.au](mailto:rob.brooks@unsw.edu.au)

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### UBourgogne TheBuffonLegacy Sep3-6

Dijon.France. The Buffon Legacy:Natural History in the 21st century. Sept3-6

Georges Louis Leclerc, Comte de Buffon was most responsible for the rise of world-wide interest in natural history. To celebrate the 300th anniversary of his birth, on 7th September 1707, the Université de Bourgogne is pleased to organize a major international scientific event, The Buffon Legacy: Natural History in the 21st century, to be held in Dijon from 3rd to 6th September,

2007.

The aim is to bring together researchers and other interested parties to discuss the fate of natural history in modern biology.

The conference will feature three and a half days of sessions on contributed talks, plus a poster session, visit to the Buffon Museum, social events and banquet. Each day will start with a plenary keynote lecture, followed by parallel symposia. Papers will cover topics such as behavioural ecology, biogeography, life-history strategies, and biodiversity in animals and plants.

Invited speakers include: Tim Birkhead (Sheffield, UK), Douglas Futuyma (Stony Brook, USA), Pierre-Henri Gouyon (Paris, France), Pierre Joly (Lyon, France) and Geoff Parker (Liverpool, UK)

<http://www.u-bourgogne.fr/buffon2007/> Deadline for abstract submission: May 30 2007

Deadline for registration: July 30 2007

Please visit this website (<http://www.u-bourgogne.fr/buffon2007/>) continuously for more information and updates. Maximum number of delegates are 300. When 300 delegates have registered, registration will close.

Loic Bollache <Loic.Bollache@u-bourgogne.fr>

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## UCaliforniaSanDiego RECOMB Sep16-18

### CALL FOR PAPERS

Fifth Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG'07) September 16-18, 2007 Center for Algorithmic and Systems Biology University of California, San Diego La Jolla, California, U.S.A. <http://casb.ucsd.edu/recombcg07> \*\*\* To be removed from or added to the CONFERENCE ANNOUNCEMENT MAILING LIST, please visit the Mailing List tab at the website above or send an email to [recombcg-info@casb.ucsd.edu](mailto:recombcg-info@casb.ucsd.edu). \*\*\*

### KEY DATES

Paper submission deadline May 6, 2007 Notification of paper acceptance June 4, 2007 Final manuscript due June 17, 2007 Poster submission deadline August 17, 2007 Pre-registration period To be announced Workshop September 16-18, 2007 Followed by RECOMB-CCB'07 September 18-20, 2007

\*\*\* Please note: RECOMB-CG'07 will be immediately followed at the same location by the new RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-CCB'07, <http://casb.ucsd.edu/recombccb07>), September 18-20, 2007. It will be organized separately, but the schedules will be coordinated, including a joint keynote by Barbara Trask (Fred Hutchinson Cancer Research Center). RECOMB-CCB'07 has a separate mailing list; see its website. \*\*\*

### THEME AND SCOPE

This workshop brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and novel experimental results. We solicit original manuscripts describing comparative genomics research on genome evolution, genetic function and cellular processes. Topics of interest include, but are not limited to

\* Algorithms in comparative genomics \* Comparative study of orthologous genes \* Gene finding using multiple genomes \* Sequence homology \* Genome rearrangements \* Measures of evolutionary distance \* Whole genome phylogeny reconstruction \* Sequence assembly using sequence comparison \* Multiple genome alignment \* Gene and genome duplication \* Gene tree reconciliation \* Identification of conserved and fast evolving sequences

### KEYNOTE SPEAKERS

Francesca Ciccarelli (European Institute of Oncology, Milan, Italy) Michael B. Eisen (University of California, San Diego) Matthew Hahn (Indiana University) Katherine S. Pollard (University of California, Davis) Oliver A. Ryder (Zoological Society of San Diego)

Joint Keynote with RECOMB Computational Cancer Biology 2007: Barbara J. Trask (Fred Hutchinson Cancer Research Center)

### CALL FOR PAPERS

Manuscripts should be no more than 10 single-spaced US letter or A4 pages with at most a 6.5x9" text area in at least an 11 point font. Title and authors, corresponding author's email address, 100-250 word abstract, references, figures, and tables all included. An optional short appendix may contain details or additional data to be consulted at the discretion of the program committee. Authors of accepted manuscripts will have to reformat them for the proceedings in LaTeX 2e (preferred) or Microsoft Word using the Springer LNCS style, which has different margins and font sizes.

Manuscripts must be submitted electronically in PDF

format via the EasyChair system. Submissions must be received in electronic form by 11:59 p.m. PDT (San Diego local time) on May 6, 2007.

Manuscripts submitted for review should represent original, previously unpublished work. At the time of submission to the workshop, and for the entire review period, the work should not be under review by any other conference or scientific journal.

Note that results accepted for publication in the workshop proceedings are considered to be preliminary and may be submitted to a journal at any time after notification of acceptance.

Accepted submissions will appear in the conference proceedings, which will be published by Springer in the "Lecture Notes in Bioinformatics" series and distributed at the workshop. Authors of accepted submissions are invited to give a 25-minute presentation at the workshop.

Address any questions to the program committee chairs, Glenn Tesler (gptesler@math.ucsd.edu) or Dannie Durand (durand@cs.cmu.edu).

#### REGISTRATION

Registration will be available soon at the conference website <http://casb.ucsd.edu/recombcg07> CONFERENCE CHAIRS

Glenn Tesler (University of California, San Diego)

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

### UGlasgow EvolSenescence Sep10-12

The British Ecological Society annual meeting will be held at the University of Glasgow, Scotland from 10th-12th Sept 2007.

We are now accepting abstracts for contributions to the following symposia:

Antioxidants as a Signal of Individual and Ecosystem Health

Endocrine Responses to Environmental Change

The Evolutionary Ecology of Senescence

More details about the conference and abstract submission (deadline is the 20th April) can be found at

<http://www.britishecologicalsociety.org/articles/-meetings/current/2007annualmeeting/> Dr. Kathryn Arnold

Royal Society University Research Fellow

Division of Environmental & Evolutionary Biology, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ

Tel. + 44 141 3302898 Fax. + 44 141 3305971 <http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PGe~Pn>  
K.Arnold@bio.gla.ac.uk K.Arnold@bio.gla.ac.uk

### UGuelph BarcodeOfLife May10-11

Meeting Announcement:

1st Scientific Symposium of the Canadian Barcode of Life Network will take place May 10-11, 2007 at the University of Guelph, Guelph, ON Canada.

The Canadian Barcode of Life Network represents the first national network dedicated to large-scale DNA barcoding. Initial work focuses on barcoding species which are of particular economic, social, or environmental importance. These research initiatives will provide important contributions to biodiversity research, and highlight Canada as a leader in the development of DNA barcoding

The May symposium has open registration and will showcase platform and poster presentations from all Network research themes. For more information and to register please visit [http://www.bolnet.ca/scientific\\_conference\\_2007.php](http://www.bolnet.ca/scientific_conference_2007.php) [http://www.bolnet.ca/scientific\\_conference\\_2007.php](http://www.bolnet.ca/scientific_conference_2007.php)

Sue-Ann Johnston Information Officer Biodiversity Institute of Ontario University of Guelph Guelph, ON N1G 2W1 Phone: (519) 824-4120 x 56393

Fax: 519-824-5703 Email: [sujohnst@uoguelph.ca](mailto:sujohnst@uoguelph.ca)

Sue-Ann Johnston <[sujohnst@uoguelph.ca](mailto:sujohnst@uoguelph.ca)>

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## Uppsala ESEB Aug20-25 announcement

The 11th congress of the European Society for Evolutionary Biology will be held at Uppsala University in Sweden, 20 - 25th August 2007. More information about the congress can be found at

<<http://www-conference.slu.se/eseb2007/index.html>>  
<http://www-conference.slu.se/eseb2007/index.html>

Deadline for submission of abstracts is April 15, 2007.

Deadline for early registration (reduced price) is April 30, 2007

All the best

Jacob Höglund, Professor Population Biology and Conservation Biology Dept. of Ecology & Evolution, Evolutionary Biology Centre Uppsala University Norbyv. 18D SE-752 36, Uppsala Sweden tel. +46-18-4712671 (office) 6473 (lab.) -100865 (home) 70-4250126 (mobile) fax. +46-18-4716424 (fax)

Jacob Höglund <jacob.hoglund@ebc.uu.se>

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## Uppsala ESEB Planteco-devo Aug20-25

Yet another call for abstracts for ESEB for the evoldir community...

We still have room left for contributed talks to our symposium on

“Plant eco-devo”: ecology and genetics of life history timing in plants

at the 11th Conference of the European Society for Evolutionary Biology (ESEBXI) in Uppsala, Sweden.

Symposium description: The timing of the crucial transitions in a plant's life (germination, onset of flowering) has strong consequences for its fitness. It is regulated by a combination of responses to environmental cues (temperature, daylength) and to internal status (age, size). Natural selection can act on variation in the way the information is used, which is important in changing environments. This symposium aims to bring together

researchers in both genetics and ecology, to discuss how our knowledge of e.g. pathways involved in flower induction in model species can help understand their role in nature.

Invited speakers: Kathleen Donohue, Harvard University, USA Outi Savolainen, University of Oulu, Finland Sonia E. Sultan, Wesleyan University, USA

ESEB XI is held from 20 to 25 August 2007 in Uppsala, our (full-day) symposium has tentatively been scheduled for the 22nd of August. Details of the conference, including an online abstract submission can be found here: <http://www-conference.slu.se/eseb2007/> Relevant dates: April 15th: Deadline for submission of abstracts. April 30th: Deadline for reduced rate registration.

Symposium organisers: Renate Wesselingh, Université catholique de Louvain, Belgium (wesselingh@ecol.ucl.ac.be) Henk van Dijk, Université de Lille 1, France (Henk.Van-Dijk@univ-lille1.fr)

Renate Wesselingh <wesselingh@ecol.ucl.ac.be>

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## Uppsala ESEB SexChromosomeEvol Aug20-25

Dear Evoldir,

we would like to invite you to submit your abstracts (talks and posters) for the symposium \*The Evolution of Sex Chromosomes\* at the 11th conference of the European Society for Evolutionary Biology (ESEB) 2007 in Uppsala, Sweden.

Symposium description: Sex chromosomes evolved repeatedly in many lineages. Repeatedly, the non-recombining, unisexually restricted chromosome has degenerated resulting in the asymmetrical chromosomal complements in the two sexes. Understanding of the evolution of sex chromosomes and of the genes located on the sex chromosomes promises to shed unique light on the key evolutionary processes affecting all genes genome-wide.

Invited speakers: Doris Bachtrog (San Diego) Antonio Bernardo Carvalho (Rio de Janeiro)

ESEB XI runs from the 20th-25th August 2007. Details of the conference, including online abstract submission can be found here: <http://www-conference.slu.se/-eseb2007/> Relevant dates: April 15th: Deadline for submission of abstracts. April 30th: Deadline for re-

duced rate registration.

Symposium organisers: Peter Arndt (MPI, Berlin)  
Dmitri Petrov (Stanford)

arndt@molgen.mpg.de arndt@molgen.mpg.de

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## Uppsala ESEB SocialEvolution Aug20-25

Call for abstracts for a symposium on 'SOCIAL EVOLUTION IN MICROBES AND PARASITES' at the European Society for Evolutionary Biology (ESEB) conference 2007, Uppsala, Sweden.

Symposium description: We will bring together researchers who have contributed to our expanding appreciation for the complexity of social interactions in microbes and parasites and discuss insights gained from the recent synthesis of evolution and microbiology. The use of micro-organisms and parasites to test theory on the evolution of social interactions has provided revolutionary insights to this field. Researchers can directly compare the fitness of alternate social strategies: aggression, exploitation and cooperation. Furthermore, many social traits have implications for the virulence of parasites and microbial disease.

Invited speakers: Angus Buckling, University of Oxford, UK Greg Velicer, Indiana University, USA

ESEB XI runs from the 20th-25th August 2007. Details of the conference, including an online abstract submission can be found here: <http://www-conference.slu.se/-eseb2007/> Relevant dates: April 15th: Deadline for submission of abstracts. April 30th: Deadline for reduced rate registration.

Symposium organisers: Ashleigh Griffin, University of Edinburgh, UK (a.griffin@ed.ac.uk) Sarah Reece, University of Edinburgh, UK (sarah.reece@ed.ac.uk)

Sarah Reece <sarah.reece@ed.ac.uk>

Eastern Great Lakes Molecular Evolution XI

FINAL ANNOUNCEMENT FOR REGISTRATION

Saturday, May 5, 2007 York University, Toronto, Ontario

The 2007 Eastern Great Lakes Molecular Evolution Meeting will be held on Saturday, May 5, 2007, at York University in Toronto. Registration, coffee, and poster setup will begin at 8:30 A.M. and the talks will end around 5 PM. Posters will be displayed all day, with a mid-day poster session set aside. The following is a confirmed list of invited speakers:

Chip Aquadro (Cornell) Patricia Wittkopp (Michigan)  
Asher Cutter (Toronto) Ben Evans (McMaster)

Further information, including information about traveling to Toronto and maps of the York campus, is available at <http://www.barnard.edu/biology/eglme.html>. If you wish to register, please follow the directions below.

Please feel free to duplicate and distribute copies of this notice to anyone who might be interested in attending the meeting, particularly students and faculty who are new to these meetings or to the field of molecular evolution. A schedule is now posted at <http://www.barnard.edu/biology/schedule.html>. To register, or if you have any questions, please contact:

Stephen Wright Department of Biology York University e-mail: stephenw (at) yorku.ca phone: 416- 736-2100 ext 20213

or

Brian Morton Department of Biological Sciences Barnard College, Columbia University e-mail: bmorton (at) barnard.edu phone: 212-854-5454

Registration: Please provide your name, institution, mailing address, email address and telephone number (please remember that this information will be made available to other registrants). Please register as soon as possible.

Organizing Committee: Stephen Wright, Brian Morton  
stephenw@yorku.ca

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## YorkU EGLME 2007 May5 final

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## GradStudentPositions

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### AberystwythU Birdsong

Birdsong in cities: effects of urban noise on song learning and female choice in great tits

Song repertoire size is an established male trait involved in both territorial defence and mate attraction in great tits (*Parus major*). Recently noise pollution has been shown to effect song learning and production in great tits as birds in noisy areas appear to drop low frequency syllables from their songs. However, it remains unclear whether these changes alter signal effectiveness when males disperse from their natal area. This project will use field observation and experimental playback experiments to investigate responses to variations in singing behaviour in different acoustic environments. It will also make predictions concerning the evolution of signalling and learning in the context of sexual selection and speciation.

Full Funding (Fees & Maintenance) at NERC standard rates for UK residents Fees only funding for EU residents

For informal enquiries & discussion, contact Dr Rupert C Marshall Email: RMM@aber.ac.uk Tel: (+44) 01970 622320 Institute of Biological Sciences, University of Wales, Aberystwyth, UK

Applications should be made on the form available at the website below, including a CV, covering letter and 2

letters of reference: <http://www.aber.ac.uk/pgs/web/-apply.htm> Deadline: 31st May

Send completed applications to:

Postgraduate Admissions Office Old College King Street Aberystwyth Ceredigion SY23 2AX UK

Rupert Marshall <rmm@aber.ac.uk>

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### EAWAG Switzerland HostParasite

Eawag is the Swiss Federal Institute for Aquatic Science and Technology, a Swiss-based and internationally operating aquatic research institute within the ETH domain.

The Department Aquatic Ecology (group of Piet Spaak) seeks for a

PhD student in host-parasite interactions

The PhD student will participate in a collaborative research project with Justyna Wolinska (presently at Indiana University, Bloomington, USA; from 2008 at Ludwig-Maximilians Universität, Munich, Germany) to study the influence of parasites on hybridization within a *Daphnia* hybrid species complex. We are interested in the population genetics of the host as well as of the parasite. Furthermore, we want to study experimentally genotype (host) x genotype (parasite) x environment

interactions.

For this, from the Swiss Science foundation financed project, we are looking for a highly motivated candidate with interests in evolutionary biology, population genetics and host-parasite interactions. Although field work is also involved, most of the work will be done in the lab (conducting experiments and screening hosts and parasites using molecular tools). Some of the work will be done in the USA and Germany.

We offer a stimulating research environment in a lively and social institute in Dübendorf (near Zürich). In a department with several other evolutionary and ecological research groups. The position will be for a period of three years, and should start as soon as possible (June 2007 or soon thereafter). The ideal candidate has both experimental as well as molecular skills (PCR, sequencing, genotyping). A Diploma or Master degree (or equivalent) in biology or related subject is necessary for admission. The working language in the group is English.

Applications should include a letter of interest with a description of pertinent experience, curriculum vitae, a list of publications (if any), the names (with e-mail address) of three potential reviewers, and copies of the certificates of academic qualifications.

Please submit your application in electronic form to Sandra Isenring, Eawag, Human Resources Department: [sandra.isenring@eawag.ch](mailto:sandra.isenring@eawag.ch). For further information, consult [www.eawag.ch](http://www.eawag.ch) or contact Piet Spaak (Tel. +41 44 823 5617) [spaak@eawag.ch](mailto:spaak@eawag.ch). Selection of candidates will start 23 April 2007.

Piet Spaak Eawag Limnologie Department  
Überlandstrasse 133 P.O. Box 611 8600 Dübendorf  
Switzerland Phone: +41 (0)44 823 56 17 Fax:  
+41 (0)44 823 58 17 [spaak@eawag.ch](mailto:spaak@eawag.ch) <http://www.eawag.ch/~spaak> <<http://www.eawag.ch/>>

[Piet.Spaak@eawag.ch](mailto:Piet.Spaak@eawag.ch) [Piet.Spaak@eawag.ch](mailto:Piet.Spaak@eawag.ch)

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## ETHZurich InsectBehaviour

We are seeking a motivated and creative PhD Student in Entomology with a Diploma (MSc) degree in Biology or related University Degree.

The project deals with the ecology and behaviour of a parasitoid wasp of practical agricultural significance, occurring naturally in Switzerland. In particular, the focus will be on the examination of the costs of inbreed-

ing and their avoidance. We expect new insights into how behavioural decisions can affect optimal sex ratios and ultimately improve the fitness of mass-reared and released parasitoids. Methods will integrate field surveys, behavioural experiments, fitness assays and the use of molecular tools. Results shall contribute to the fundamental understanding of sex allocation and mating structures in parasitoids, as well as to a sound application of biological control strategies.

Languages spoken in the group are mainly German and English.

The position is funded for a duration of three years, and is open until filled.

Interested candidates should submit a curriculum vitae and certificates, along with name, address and phone number of three references by e-mail or post to:

Prof. Dr. Silvia Dorn Reference Code PhD-InsBeh  
Institute of Plant Sciences/ Applied Entomology ETH  
Zurich Schmelzbergstr. 9 / LFO CH - 8092 Zurich  
Switzerland

[silvia.dorn@ipw.agrl.ethz.ch](mailto:silvia.dorn@ipw.agrl.ethz.ch)

Informal inquiries should be directed to Dr. Dominique Mazzi ([dominique.mazzi@ipw.agrl.ethz.ch](mailto:dominique.mazzi@ipw.agrl.ethz.ch)).

[dominique.mazzi@ipw.agrl.ethz.ch](mailto:dominique.mazzi@ipw.agrl.ethz.ch)

[do-](mailto:dominique.mazzi@ipw.agrl.ethz.ch)

[minique.mazzi@ipw.agrl.ethz.ch](mailto:dominique.mazzi@ipw.agrl.ethz.ch)

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## LeidenU GMcarrot

PhD position Introgression in GM carrot, Leiden, the Netherlands

1 PhD (F/M) (full time position, 4 years), vacancy reference number: 7-084 At the Centre of Environmental Sciences (CML), Leiden University

The project: Through outcrossing, genes from cultivars can be taken up by wild relatives, this is called introgression. There is growing economical interest and concern about the genetic modification of crops and the introgression of transgenes to wild relatives. Estimates of the rate and probability of introgression are therefore needed.

Random events play a large role in the introgression process, resulting in a large variation between genotypes of hybrids in their reproductive success. Aim of the project is to develop an accurate measure of the chance of the introgression of transgenes: the "hazard



rate". This measure will be calculated on the basis of mathematical models. The parameters for the developed models will be estimated from crossing experiments, molecular- and field work. A model study is carried out on carrot and its wild relatives.

This project is a part of a collaboration between mathematicians, ecologists and molecular biologists. Within this program 2 PhD's and 1 Postdoc will be appointed.

PhD position In this PhD project the fitness of hybrids between crosses of wild and cultivated carrots will be determined under varying environmental conditions. In collaboration with the postdoc the PhD student will estimate with molecular techniques which part of the genome have the highest fitness effects. Together with the postdoc and the other PhD student the amount of gene flow between wild and cultivated carrot will be estimated on the basis of field surveys.

The candidate should have: - a degree in ecology (population dynamics), plant breeding or environmental biology - knowledge of modern molecular techniques - experience with growing plants - affinity with GIS, database manipulations and internet applications - drivers license - Sufficient fluency in writing and speaking English

The salary in the first year is 1956,00 gross per month increasing to 2502,00 gross per month in the fourth year. The appointment is temporal with a duration of 4 years, and must be concluded with a PhD thesis. After one year an assessment will be made of the project and the candidate.

For more information contact: Dr. W.L.M. Tamis, email: [tamis@cml.leidenuniv.nl](mailto:tamis@cml.leidenuniv.nl), tel: +31 71-5275618 Dr. T.J. de Jong, email: [t.j.de.Jong@ibl.leidenuniv.nl](mailto:t.j.de.Jong@ibl.leidenuniv.nl), tel: +31 71-5275118 Dr. P. Haccou, email: [p.haccou@ibl.leidenuniv.nl](mailto:p.haccou@ibl.leidenuniv.nl), tel: +31 7171-5274917. For the ERGO program see: [www.nwo.nl/nwohome.nsf/pages/NWOA\\_6JNP94\\_Eng](http://www.nwo.nl/nwohome.nsf/pages/NWOA_6JNP94_Eng) The full text of this grant is available from our website: <http://biology.leidenuniv.nl/ibl/S11/docs/ERGOproject.pdf> Application: Applications with vacancy number on the letter and envelope can be sent until 25 April to: Faculty of Sciences, Leiden University, Dienst P&O, Mrs. L. den Hollander, PO Box 9504, 2300 RA LEIDEN, The Netherlands, e-mail: [l.den.hollander@science.leidenuniv.nl](mailto:l.den.hollander@science.leidenuniv.nl)

Tom de Jong

"T.J. de Jong" <[T.J.de.Jong@biology.leidenuniv.nl](mailto:T.J.de.Jong@biology.leidenuniv.nl)>

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## McGillU PlantEvolution

Ph.D. Position at McGill University, Montreal

I am seeking a motivated and independent student to study the evolution and breakdown of self-incompatibility in the plant genus *Leavenworthia*. This work involves a combination of lab and field studies, and is part of a 5-year NSERC-funded study. Molecular lab experience is an asset but not a necessity. The Biology Department at McGill University is a vibrant and interactive group of staff, graduate students, and post-docs with expertise in all aspects of ecology, evolution, and conservation biology. Montreal is a safe, bilingual, and cosmopolitan city. This position is open to students from both inside and outside of Canada. Please contact me for details at: [Daniel.Schoen@McGill.CA](mailto:Daniel.Schoen@McGill.CA). Include in your e-mail message a short description of your educational background and qualifications. I will be happy to provide details about formal application procedures for the graduate program at McGill.

Dan Schoen

[daniel.schoen@mcgill.ca](mailto:daniel.schoen@mcgill.ca) [daniel.schoen@mcgill.ca](mailto:daniel.schoen@mcgill.ca)

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## SouthernIllinoisU SturgeonGenetics

Graduate Positions - Sturgeon Conservation Genetics

Ph.D. and MS research assistantships including stipend and tuition waiver are available to begin as early as August 2007 in the laboratory of Dr. Ed Heist at Southern Illinois University (<http://www.science.siu.edu/zoology/heist/index.html>) in conjunction with the Fisheries and Illinois Aquaculture Center (<<http://fisheries.siu.edu/>><http://fisheries.siu.edu/>). Research projects will involve development and scoring of molecular markers for conservation of endangered pallid sturgeon. Opportunities exist for field work in addition to laboratory analyses. Ideal candidates will have prior experience with molecular genetics techniques (e.g. DNA sequencing) but students without prior experience will be considered provided they are interested in the use of genetic markers for endangered species conservation. Interested students should contact Dr. Ed Heist

at [edheist@siu.edu](mailto:edheist@siu.edu) . Edward J. Heist, Ph.D. Southern Illinois University at Carbondale Fisheries and Illinois Aquaculture Center Life Sciences II, 1125 Lincoln Drive Carbondale, IL 62901-6511 Voice: (618) 453-4131 Fax: (618) 453-6095 email: [edheist@siu.edu](mailto:edheist@siu.edu) web: <http://www.science.siu.edu/zoology/heist/index.html> [edheist@siu.edu](mailto:edheist@siu.edu)

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## UAdelaide PlantBiogeography

A highly motivated student is required to undertake a Phd project in plant biogeography.

The role of long distance dispersal in the evolution of the Australasian and southwest Pacific flora is hotly contended, but appropriate tests of alternative hypotheses are still lacking. This position will develop a new comparative method for biogeography, contrasting biogeographic estimates of long distance dispersal from species phylogenies with phylogeographic estimates obtained from wide ranging species. This unique approach will be applied to the Podocarpaceae, southern pines, to test central premises of biogeographic theory, examine differences in long distance dispersal dynamics, and coincidence with major past climatic changes.

Eligibility: Only Australian and New Zealand permanent residents or citizens.

Experience required: 1. First or exceptional upper second class Bachelor of Science Degree with Honours or Masters in evolutionary or biological sciences. 2. Interest in the application of molecular tools to dissect and understand fundamental evolutionary processes at molecular and ecological levels

Contact Andrew Lowe ([andrew.lowe@adelaide.edu.au](mailto:andrew.lowe@adelaide.edu.au)) for more details.

[peter.prentis@adelaide.edu.au](mailto:peter.prentis@adelaide.edu.au)  
[peter.prentis@adelaide.edu.au](mailto:peter.prentis@adelaide.edu.au)

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## UAdelaide PlantEvolution

Plant evolution: mapping invasiveness of weeds

A highly motivated student is required to undertake a PhD project to examine the link between adaptive

evolution and invasiveness in fireweed (*Senecio madagascariensis*), a highly invasive weed in the Southern Hemisphere. Genomic changes as a result of selection and hybridisation have been implicated in the evolution of invasiveness in several weed species. Currently, the Lowe lab is investigating the role of selection, admixture and hybridisation (with *Senecio pinnatifolius*) on the genome and gene expression of fireweed. The project requires generation of genetic linkage maps to test for associations between candidate genes under selection, phenotypic traits and invasiveness; differences in genetic architecture between source and introduced populations of fireweed; and differences in the genetic architecture of *S. madagascariensis* and *S. pinnatifolius*.

Eligibility: Only Australian and New Zealand permanent residents or citizens.

Experience required: 1. First or exceptional upper second class Bachelor of Science Degree with Honours or Masters in evolutionary or biological sciences. 2. Interest in the application of molecular tools to dissect and understand fundamental evolutionary processes at molecular and ecological levels.

The position will remain open until a suitable applicant is found. Please contact Dr. Peter Prentis for further details: [peter.prentis@adelaide.edu.au](mailto:peter.prentis@adelaide.edu.au)

[peter.prentis@adelaide.edu.au](mailto:peter.prentis@adelaide.edu.au)  
[peter.prentis@adelaide.edu.au](mailto:peter.prentis@adelaide.edu.au)

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## UBasel 2 PlantPopGenet

Botanical Institute, Unit of Plant Ecology, University of Basel, Schönbeinstr. 6, 4056 Basel, Switzerland

2 PhD Studentships available (funded by the Swiss National Science Foundation)

POSITION DESCRIPTION: Two PhD positions are available in the Group of Plant Population Ecology at the Botanical Institute, University of Basel in a research project with the title: "How glacial history, selection and current gene flow affect alpine plants: Population differentiation, local adaptation and demography in a fragmented landscape". The proposal is an experimentally-based field study, including molecular and modeling work. The project is based on results from earlier and ongoing research. As a whole, the question is addressed of how plant species are able to survive and perform in the naturally fragmented alpine landscape. Typically, widespread alpine plants show

high levels of genetic variation and adaptation to local conditions. The project includes several parts: (1) Experiments in the common garden and reciprocal transplantation with plant material from the entire alpine belt will serve to test for population differentiation and local adaptation in alpine species due to geographic origin (i.e. glacial history) and environmental conditions. (2) Specific experiments will be performed to test adaptation to particular selection regimes. (3) Genetic diversity and gene flow will be analyzed using molecular markers and field experiments. By combining experiments with widespread alpine plant species, measurements of actual gene flow and colonization potential, and modeling of meta-population dynamics in a real landscape, the project links processes operating at different time and spatial scales. Students have the chance to work in a small and motivated research group. The positions are founded for three years. Preferably, work starts in June or by arrangement. Starting salary will be CHF 34'200.- per year.

**REQUIREMENTS:** The successful candidates should be motivated to work on alpine ecology. Experiences in experimental population biology, a sound background in statistics, and skills or interest in molecular work would be appreciated. Applicants should enjoy working in the field, as well as in the lab. There will be a clear distribution of responsibilities among the two PhD-students and a strong emphasis on cooperation for practical work.

**HOW TO APPLY:** Send your application preferably by regular mail to Prof. Dr. Jürg Stöcklin, Botanical Institute, Schönbeinstr 6, 4056 Basel, Switzerland. Application should include: a statement of interest, CV, and the names and addresses of two academic references.

11. 04.2007

Prof. Dr. Jürg Stöcklin Botanical Institute, Dep. of Ecology, University of Basel Schönbeinstr. 6, 4056 BASEL, Switzerland +41 61 267 35 01, [juerg.stoecklin@unibas.ch](mailto:juerg.stoecklin@unibas.ch) <http://pages.unibas.ch/botschoen/stoecklin/index.shtml> [sylvia.martinez@unibas.ch](mailto:sylvia.martinez@unibas.ch)

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## UBremen WeevilEvol

PhD position in a collaborative project of the University of Bremen and the ICIPE at Nairobi, Kenya.

Project title: Mango seed weevil bioecology and man-

agement in Kenya

**Description:** We are looking for a PhD student to study the bioecology and management of the mango seed weevil (MSW) (*Sternochetus mangiferae*) using entomopathogenic fungi and soft pesticides.

The mango seed weevil is an important pest of mango that is responsible for direct damage to fruit pulp, premature fruit drop and sometimes associated with reduced seed germination. It is also a major quarantine pest in many countries thereby limiting export of mango from Africa to lucrative markets in the EU, the Middle East and USA. The overall goals of this project are to quantify the level of damage by MSW to mango in relation to variety, season and locality and better understand ecological aspects of the pest with regard to its dynamics and distribution to guide in the deployment of control strategies. Our short term goals with regard to management is to identify candidate entomopathogenic fungi and or soft pesticide that could be used for management of the pest and to develop appropriate field application strategy based on soil or trunk application. The successful candidate will screen different isolates of entomopathogenic fungi, evaluate the effect of abiotic factors on candidate isolates, develop appropriate formulation of the pathogen and assess field persistence and application strategy. The research activity is a component of a mango IPM project targeting other mango pests such as fruit flies and mealybugs in sub-Saharan Africa and the position is based at icipe, Nairobi, Kenya. The experimental work will be carried out at the icipe, Nairobi, Kenya and the successful candidate will obtain a PhD in Biology at the University of Bremen, Germany.

**Qualifications.** This position requires a MSc or equivalent in entomology, biology, ecology or related fields. Familiarity with insect pathology is desirable.

**Available:** Immediately

**Duration:** 3 years with possibility of 1 yr extension

**Contact:** For further information and application, please contact Prof. Dr. Thomas S. Hoffmeister, Institute of Ecology and Evolutionary Biology, University of Bremen, e-mail [hoffmeister@uni-bremen.de](mailto:hoffmeister@uni-bremen.de)

Applicants should send an application until May 7 to [hoffmeister@uni-bremen.de](mailto:hoffmeister@uni-bremen.de) that includes an explanation of research experience and interests, a CV, and contact details of two persons who can provide letters of reference. Copies of relevant earlier publications can also be useful.

Thomas Hoffmeister <[hoffmeister@uni-bremen.de](mailto:hoffmeister@uni-bremen.de)>

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## UCollegeLondon ButterflyEvol

Three PhD studentships are available (for UK residents). The studentships cover a variety of environmental science topics, including my own topic on butterflies: Effects of climate warming on biodiversity at the edge of the Amazon basin. (see: [www.ucl.ac.uk/-environment-institute/jobs/docs/Mallet.pdf](http://www.ucl.ac.uk/-environment-institute/jobs/docs/Mallet.pdf))

Further details and application forms: <http://www.ucl.ac.uk/environment-institute/jobs/>  
 James Mallet <http://www.ucl.ac.uk/taxome/jim/>  
[j.mallet@ucl.ac.uk](mailto:j.mallet@ucl.ac.uk) [j.mallet@ucl.ac.uk](mailto:j.mallet@ucl.ac.uk)

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## UEdinburgh epiphytes

Lichen Diversity of Aspen - a Component of the Extended Phenotype

BBSRC CASE Studentship with Macaulay Institute

This study will test the hypotheses that the lichen flora associated with aspen (*Populus tremula*), varies between aspen clones and represents a component of the tree's extended phenotype, which is genetically based and mediated by its phenolic secondary metabolites. Lichens are a very species rich component of the biodiversity of oceanic regions and in Scotland alone, epiphytic lichens on aspen comprise over 300 species. Selection of genotypes and management of aspen woodlands for conservation and biomass production, could thereby have a profound influence on the associated biodiversity, particularly the lichens.

The overall approach will be to implement an inductive field-monitoring programme complemented by field experiments. The role of host genotypic variation and bark phytochemistry as determinants of lichen distribution, abundance and species richness will be determined between populations along a climatic gradient, and in relation to a range of physical factors. These include age of stand, light, water stress, host bark topography and nutrients. Variation in lichen communities within populations between aspen clones, characterised using existing microsatellite markers, and independently of biogeographic factors, will be established. Experimen-

tal approaches will manipulate leachate quality and quantity in stemflow whilst measuring rates of colonisation and community succession between individual trees with contrasting phytochemistry.

Supervisors: Richard Ennos (University of Edinburgh) Glenn Iason (Macaulay Institute) Chris Ellis (Royal Botanic Gardens Edinburgh)

Applications including a CV, the names and contact details of two referees, and a one page statement of your research interests should be sent to Dr. Richard Ennos ([rennos@ed.ac.uk](mailto:rennos@ed.ac.uk)) by 30th April 2007.

[R.Yahr@rbge.ac.uk](mailto:R.Yahr@rbge.ac.uk)

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## UGuelph 2 MolEvol

I am looking for two PhD candidates with research interests in molecular evolution to start in September 2007. These positions will be partially supported by funds provided by a special program at the University of Guelph and are only open to Canadian citizens. Interested students should contact Dr. Teresa Crease at [tcrease@uoguelph.ca](mailto:tcrease@uoguelph.ca). Additional information about the Zoology graduate program at the University of Guelph can be found at [http://www.uoguelph.ca/-ib/graduate\\_zoology2.shtml](http://www.uoguelph.ca/-ib/graduate_zoology2.shtml). A description of my research interests is provided below.

Ribosomal DNA (rDNA) is an important multigene family that codes for the structural RNA molecules that make up ribosomes. One unit of rDNA consists of 3 genes encoding ribosomal RNA (rRNA) separated by intergenic spacers. The spacers contain sequences that control the expression of the rRNA genes. Some regions of these genes evolve very slowly while other regions, known as expansion segments, and the intergenic spacers evolve very rapidly. Despite this rapid evolution in their sequence, they still maintain their function. In addition, it has been observed that sequence similarity among the members of this multigene family is high within species relative to similarity between copies from different species. This phenomenon is known as 'concerted evolution'.

Due to variation in the rate of evolution in different parts of the same repeat unit, rDNA is an excellent model system with which to study the interaction between the molecular processes that cause concerted evolution, and natural selection to maintain the structure and function of the molecule. I use freshwater crus-

taceans in the genus *Daphnia* as a model organism for this work as they contain unusually long expansion segments, and show variation in breeding system with some populations reproducing by cyclical and others by obligate parthenogenesis.

The current goals of my research program are to:

- 1) test the hypothesis that rates of recombination and rDNA copy number differ between *Daphnia* species, and thus cause differences in their rates of concerted evolution
- 2) test the hypothesis that natural selection is acting on rRNA gene expansion segment length variation within species
- 3) identify proteins that bind to the ribosomal intergenic spacer, and determine the impact of intra- and interspecific variation on the interaction between this sequence and these proteins
- 4) determine the impact of breeding system and genomic location on the evolution of a *Daphnia* transposon, Pokey, that is found both inside and outside of the rDNA.

– Dr. Teresa Crease Professor Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 Canada

Phone: 519-824-4120 ext 52723 Fax: 519-767-1656  
Email: tcrease@uoguelph.ca

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## UGuelph Barcoding and TEs

Up to two graduate positions (MSc or PhD) \*may\* be available for Canadian students beginning in September, 2007, in the areas of evolutionary biology, genomics, and biodiversity science. These positions will be contingent on funding that is being made available at the University of Guelph – once suitable candidates are identified, they will be included in an application for this funding. If either of the positions is of interest \*and\* you are a Canadian student \*and\* you would be available to commence graduate studies in Fall 2007, please contact Dr. T. Ryan Gregory (rgregory@uoguelph.ca) as soon as possible.

**\*\*DNA BARCODING AND GENOMIC DIVERSITY OF ECONOMICALLY AND SOCIALLY IMPORTANT INVERTEBRATES\*\***

A student engaged in this project will focus on devel-

oping a DNA barcode library and applied identification tools for pests, parasites, disease vectors, pollinators, invasives, and other economically important invertebrates. In addition, the project will involve measurements of genomic diversity (especially genome size) in these and other species, including investigations of any links between DNA content and invasiveness, parasitism, and other ecological traits. The project will involve collaborations with government and industry and will provide an opportunity to work with a wide range of organisms and methodologies. Some experience with PCR, DNA sequencing, field work, and cytogenetics would be desirable but is not required. This project will be co-supervised by Dr. T.R. Gregory and Dr. R.H. Hanner in the Department of Integrative Biology and the Biodiversity Institute of Ontario.

**\*\*BIOINFORMATICS AND TRANSPOSABLE ELEMENT EVOLUTION\*\***

A student with expertise in bioinformatics and large-scale sequence analysis is sought to explore the evolution of transposable elements in genomes of different sizes. In particular, efforts will be made to test models of competition and diversification of transposable elements, host-TE interactions, and TE-TE coevolution. This will include investigating proposed similarities between genome-level evolution and processes occurring in ecosystems. Students engaged in this project will work jointly with Dr. T.R. Gregory and bioinformaticians and computer scientists on campus and at other collaborating institutions.

PLEASE NOTE: These positions are contingent on successful applications for support, for which high quality candidates must be identified prior to application. Decisions about funding will be made relatively quickly, but it is necessary to identify potential students prior to application for the available funds. These positions are open only to Canadian students.

Dr. T. Ryan Gregory Assistant Professor Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 CANADA

<http://www.genomesize.com/gregorylab/>      trgregory@netzero.net

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## ULiverpool RodentReproductiveStrategies

Project Supervisor: Prof Jane Hurst, University of Liv-

erpool UK (jane.hurst@liv.ac.uk)

Funding: Funding is available to students from the UK ONLY

Application Deadline: 31st May 2007, available immediately

PhD in animal behaviour: Communication and Reproductive Strategies in Rodents

Inbred laboratory animals provide powerful tools to dissect the detailed molecular mechanisms underlying animal behaviour and physiology under highly controlled conditions that strictly limit experience and avoid “unwanted” individual variation. However, understanding the functions and evolution of species-specific behaviour patterns and strategies requires a much more naturalistic approach, taking into account the normal conditions, genetic variability and prior experience of animals in natural populations. Rodents use scent cues to recognize each other, assess each individual’s current status and prime their reproductive physiology according to the local social environment. As yet, we have little understanding of how these cues are used to modify reproductive strategies in normal populations. This project will use carefully controlled, non-invasive experiments to understand how and why animals use these cues under naturalistic social conditions. The student will join our Mammalian Behaviour and Evolution Group ([www.liv.ac.uk/mbe](http://www.liv.ac.uk/mbe)) which has strong interests in mammalian communication and reproductive strategies and excellent facilities for studying rodents under a wide range of conditions. This is part of a long term research programme conducted in close collaboration with the Proteomics and Functional Genomics Group ([www.liv.ac.uk/pfg](http://www.liv.ac.uk/pfg)), providing opportunities to explore the molecular basis of scent cues in addition to the behavioural and reproductive responses to social signals. You will gain a first class training in experimental approaches in behavioural and evolutionary biology, and a detailed understanding of both chemical communication in animals and the evolution of their reproductive strategies. We are looking for an individual with a strong interest and background in animal behaviour and evolutionary biology (Upper Second or First Class Honours degree achieved or anticipated). The studentship is subject to BBSRC restrictions ([www.bbsrc.ac.uk/funding/training](http://www.bbsrc.ac.uk/funding/training)). Non-EU students are not eligible. The studentship is available immediately (a start date before 31 July is preferable).

\* Hurst, J.L. (2005) Scent marking and social communication. In: *Animal Communication Networks* (Ed P.K. McGregor), pp 219-243, Cambridge University Press, Cambridge.

\* Hurst, J.L. & Beynon, R.J. (2004) Scent wars: the chemobiology of competitive signalling in mice. *Bioessays* 26, 1288-1298.

\* Thom, M.D. & Hurst, J.L. (2004) Individual recognition by scent. *Annales Zoologici Fennici*, 41, 765-787.

\* Hurst, J.L., Thom, M.D., Nevison, C.M., Humphries, R.E. & Beynon R.J. (2005) MHC odours are not required or sufficient for recognition of individual scent owners. *Proceedings of the Royal Society series B*, 272, 715-724.

\* Robertson D H, Hurst J L, Searle J B, Gunduz I and Beynon R J (2007) Characterization and Comparison of Major Urinary Proteins from the House Mouse, *Mus musculus domesticus*, and the Aboriginal Mouse, *Mus macedonicus*. *J Chem Ecol* (in press)

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Prof J L Hurst Mammalian Behaviour & Evolution Group Faculty of Veterinary Science University of Liverpool

Leahurst Veterinary Field Station Neston CH64 7TE, UK

Phone: +44 151 794 6100

Fax: +44 151 794 6107

mailto: [jane.hurst@liv.ac.uk](mailto:jane.hurst@liv.ac.uk)

<http://www.liv.ac.uk/mbe>

“Hurst, Jane” <[Jane.Hurst@liverpool.ac.uk](mailto:Jane.Hurst@liverpool.ac.uk)>

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## UMontreal HemichordateSystematics

Graduate Positions: Hemichordate systematics and functional biology Université de Montreal, Montreal, QC, Canada

Two graduate positions are available in the laboratory of Dr. Chris Cameron. One student will sequence genes from a suite of hemichordates and deuterostome invertebrates for molecular phylogenetic analysis. Preference will be given to applicants with demonstrated experience in basic molecular methods and bioinformatics.

The second position will examine filter-feeding in the enteropneust and pterobranch hemichordates using microscopy and computational fluid dynamic modeling. Preference will be given to applicants with demon-

strated experience in microscopy and computer skills.

Applicants should send a C.V., a 1 page statement of research accomplishments and interests, names and contact information for two references by email to <c.cameron@umontreal.ca>.

More information on the Cameron laboratory and on the Integrative Biology group at the University of Montreal may be found at the following links:

<http://www.bio.umontreal.ca/profs/Cameron/>  
<http://www.bio.umontreal.ca/> <http://www.umontreal.ca/> [http://en.wikipedia.org/wiki/Universit%C3%A9\\_de\\_Montr%C3%A9al](http://en.wikipedia.org/wiki/Universit%C3%A9_de_Montr%C3%A9al) Applicants should have a basic working knowledge of french and english.

Chris Cameron Sciences biologiques Université de Montréal C.P. 6128, Succ. Centre-ville Montreal, QC, Canada H3C 3J7

Cameron Christopher <c.cameron@umontreal.ca>

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## UMunich EvoBiol

\*Master Program in Evolution, Ecology and Systematics in Munich\*

The University of Munich (LMU) is launching a new, 2-year, international master program for highly motivated students from Germany and abroad with a background in biology or a related subject. The program starts in the winter semester 07/08 and all courses will be offered in English. The EESlmu Master contains many innovative elements such as a mentoring program, integrated skills courses and individual research training. We also apply a feedback and revision system instead of simple grading. Thanks to funding by the Volkswagen Foundation, students can apply for their own research and travel money and for money to invite international speakers.

Application deadline is the 30th of June 2007. For more information, please have a look at our website (<http://www.eeslmu.de>) or contact me by e-mail.

Best wishes, Pleuni Pennings –

Ms Pleuni S. Pennings, PhD

\* Program Coordinator of the Munich Graduate School for Evolution, Ecology, and Systematics

\* Postdoc in theoretical evolutionary biology

Evolutionary Biology, Department Biologie II University of Munich (LMU) Großhaderner Str. 2 D-82152 Planegg-Martinsried

Tel: 0049 89 2180 74 234 <http://www.biologie.uni-muenchen.de/ou/theopopgen/index.htm> <http://www.eeslmu.de> pennings@lmu.de

Pleuni PENNINGS <pennings@zi.biologie.uni-muenchen.de>

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## UNewBrunswick EvoOfMulticellularity

A graduate student position is available in the laboratory of Aurora Nedelcu, in the Department of Biology (<http://www.unb.ca/fredericton/science/biology/>) at the University of New Brunswick (<http://www.unb.ca/>), Canada. Research in our laboratory is directed towards understanding general, fundamental issues in evolution such as the evolution of multicellularity, development, cell differentiation, sex, programmed cell death, altruism. Our research is rooted in the framework of transitions in individuality and evolution of complexity (at a conceptual level), and of cellular responses to stress (at a more mechanistic level) (<http://www.unbf.ca/vip/amnedelcu/>). The experimental model-system we are currently using is the green algal group, Volvocales (see our Volvocales Information Project; <http://www.unbf.ca/vip>). Highly motivated students with interests in either theoretical or experimental approaches, and previous research experience are encouraged to apply. Interested applicants should e-mail a CV, summary of research experience and interests, unofficial transcripts, and contact information for at least two referees to [anedelcu@unb.ca](mailto:anedelcu@unb.ca). Applicants should meet the minimum requirements for acceptance in the Biology Department Graduate Program (see [http://www.unb.ca/fredericton/science/biology/-Degree\\_Info/Graduate.html](http://www.unb.ca/fredericton/science/biology/-Degree_Info/Graduate.html)).

[anedelcu@unb.ca](mailto:anedelcu@unb.ca)

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## UNewSouthWales EvoBiol

University of New South Wales, Sydney: Evolutionary biology

A full-stipend scholarship is available for PhD studies in the laboratory of Dr. Russell Bonduriansky in the School of Biological, Earth and Environmental Sciences at the University of New South Wales. Our lab pursues research on sexual selection and sexual dimorphism, evolutionary genetics, and the evolution of ageing through laboratory and field research on flies and other insects, as well as the development of new theory. The successful applicant will have the opportunity to choose from several interesting projects, or to develop their own project within this broad area, in consultation with Dr. Bonduriansky.

The School includes one of Australia's most research-active clusters in the area of ecology and evolution, and the evolutionary biology group is currently expanding. The University of New South Wales is located in Sydney's eastern suburbs, about 5 km from the city centre.

For more information, visit: <http://www.bees.unsw.edu.au/research/research.html>  
<http://www.bees.unsw.edu.au/school/researchstaff/-bonduriansky/bondurianskyrussel1.html>

To apply, submit a CV, contact details for two academic referees, and a one-page statement of research interests to Dr. Russell Bonduriansky (r.bonduriansky@unsw.edu.au). Note that the successful applicant, if not an Australian citizen/resident, will also need to apply to the University for a fee-waiver scholarship.

r.bonduriansky@unsw.edu.au

r.bonduriansky@unsw.edu.au

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## UPierreMarieCurie EvoOriginOfNerveCells

PhD position in Evo-Devo (Paris, France). A position for a PhD student is available at the University Pierre et Marie Curie, Paris (Ecole Doctorale Diversite du Vivant) on the following subject: "The molecular toolkit of the ancestral nerve cell: reconstructing its content and evolutionary origin. A comparative approach using sponge, ctenophore and cnidarian transcriptomes". The nerve cell was acquired in a common ancestor of cnidarians, ctenophores and Bilateria, while the sponges retained the primitive absence of a nervous system. Abundant data are available on the "molecular toolkit" used for the specification and differentiation of nerve cells in the Bi-

lateria. This PhD project aims at reconstructing the ancestral molecular toolkit of the nerve cell and its evolutionary origin. The work will start from existing EST collections, recently sequenced by the Genome, from the sponge *Sycon raphanus*, the cnidarian *Clytia hemisphaerica* and the ctenophore *Pleurobrachia pileus*. The first step will be to look for orthologues of bilaterian structural or regulatory genes involved in specification/differentiation of nerve cells. Their expression will be studied by *in situ* hybridisation and compared, between the three model species. Evolutionary scenarios will then be formalised, by mapping characters on the phylogeny. For example, data from the sponge may give insights about the ancestral functions of these molecules, before their recruitment in the nervous system. The project also comprises a phylogenomic part, in order to improve the resolution of relationships between sponges, cnidarians, ctenophores and bilaterians.

The PhD student will work in the Department UMR 7138 "Systematique, Adaptation, Evolution"; (Head of Dept: Herve Le Guyader), in the "Evolution and Development" team. Dr Michael Manuel will be the supervisor of the thesis. Starting date September 2007. Applicants must have a strong background in zoology, and must be familiar with the concepts and methods of phylogeny and Evo-Devo. An experience with molecular biology lab work will also be appreciated. Applicants must be citizens of the European Union or associated countries. The application file (single pdf file) will comprise: - a complete CV (max 4 pages), with all details about University studies and Master courses, and including a presentation of the Master lab training and other lab trainings, - a letter of motivation. All applications must be sent by e-mail (Michael.Manuel@snv.jussieu.fr). The application deadline is 25 April 2007. One referee (e.g. the supervisor of a lab training) must send a letter of appreciation on the applicant, by e-mail to Michael.Manuel@snv.jussieu.fr, before the deadline. Selected applicants will have to make an oral presentation on the 10th May 2007, in Paris.

- Dr. Michael MANUEL

Maître de Conférences (Assistant Professor) Université Pierre et Marie Curie (Paris 6) Equipe Evolution et Developpement, UMR 7138 "Systematique, Adaptation, Evolution" Bat. A, 4eme etage, piece 425 7 quai St Bernard 75 005 Paris, FRANCE

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Michael MANUEL <mmanuel@snv.jussieu.fr>

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Hinrich Schulenburg <hinrich.schulenburg@uni-tuebingen.de>

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## UTuebingen ExperimentalEvol

PhD on Experimental host-parasite coevolution

The PhD project aims at a comprehensive experimental test of the consequences of host-parasite co-evolution. It is based on a selection experiment followed by extensive phenotypic and molecular analysis. The approach relies on a unique model system, consisting of the nematode *Caenorhabditis elegans* as a host and its micro-parasite *Bacillus thuringiensis*, which are both ideally suited to experimental analysis. The results of this project are expected to have an impact on four biological research themes that are of particular current interest: the animal innate immune system, bacterial virulence, life-history trade-offs, and the generation of biological diversity.

The project is supervised by Dr. Hinrich Schulenburg and funded by the German Science Foundation (SCHU 1415/5-1; position according to 13 TV-L/2). It is based in the Department of Animal Evolutionary Ecology at the University of Tübingen, Germany. The department is active in various fields of evolutionary ecology and it provides an international and interactive atmosphere.

Requirements for the position: High motivation, excellent background in evolutionary ecology (especially host-parasite evolution) and statistics, knowledge of basic molecular techniques (PCR, fragment analysis), handling of complex experimental set-up, teamwork, ideally some experience with *C. elegans* or bacteria, fluency in English.

Please send applications with CV, brief statement of research interests, and two references, as a pdf-file by email to hinrich.schulenburg<at>uni-tuebingen.de. Deadline for applications: 1st June 2007. Start of position: September 2007. Women are especially encouraged to apply. Severely handicapped people will be preferentially considered in case of equivalent qualifications. For further details + questions, send an email to hinrich.schulenburg<at>uni-tuebingen.de or check: [www.uni-tuebingen.de/evoeco/](http://www.uni-tuebingen.de/evoeco/) . Dr. Hinrich Schulenburg

Department of Animal Evolutionary Ecology Zoological Institute University of Tuebingen Auf der Morgenstelle 28 72076 Tuebingen Germany Tel.: +49-7071-2975342 Fax: +49-7071-295634 Email:

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## UWyoming EvolGenetics

Position: Ph.D. research assistantship (starting fall 2007)

Project: Analytical tools for studies of the genomics of isolation between plant taxa

A Ph.D. research assistantship is available in the Buerkle lab at the University of Wyoming to work in the area of evolutionary genetics and computational biology.

The goal of the research is to continue the development of methods and software tools for the analysis of genomics of isolation between plant taxa. Initially we are interested in developing tools for the study of hybrid zones between *Populus* species and the movement of genes between crop and wild sunflowers. The statistical methods will identify genes that are likely to experience divergent selection between taxa or that easily cross boundaries between taxa. In addition, we will advance related methods and write software for admixture mapping in natural populations.

This research assistantship is a good opportunity for a student to gain skills in computational biology and statistical genetics in the context of interesting evolutionary questions. The central tasks for the assistantship are computational, and applicants with experience in computer programming, modeling and statistical analysis (R/S-Plus, Perl, C/C++, Maple/Mathematica, etc.), or a demonstrated aptitude for and an interest in learning skills of this type, will be preferred.

The position will begin in late August 2007 and is federally funded for three years (university funding for assistantship thereafter). Review of applications will begin 1 May 2007 and will continue until the position is filled.

Preliminary inquiries are encouraged and should be directed to Alex Buerkle (buerkle@uwyo.edu). Additional information about the lab, the University and the position is available from [http://www.uwyo.edu/buerkle/students/phd\\_pos\\_2007.asp](http://www.uwyo.edu/buerkle/students/phd_pos_2007.asp)

Buerkle@uwyo.edu Buerkle@uwyo.edu

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## UZurich 2 PlantEvol

Dear Colleagues,

I would be very grateful if you could circulate the following announcement for two Ph.D. positions in plant evolution among your colleagues and students:

Ph.D. ASSISTANTSHIPS IN PLANT MOLECULAR SYSTEMATICS/ EVOLUTIONARY ECOLOGY AT THE UNIVERSITY OF ZURICH

POSITION DESCRIPTION: Two 3-year Ph.D. Assistantships (extendable to a 4th yr., if appropriate) are available in the area of Plant Molecular Systematics/Evolutionary Ecology at the Institute of Systematic Botany of the University of Zurich, under the supervision of Prof. Elena Conti. The Ph.D. projects will build upon an existing research program on macro- and micro-evolutionary aspects of the plant genus *Primula*: i) Macro-evolutionary project: Evolution of breeding systems, ploidy levels, and biogeographic patterns in the framework of dated chloroplast and nuclear phylogenies at the genus-wide level; ii) Micro-evolutionary project: Hybridization, pollination biology, and floral development in selected hybrid complexes. Further details about the research projects will be discussed upon interviews with the best-qualified applicants. (<http://www.systbot.unizh.ch/institut/-personen/person.php?l=d&id=24>). DEADLINE FOR APPLICATION: April 30, 2007. If needed, the position will remain open until a suitable candidate is found. STARTING DATE: Ideally October 1, 2007, but earlier or later dates could be discussed. REQUIREMENTS: Perspective students are expected to have received their Master's degree or equivalent by the start of the Ph.D. program. Good knowledge of English and, possibly, German highly desirable. The ideal candidate will have documented experience/knowledge in one or more of the following areas: molecular biology, phylogeny reconstruction, population genetics, evolutionary ecology, plant breeding systems, pollination biology. The selected candidate will be expected to help in teaching (3 to 5 hours weekly average, 3-4 months per year) and writing proposals to raise additional research funds. HOW TO APPLY: Send the following by regular mail (preferred) or email to: Prof. Elena Conti, Institute for Systematic Botany, Zollikerstrasse 107, 8008, Zurich, Switzerland: I) a one- to two-page application letter addressing, but not limited to the

following questions: a) Why are you interested in a Ph.D. in this research area? b) What are your career goals? II) Your detailed curriculum vitae, including a list of field-collecting, molecular, analytical, and linguistic skills, presentations at scientific meetings, and publications (if applicable); III) a copy of your undergraduate and graduate academic records, with grades and an explanation of the grading system; IV) two or three letters from your academic advisors addressing: a) your intellectual and academic skills; b) your dedication to science; c) your ability to work cooperatively in a team. Please, follow the directions for application carefully. FACILITIES: The Institute of Plant Systematics of the University of Zurich offers state-of-the-art research facilities in an international and stimulating academic environment. Located in the heart of Europe, Zurich offers all the cultural opportunities of a major European city in close proximity to the Alps.

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Prof. Elena Conti, Ph.D. University of Zuerich, Institute for Systematic Botany Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 1 634 8424 Fax: 0041 1 634 84 03 email: [ContiElena@access.unizh.ch](mailto:ContiElena@access.unizh.ch) <http://www.systbot.unizh.ch/institut/personen/-person.php?l=d&id> UPCOMING INTERNATIONAL CONFERENCE: July 14-15, 2007, University of Zurich:

“Origin and Evolution of Biota in Mediterranean Climate Zones”

<http://www.systbot.unizh.ch/mediterranean/-index.htm> [ContiElena@access.unizh.ch](mailto:ContiElena@access.unizh.ch)

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## UZurich ComparativeAnatomy

Open PhD position

The new research group working on Vertebrate Comparative Ontogeny and Palaeobiology at the Palaeontological Institute of the University of Zürich invites applications for a PhD position (3 years funding, with potential extension). The successful candidate will work in a Swiss National Science Foundation supported research project about skeletal heterochronies in mammals and other amniotes, under the supervision of Prof. Marcelo Sánchez. The Ph.D. project will build upon an existing research program (<http://www.pim.uzh.ch/de/Institut/-Mitarbeitende/index.php?show=34>) and includes mu-

seum visits world wide and extensive lab work. Interested applicants should check our website for our publications and current research projects. Details about the PhD project will be discussed upon interviews with the best-qualified applicants.

The ideal candidate will be a highly-motivated zoologist with neontological or palaeontological background. Previous participation in research activities and excellent writing skills in English are required, knowledge of speaking German is desirable. Perspective students are expected to have received their Master's degree or equivalent by the start of the Ph.D. program. The selected candidate will be expected to help in teaching (3 to 5 hours weekly average, 3-4 months per year) and writing proposals to raise additional research funds.

**HOW TO APPLY:** Send the following by regular mail or email to: Prof. Marcelo Sánchez: I) a one- to two-page application letter addressing, but not limited to the following questions: a) Why are you interested in a Ph.D. in this research area? b) What are your career goals? II) Your detailed curriculum vitae, including a list of lab, field, analytical, and linguistic skills, presentations at scientific meetings, and publications (if applicable); III) a copy of your undergraduate and graduate academic records, with grades and an explanation of the grading system; IV) two or three letters from your academic advisors addressing: a) your intellectual and academic skills; b) your dedication to science; c) your ability to work cooperatively in a team. Please, follow the directions for application carefully. **DEADLINE FOR APPLICATION:** May 1, 2007. If needed, the position will remain open until a suitable candidate is found. **STARTING DATE:** Summer or early Fall 2007 (negotiable).

The University is one of the top comprehensive institutions in Europe and Zürich, in close proximity to the Alps, offers the conditions for an excellent quality of life. With a critical mass of researchers in Palaeontology and Evolutionary Biology at the University and the neighbouring Swiss Federal Institute of Technology (ETH Zürich), Zurich offers an exceptional academic environment for research and study. The Institute of Palaeontology of the University of Zürich offers state-of-the-art research facilities in an international and stimulating academic environment.

Please send enquiries and applications (letter of application, Curriculum Vitae and two references) by regular mail or by email to Prof. Marcelo Sánchez (e-mail: m.sanchez@pim.uzh.ch)

– Marcelo Sánchez Assistant Professor of Palaeontology Paläontologisches Institut und Museum Universität Zürich Karl Schmid-Strasse 4 CH-8006 Zürich Switzerland

land Phone: +41 (0)44 634 23 42 Fax +41 (0)44 634 49 23 For deliveries (please add): Raum KO2 E63e Email: m.sanchez@pim.uzh.ch <http://www.pim.uzh.ch/de/-Institut/Mitarbeitende/index.php?show4> Marcelo Sánchez <m.sanchez@pim.uzh.ch>

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## UZurich PlantEvol

TWO Ph.D. ASSISTANTSHIPS IN PLANT PHYLOGENETICS/ EVOLUTIONARY ECOLOGY AT THE UNIVERSITY OF ZURICH: second announcement

**POSITION DESCRIPTION:** Two 3-year Ph.D. Assistantships (extendable to a 4th yr., if appropriate) are available in the area of Plant Molecular Systematics/Evolutionary Ecology at the Institute of Systematic Botany of the University of Zurich, under the supervision of Prof. Elena Conti. The Ph.D. projects will build upon an existing research program on macro- and micro-evolutionary aspects of the plant genus *Primula*: i) Macro-evolutionary project: Evolution of breeding systems, ploidy levels, and biogeographic patterns in the framework of dated chloroplast and nuclear phylogenies at the genus-wide level; ii) Micro-evolutionary project: Hybridization, pollination biology, and floral development in selected hybrid complexes. Further details about the research projects will be discussed upon interviews with the best-qualified applicants. (<http://www.systbot.unizh.ch/institut/-personen/person.php?l=d&id=24>).

**DEADLINE FOR APPLICATION:** April 30, 2007. If needed, the position will remain open until a suitable candidate is found.

**STARTING DATE:** Ideally October 1, 2007, but earlier or later dates could be discussed.

**REQUIREMENTS:** Perspective students are expected to have received their Master's degree or equivalent by the start of the Ph.D. program. Good knowledge of English and, possibly, German highly desirable. The ideal candidate will have documented experience/knowledge in one or more of the following areas: molecular techniques, phylogeny reconstruction, population genetics, evolutionary ecology, plant breeding systems, pollination biology.

**HOW TO APPLY:** Send the following by regular mail (preferred) or email to: Prof. Elena Conti, Institute for Systematic Botany, Zollikerstrasse 107, 8008, Zurich, Switzerland: I) a one- to two-page application letter ad-

dressings, but not limited to the following questions: a) Why are you interested in a Ph.D. in this research area? b) What are your career goals? II) Your detailed curriculum vitae, including a list of field-collecting, molecular, analytical, and linguistic skills, presentations at scientific meetings, and publications (if applicable); III) a copy of your undergraduate and graduate academic records, with grades and an explanation of the grading system; IV) two or three letters from your academic advisors addressing: a) your intellectual and academic skills; b) your dedication to science; c) your ability to work cooperatively in a team. Please, follow the directions for application carefully.

**FACILITIES:** The Institute of Plant Systematics of the University of Zurich offers state-of-the-art research facilities in an international and stimulating academic environment. Located in the heart of Europe, Zurich of-

fers all the cultural opportunities of a major European city in close proximity to the Alps.

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Prof. Elena Conti, Ph.D. University of Zuerich, Institute for Systematic Botany Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 1 634 8424 Fax: 0041 1 634 84 03 email: ContiElena@access.unizh.ch <http://www.systbot.unizh.ch/institut/personen/-person.php?l=d&id> UPCOMING INTERNATIONAL CONFERENCE: July 14-15, 2007, University of Zurich:

“Origin and Evolution of Biota in Mediterranean Climate Zones”

<http://www.systbot.unizh.ch/mediterranean/-index.htm> ContiElena@access.unizh.ch

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### CSIRO Canberra PlantPopGenet

RESEARCH SCIENTIST (POPULATION GENETICS) - CSIRO Entomology (Canberra, Australia)

APPLICATIONS CLOSE 4 MAY 2007

Testing and developing evolutionary theory using natural populations is always challenging. We seek a population geneticist who can rise to this challenge. You will develop and lead research that focuses on population structure and gene flow in natural populations of invertebrates relevant to major issues for Australia. In the first instance you will contribute to CSIRO's research in the CRC for National Plant Biosecurity, with the longer term expectation for you to develop a wider CSIRO research program with a range of organisms

in collaboration with Universities and other research providers.

This position suits an early career scientist keen to establish their own research group using excellent science to progress theory while at the same time giving insight to practical problems and their solutions. More information about the CSIRO can be found at [www.csiro.au](http://www.csiro.au) <<http://www.csiro.au/>> under Careers

CSIRO prefers applications be lodged online via this careers site.

You are required to include two documents (1) "A document Addressing the Selection Criteria" and (2) a "Resume or CV" including the names of at least two referees. Note: Applications that do not address the selection criteria will not be considered.

If you experience difficulties applying online call 1300 301 509 and someone will be able to assist you. Outside business hours please email: [csiro-careers@csiro.au](mailto:csiro-careers@csiro.au) <<mailto:csiro-careers@csiro.au>> .

If you are unable to lodge your application online, please fax your application quoting reference number 2007/54 to (02) 6246 4068 or alternatively post to:

CSIRO Careers Online PO Box 225 DICKSON ACT 2602

If after reading the selection documentation you have any questions specifically relating to this position, please contact Gary Fitt on + 61 7 3214 2828 or [gary.fitt@csiro.au](mailto:gary.fitt@csiro.au) <<mailto:gary.fitt@csiro.au>> Do not apply to Dr Fitt. Any applications received by this method will not be accepted.

Owain Edwards, Principal Research Scientist Stream Leader, Applied Genomics CSIRO Entomology Centre for Environment and Life Sciences (CELS) Floreat Park, WA 6014 AUSTRALIA

[Owain.Edwards@csiro.au](mailto:Owain.Edwards@csiro.au)

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## DukeU SpeciationGenetics LabTech

An Associate in Research ("lab technician") position is available in the Duke University laboratory of Biology Department Associate Professor Mohamed Noor beginning June, 2007. Responsibilities: 50% Isolation and molecular analysis of DNA using PCR and other techniques; 20% Maintenance of fruit fly cultures and collection of unmated flies; 10% Supervision of undergraduates; 10% Data entry and analysis of results from

molecular and phenotypic assessments; 10% Ordering and laboratory maintenance. Required qualifications: B.S. or B.A. degree in biology or related field, some experience with basic laboratory techniques. Additional qualifications desired: experience with molecular biology protocols, experience with handling of *Drosophila* fruit flies, experience with supervising others. Applications will be reviewed as they are received until candidate is selected. Please ONLY send an e-mail of intent (no attachments!) that indicates your experience and interest to: Dr. Mohamed Noor, [NOOR@DUKE.EDU](mailto:NOOR@DUKE.EDU) . Duke University is an Equal Opportunity/ Affirmative Action Employer.

Mohamed A. F. Noor [noor@duke.edu](mailto:noor@duke.edu) Associate Professor Tel: 919-613-8156 DCMB Group/ Biology Lab: 919-613-8193 Box 91000 FAX: 919-613-8177 Duke University Durham, NC 27708 USA <http://www.biology.duke.edu/noorlab/> [noor@duke.edu](mailto:noor@duke.edu)

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## LudwigMaximiliansU QuantGenetics

The FACULTY of BIOLOGY at the LUDWIG-MAXIMILIANS-UNIVERSITY of MUNICH

invites applications for an

ASSOCIATE PROFESSORSHIP (W2, tenure track) for Quantitative Genetics

The successful candidate is expected to have a strong research record in the areas of quantitative and/or statistical genetics with an emphasis on theory and the analysis of the genetic basis of adaptive traits. This may include, but is not limited to: QTL analysis, association mapping, or systems biology. The research should complement the current focus of the groups working in population genetics, evolutionary genomics, and evolutionary ecology.

The Faculty of Biology has strengths in both organismal and molecular/ cellular biology. It is located at the high-Tech-CampusLMU Martinsried, in close proximity to other life science departments and Max-Planck-Research Institutes. Close ties also exist with the Technical University of Munich and the Research Center for Environment and Health. The professorship will be integrated into the planned interdisciplinary "Center of Quantitative Methods" (run jointly by the Faculties of Biology, Medicine, Physics, Mathematics/ Informatics

and Statistics).

The successful candidate must be able to establish international competitive research programs with extramural funding. Teaching obligations include courses for both undergraduate and graduate students in evolutionary biology and quantitative biology.

Prerequisites for the application are a doctoral degree, teaching skills and a record of research equivalent to the German "Habilitation". Scientific qualifications achieved in the private sector, outside Germany or as Junior professor will also be considered.

Applicants must be younger than 52 at the time of appointment. Exceptions to this rule may be considered if outstanding.

The University of Munich is interested in increasing the number of female faculty members and encourages women to apply. The University supports dual carrier couples.

The university is an equal opportunity employer and handicapped candidates with equal qualifications will be given preference. Further information concerning the equal opportunity policy of the LMU can be obtained from Prof. K. Jung (kirsten.jung@lrz.uni-muenchen.de), concerning teaching from Prof. M. Starck (starck@uni-muenchen.de), concerning the structure of the Faculty from Prof. J. Soll (dekanat19@lmu.de), and concerning the scientific scope of the position from Prof. W. Stephan (stephan@zi.biologie.uni-muenchen.de).

Applications including CV, list of publications, a brief summary of present and future research interests, proof of teaching experience, five selected reprints and copies of relevant documents should be sent and a CD containing these documents before May 20, 2007 to Prof. Dr. Jürgen Soll, Dean of the Faculty of Biology, Ludwig-Maximilians-University of Munich, Großhaderner Str. 2, 82152 Planegg-Martinsried, Germany.

rose@zi.biologie.uni-muenchen.de rose@zi.biologie.uni-muenchen.de

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## Milan EvolGenomics

Postdoctoral Fellowship in Evolutionary Genomics and Bioinformatics

A postdoctoral position is available in the group of Bioinformatics and Evolutionary Genomics of Cancer

at the European Institute of Oncology in Milan (Italy).

The group is interested in detecting the genotypic determinants of human cancer through the study different features of human genes, proteins and of the entire genome. A number of projects are currently going on in the lab. Therefore, a certain flexibility in the choice of the project is allowed. In all cases, the successful candidate will deal with well-assessed procedures for data analysis as well as with the development of tools for solving specific problems. A tight collaboration with the many wet labs in the campus is a major trait of the job.

Qualifications: A PhD in bioinformatics, theoretical biology, genetics or equivalent is required. Computational skills (Perl, Python, C++) are mandatory. A background in evolution and developmental biology would be favourable.

To apply: send, via email, a CV, a statement of research interests, and the names and contact information for two references. Applications and inquiries should be addressed to Francesca Ciccarelli francesca.ciccarelli@ifom-ieo-campus.it

Francesca D. Ciccarelli, PhD IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303-053 fax +39-02574303-231 web: <http://-ciccarelli.group.ifom-ieo-campus.it/fewiki/> francesca.ciccarelli

francesca.ciccarelli@ifom-ieo-campus.it  
francesca.ciccarelli@ifom-ieo-campus.it

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## Muenster 2 CompBiol

Jobs in Computational Biology - University of Muenster, Germany

The newly founded Institute for Bioinformatics at the University of Muenster is looking for highly motivated people to work in multidisciplinary group in the area of comparative genomics and systems biology. The official language of the Institute is English. Two positions are currently open but several others for graduate and diploma students are expected to be available in near future.

SCIENTIFIC PROGRAMMER The ideal candidate will have a master degree in computer science with strong experience in programming (Perl, Python, C++) in UNIX environment (familiarity with Solaris sys-

tem is a plus). The successful candidate will be responsible to provide programming services for several research projects ongoing in the Institute mostly related to development of specialized databases and creating Web-based user interfaces to these databases. See for example the Database of Evolutionary Distances (<http://warta.bio.psu.edu/DED/>) or the ScrapYard Database (<http://warta.bio.psu.edu/ScrapYard/database.html>). This person will also administrate Solaris-based servers and provide help and advise to other members of the Institute.

POSTDOCTORAL FELLOW Research projects might be (but are not limited to) in one of the following areas: - evolutionary comparative genomics - evolutionary systems biology - evolution of alternative splicing - see <http://warta.bio.psu.edu/Research.html> for other research projects and current papers Required qualifications include: - Ph.D. in bioinformatics or computer science with strong interest in biology - Fluency in English - Basic skills in statistics - Programming skills (in either PERL, C, or PYTHON) - UNIX literacy - Motivation and proven ability to carry out bioinformatics research independently - Good social skills; capacity and willingness to develop teamwork

Expected starting date for both positions is June 2007. Applications should include a CV, list of publications, and addresses of three references. Candidates are encouraged to send informal inquiries to: Mr. Wolfgang Garbers [GarberW@mednet.uni-muenster.de](mailto:GarberW@mednet.uni-muenster.de) Institute for Bioinformatics University of Muenster or Dr. Wojciech Makalowski [wojmak@uni-muenster.de](mailto:wojmak@uni-muenster.de)

Muenster hosts many excellent scientific institutions such as a newly founded Max-Planck Institute for biomedical research and newly founded Institute of Evolution and Biodiversity, a Centre for Nanotechnology, and a great number of specialized research areas. Muenster is a dynamic city with a world-famous heritage center and is located in the middle of the beautiful "Muensterland". It is very lively, last but not least because of the high number of students (around 20% of the residents) and the rich choice of social, cultural and sporting facilities (see [www.muenster.de](http://www.muenster.de) for further details).

[wojtekw@warta.bio.psu.edu](mailto:wojtekw@warta.bio.psu.edu) [wojtekw@warta.bio.psu.edu](mailto:wojtekw@warta.bio.psu.edu)

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**NatureSourceGenetics  
Bioinformatics**

Our new company, working on computational genomics towards crop improvement, has a position open for a Bioinformaticist/Programmer. Info is available on our website below.

If you feel you have members that may be interested in this, please post, or let me know what additional info you need to do so. Thanks, Theresa Fulton

- Theresa M. Fulton, Ph.D. Director of Operations Nature Source Genetics, LLC. <http://naturesourcegenetics.com>

[tfulton@naturesourcegenetics.com](mailto:tfulton@naturesourcegenetics.com)

[tful-ton@naturesourcegenetics.com](mailto:tful-ton@naturesourcegenetics.com)

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## NewYorkU Tech CompFuncGenomics

JOB OPENING: Technician/Lab Manager

We have an opening for a technician/lab manager at the Purugganan Laboratory in the Department of Biology/Center for Comparative Functional Genomics at New York University. The duties include management of laboratory operations and technical support for various projects. Experience in molecular genetic techniques and in the care of plants is desirable. Salary is commensurate with experience, and will start at \$36,000/year plus full benefits.

If you are interested, please send me a CV at [mp132@nyu.edu](mailto:mp132@nyu.edu). If you want to know more about our laboratory, check out our website at <http://www.nyu.edu/fas/dept/biology/faculty/purugganan/index.html>

The position will be in NYU's main campus in Washington Square at the heart of Greenwich Village in downtown Manhattan.

Michael Purugganan Dorothy Schiff Professor of Genomics

Department of Biology Center for Comparative Functional Genomics 100 Washington Square East New York University New York, NY 10003

Tel. (212) 992 9628

Michael Purugganan <[mp132@nyu.edu](mailto:mp132@nyu.edu)>

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## NorthDakotaStateU PlantConsBiol

Plant Conservation Biologist Biological Sciences Department North Dakota State University

The NDSU Department of Biological Sciences invites applications for a tenure-track Assistant Professor in Plant Conservation Biology. Inquiries about a more advanced position will be considered. A Ph.D. in Biology or a related field is required. The successful candidate must develop an externally funded, nationally competitive research program in the area of conservation biology focusing on the evolutionary-ecology of plant and/or plant systems. The candidate must demonstrate a commitment to teaching at the undergraduate and graduate levels, have strong oral and written English communication skills, and an established record of peer-reviewed publication. The candidate will be expected to participate in the interdisciplinary Environmental and Conservation Sciences Graduate program, and be able to integrate across existing strengths in the department, which include evolutionary conservation biology, regulatory-developmental biology and science education. Duties will include teaching in the general areas of conservation biology, evolutionary ecology, and plant biology. The candidate will have the opportunity to participate in the development of a new environmental field school in central North Dakota. Demonstrated ability to obtain extramural funding is strongly preferred. Postdoctoral and teaching experience preferred. We especially encourage applicants who will increase the participation of women and minorities in the sciences. Information about NDSU can be found at <<http://www.ndsu.edu/>>[www.ndsu.edu](http://www.ndsu.edu). The position will begin August 15, 2007. Review of applications will begin December 1, 2006 and continue until the position is filled. Applications by email will be accepted. Please send a letter of application, curriculum vitae, up to three representative publications, statements of research and teaching interests, and contact information (including telephone numbers and e-mail addresses) for three professional references to: Plant Conservation Biology Search Committee, Department of Biological Sciences, North Dakota State University, Fargo, ND 58105 USA; (701) 231-7087; [Craig.Stockwell@ndsu.edu](mailto:Craig.Stockwell@ndsu.edu). NDSU is an equal opportunity institution.

For more information contact Craig Stockwell Craig A. Stockwell Associate Professor Department of Biological Sciences Environmental & Conservation Sciences Grad-

uate Program Stevens Hall North Dakota State University Fargo, ND 58105

phone (701) 231-8449 fax (701) 231-7149  
e-mail [Craig.Stockwell@ndsu.edu](mailto:Craig.Stockwell@ndsu.edu) web site:  
<http://www.ndsu.nodak.edu/ndsu/stockwell/>  
[craig.stockwell@ndsu.edu](mailto:craig.stockwell@ndsu.edu) [craig.stockwell@ndsu.edu](mailto:craig.stockwell@ndsu.edu)

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## OhioStateU BiomedicalInformatics DatabaseWebInterface

Title: Jobs for Database and Web Interface Programmers

Location: Ohio State University Department of Biomedical Informatics, Columbus OH ([bmi.osu.edu](http://bmi.osu.edu))

Duration: Summer 2007 and perhaps ongoing for the right programmers.

Ground-up design of phylogeographic services and workflow.

Database Programmer: The database programmer is responsible for reviewing, analyzing and modifying PostGIS enabled PostgreSQL database architecture. In addition, the position is responsible for reviewing and designing efficient query approaches for both spatial and standard SQL statements.

The database programmer will be responsible for the technical and administrative maintenance and design of PostgreSQL databases. Other duties include:

Implementation of data models and database designs, data access and table/view maintenance codes.

Resolution of database capacity issues, replication, and other distributed data issues.

Web Interface Developer: The web developer will design a graphical user interface to create SQL queries for the non-SQL versed user, and reformat/manipulate results.

Successful candidates will have demonstrated strength in analyzing and troubleshooting data and processing issues.

You must have a desire to learn and understand the data in order to work incrementally towards a comprehensive workflow with intermediate milestones. Finally, you should be able to work independently and make decisions confidently.

2 years PostgreSQL experience desired Current stu-



dent in Computer Science or related field Experience with JAVA and/or PHP Domian Knowledge in genomics and or cartography a plus

Salary commensurate with experience Please send CV and links to relevant examples of previous work. Contact: Daniel Janies, (danjanies@hotmail.com) for more information.

danjanies@hotmail.com

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### Smithsonian DNABarcodes

An excellent opportunity exists for a qualified student or recent graduate (undergraduate or graduate degree received within the last 24 months) to provide services under a contractual agreement in support of research to develop and evaluate DNA barcodes for stream macroinvertebrates in the state of Maryland, USA. The individual hired will contribute to an important collaborative research project involving the United States Environmental Protection Agency, the Smithsonian Institution's National Museum of Natural History, the Maryland Department of Natural Resources, and the Consortium for the Barcode of Life. The individual hired will be stationed at the Smithsonian Institution's Laboratories for Analytical Biology, 4210 Silver Hill Rd, Suitland MD 20746.

The research is expected to advance the fields of water quality monitoring and aquatic ecosystem assessment by incorporating DNA diagnostic procedures into existing bioassessment protocols. The selected individual will provide technical support for the DNA barcode research project by (1) aiding in development of DNA barcode reference libraries for Ephemeroptera (mayflies), Plecoptera (stoneflies), and Tricoptera (caddisflies) established in Maryland freshwater streams and (2) using DNA barcodes to identify macroinvertebrate samples collected by Maryland Department of Natural Resources as part of the project.

Please note that applications must be received by April 26, 2007. For details on the requirements for the position and instructions to apply, you must visit <http://www.epa.gov/oamrtpnc/q0700114/index.htm> For more information on the research project and technical aspects of the work please contact Mark Bagley at [bagley.mark@epa.gov](mailto:bagley.mark@epa.gov) or (513) 240-0950

Bagley.Mark@epamail.epa.gov  
Bagley.Mark@epamail.epa.gov

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### SouthAfrica FieldAssist SmallMammals

Volunteer needed as field assistants for the project:

Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

July/August to Ovtober/November 2007

>From November 2007 onwards

Project: We study the reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students with a BSC/Vordiplom or equivalent are preferred as candidates. Applicants must have an interest in working in the field and with animals. Whereas the research is mainly non-invasive, this is no job for extreme animal right persons (we take tissue and blood samples). Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5-6 days a week. Applicants must be able to manage extreme temperatures (below 0 at night, sometimes over 40C during days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

Work of field assistants: Trapping and marking of mice and rats; radio-tracking to determine home ranges and nest sites; direct behavioral observations in the field; experiments and observations with captive specimen under natural weather conditions; maintenance and cleaning of the research station.

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for the masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 500 (around 70 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 1500 or 200 Euro/month). Including extras, you should expect to

pay about 300 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: Currently we are looking for a volunteer for the period July/August to October/ November 2007, the breeding season. The next open positions will be December 2007 and January 2008.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to [carsten.schradin@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch).

More information under [www.stripedmouse.com](http://www.stripedmouse.com) Contact via e-mail: [carsten.schradin@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch)

Dr. Carsten Schradin Research Assistant, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Dr. Carsten Schradin Research Associate, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel; +41 - (0)44 635 5486 Fax: +41 - (0)44 635 5490

(Tel. secretary: +41 - (0)44 635 5271)

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Succulent Karoo Research Station, Goegap Nature Reserve, Private Bag X1, 8240 Springbok, South Africa.

visit <http://www.stripedmouse.com> The university of Zurich decided to change the email addresses to "uzh" instead of "unizh" at the end. "unizh" remains valid until 2008.

Carsten Schradin <[carsten.schradin@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch)>

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**UArkansas InsectSystematics**

Position Title: Insect Systematist Position Rank: Assistant Professor, 12-month appointment, Tenure Track Location: Department of Entomology, University of Arkansas, Fayetteville Appointment: 80% Research/20% Teaching Date Available: Tentatively, August 2007 or negotiable

Responsibilities: Develop an independent, recognized research program in insect systematics, with relevance to insect diversity, evolution and ecology. This position is open to specialists in all insect taxa, especially taxa with relevance to crop pests, aquatic insects or insect natural enemies. The incumbent will seek extramural funding, train graduate students, and coordinate with the curator of the Departments Arthropod Collection in managing the collection. Teaching responsibilities will include an undergraduate course in General Entomology and a graduate-level advanced systematics course.

Qualifications: Ph.D. in entomology or a related field (by date of hire), with a strong background in contemporary systematics techniques and demonstrated excellence or potential in research and publication. Preference will be given to candidates with prior experience in teaching, grantsmanship and collaborative research.

Application: Review of applications will begin May 1, 2007, and will continue until the position is filed. Applicants should submit CV, statement of research and teaching plans and objectives, up to 5 reprints, names and contact information for at least three professional references, and arrange for transcripts to be submitted.

All application materials should be sent (electronic submissions preferred) to:

Dr. Fiona L. Goggin Chair, Search Committee c/o Janet Funk, Administrative Assistant Department of Entomology AGRI 319 University of Arkansas Fayetteville, AR 72701 [jfunk@uark.edu](mailto:jfunk@uark.edu) [fgoggin@uark.edu](mailto:fgoggin@uark.edu)

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## UCC Cork Ireland ProgramManager InformaticsSpecialist

Program Manager with Informatics Skills

5 Year Fixed Term Contract Post beginning 01.06.2007

Applications are invited for the post of Program Manager in the newly created research group on Microbial Population Genetics and Genomics, University College Cork, Ireland. This is a key post within the newly es-

tablished group and will report directly to the group leader, Prof. Mark Achtman. The post holder will have responsibility for administering, developing and installing software and hardware as well as administering purchasing and accounting for various research projects. He/she will work with research scientists to continuously improve the informatics and bioinformatics environment for a variety of projects.

UCC is seeking to appoint an enthusiastic and motivated person to drive the following agenda: "Installation of a small network of PCs and a small UNIX cluster. Administration of this network including the installation of programs and regular backups." "Installation of a PostgreSQL database server and administration of access rights to the database." "Maintenance and improvement of a WEB site designed in Python and Zope. Implementation of a SOAP interface and adaptation of additional pre-existing modules written in Perl." "Write programming scripts in a variety of languages to support molecular biologists who have limited programming experience." "Administration of purchasing and accounting of equipment and supplies

Suitable candidate should have a degree in informatics, bioinformatics, molecular biology or genetics, preferably to an advanced level, and have excellent communication and organisational skills.. Experience in informatics and/or bioinformatics in an academic or industry setting is a prerequisite as are experience in administration of networks and relational databases, Web page design and extensive programming skills. A further requirement is the ability to assimilate and understand scientific and technological issues. The appointee will be flexible, confident, energetic and enthusiastic with an ability to manage and prioritize a demanding workload.

A competitive salary, up to an initial maximal annual salary of 54,178, will be offered to the successful candidate, commensurate with experience and qualifications. Closing Date for informal discussions: 17 April, 2007

For informal discussions on this post, please contact Dr. Mark Achtman. [achtman@mpiib-berlin.mpg.de](mailto:achtman@mpiib-berlin.mpg.de). Selected applicants will then be requested to submit completed application forms by mail.

UCC IS AN EQUAL OPPORTUNITIES EMPLOYER

Mark Achtman Max-Planck Institut für Infektionsbiologie Schumannstr. 21/22 10117 Berlin, Germany Tel: +4930 28460751 Fax: +4930 28460750 e-mail: [achtman@mpiib-berlin.mpg.de](mailto:achtman@mpiib-berlin.mpg.de)

Mark Achtman <[achtman@mpiib-berlin.mpg.de](mailto:achtman@mpiib-berlin.mpg.de)>

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## UCaliforniaBerkeley HerpetologyCurator

### ACTING CURATOR OF HERPETOLOGY MUSEUM OF VERTEBRATE ZOOLOGY UNIVERSITY OF CALIFORNIA, BERKELEY

The Museum of Vertebrate Zoology at the University of California, Berkeley seeks to fill a three-year appointment as a full-time Associate Specialist, \$46,872 - \$50,112 annually. The successful applicant will work with the curators and staff on the herpetological preserved and tissue collections, with particular attention to accessioning of specimens, reorganization of the collections to reflect current taxonomy, as well as managing day-to-day activities such as specimen loans. Undertake herpetological analysis in support of major MVZ projects, including collaborative or independent research, as appropriate. Applicants should have: \* An advanced degree in a relevant area (or expecting to file prior to commencement of employment) \* A sound working knowledge of systematic herpetology \* A record of research in systematic or evolutionary biology of reptiles or amphibians \* Relevant experience working in museum collections or with museum specimens

Interested persons should send a curriculum vitae, statement of purpose, and the names of three references to: Prof. Craig Moritz, Director, Museum of Vertebrate Zoology, University of California, Berkeley, CA 94720-3160. Further information about this position can be obtained from the MVZ website ([mvz.berkeley.edu/Job\\_Listings.php](http://mvz.berkeley.edu/Job_Listings.php)), or you can address questions to Jimmy A. McGuire (Curator, MVZ, [mcguirej@berkeley.edu](mailto:mcguirej@berkeley.edu)).

Deadline for receipt of applications is June 1, 2007, with an anticipated starting date of September 1, 2007.

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

Jeanne G. Kassis Human Resources Manager Berkeley Natural History Museums 3101 VLSB Berkeley, CA 94720-3070 phone:(510) 642-3568 fax:(510) 642-6984

[kassj@berkeley.edu](mailto:kassj@berkeley.edu) [kassj@berkeley.edu](mailto:kassj@berkeley.edu)

V Sork <vlsork@ucla.edu>

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## UCaliforniaLosAngeles PopGenet ResTech

Research Technician Position at UCLA:

Plant Population Genetics/ Molecular Ecology

Description of Responsibilities:

Under supervision from Victoria Sork or Senior post-doc, research technician will perform standard laboratory procedure and data management for research in plant population and conservation genetics. Right now we are studying contemporary gene flow with microsatellite markers and comparative phylogeography with gene sequences. The technician will conduct molecular analyses, including DNA extraction, PCR, genotyping with microsatellite DNA and sequencing, using standard methods and by developing modifications of standard methods. Other duties include: oversee day-to-day management of laboratory including purchase of supplies and equipment; insuring proper operation and maintenance of laboratory equipment; entering and managing electronic data files; working with undergraduate research assistants; maintaining greenhouse plants, and occasional training of students.

Details: The position is classified as Staff Research Associate II (SRAII), according to the UC human resources system. The salary will start at \$3045 per month for full time, and the position could be 75% to 100%.

Minimum Qualifications: Bachelor's Degree in an appropriate field of technology or science such as Biological Sciences, Molecular Biology, or Genetics, PLUS research experience in an appropriate field of science or technology. Experience with microsatellites or gene sequencing is required. Knowledge of evolutionary biology or population genetics and statistical software preferred.

Please apply on-line by April 30, 2007 to: <https://hr.mycareer.ucla.edu/> (job #10104)

Questions? Please contact Victoria Sork at: vlsork@ucla.edu

Victoria Sork UCLA Professor, Dept of Ecol & Evol Biology Professor, Institute of the Environment

Victoria Sork Professor, Dept of Ecol & Evol Biology Professor, Institute of the Environment UCLA vlsork@ucla.edu

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## UGeorgia BiodiversityGenetics ResAssist

Research Assistant: Biodiversity Genetics Research assistant wanted for project studying freshwater mollusk communities in Georgia for the duration of May 28th 2007 to August 20th 2007. Position will require 50% fieldwork and 50% lab work. Fieldwork will be 2-3 days per week and will encompass trips to 4 different rivers in Georgia that make up the Altamaha River Basin. Transects will be performed via kayak or canoe (experience preferred), applicants must be comfortable with camping in river wilderness areas. Lab work will encompass DNA and molecular techniques (PCR, sequencing, and electrophoresis), experience required though some training will be provided. Position is salaried through the University of Georgia in Athens, approximately \$1500.00 per month; applicant must have a valid driver's license and clean driving record. All inquires please send CV and three references (at least one specifically noting the extent of lab techniques) to Scott T. Small via email [stsmall@uga.edu](mailto:stsmall@uga.edu), OR snail-mail to: Scott Small, Dept of Genetics, University of Georgia, Athens, GA, 30602. For more information on my research and the research of my associated lab check out: <http://www.genetics.uga.edu/-wareslab/biodiversity.html> Scott T. Small Department of Genetics University of Georgia Athens, GA 30602

stsmall@gmail.com

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## UIdaho Undergrad Assist

Project: I am trying to determine if coevolution shapes the way that plants and insects adapt to their environment. To do this I will study the way a native plant-Round Leaved Alumroot, responds to different habitats and different plant-feeding insects. This project will involve a great deal of field work along Clearwater River of Idaho the Blue Mountains of Washington.

Responsibilities: The applicant will be expected to help establish ecological experiments and then conduct detailed surveys on Round Leaf Alumroot and its asso-

ciated insects. This project will provide training on methods in field ecology, experimental design and natural history in the Pacific Northwest.

This position will consist of an eight week REU (research experience for undergraduates) with a salary of 4880 dollars.

Interested applicants should contact

William Godsoe gods9193@uidaho.edu Biological sciences University of Idaho

<http://www.webpages.uidaho.edu/~pellmyr/-pellmyr/labfront.htm> "The pure and simple truth is rarely pure and never simple."

gods9193@uidaho.edu gods9193@uidaho.edu

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## UKwazuluNatal EvolBiol

### UNIVERSITY OF KWAZULU-NATAL

All appointments will be in terms of the prevailing University Employment Equity Policy and the Employment Equity Plan of the faculty/division (available at <http://www.ukzn.ac.za/ESU>). The University reserves the right not to make an appointment or to stop the process at any stage to headhunt or re-advertise the post to meet its equity goals. Candidates who do not meet the minimum criteria will not be considered.

SENIOR LECTURER/ASSOCIATE PROFESSOR (1 POST)

5-YEAR FIXED-TERM APPOINTMENT EVOLUTIONARY BIOLOGY

SCHOOL OF BIOLOGICAL & CONSERVATION SCIENCES

PIETERMARITZBURG CAMPUS

REF NO.: SA17/2007

The School of Biological and Conservation Sciences is well established with a very active research profile and a substantial graduate school. It has excellent research facilities, including an animal house, comprehensive herbarium and botanical garden.

We are seeking a plant evolutionary biologist for a five-year fixed-term appointment associated with a newly established South African Research Chair in Evolutionary Biology. The successful applicant, who will support the teaching and research activities of the Chairholder, will have a strong background in evolutionary biol-

ogy and an established record of publications in peer-reviewed journals. The responsibilities will include teaching of undergraduate and Honours-level modules in the fields of evolutionary and pollination biology, and supervision of postgraduate students. The appointee will also be expected to conduct independent research as part of a group that focuses on the evolution of pollination systems in plants.

#### MINIMUM REQUIREMENTS:

A PhD and postdoctoral experience in a relevant field; Research experience in the fields of evolutionary biology and/or plant-animal interactions; Evidence of current research activity shown by at least five recent publications in the international peer-reviewed scientific literature; Relevant teaching experience at tertiary level.

#### ADVANTAGES:

A good working knowledge of molecular methods in evolutionary biology; Successful supervision of postgraduate students.

For further information visit the School website at <http://www.ukzn.ac.za/biology> or contact Prof. Steve Johnson at johnsonsd@ukzn.ac.za .

The remuneration package offered includes benefits and will be dependent on the qualifications and/or experience of the successful applicant. The selection process will commence on 30 April 2007 and will continue until a suitable candidate is appointed or a decision is taken not to fill the post.

Applicants are required to submit a covering letter highlighting their experience in, and providing evidence for, each of the minimum requirements and advantages as listed above, together with a detailed CV including the names, full addresses, fax numbers and e-mail addresses of three referees, to Mrs. CJ Bhebhe, Human Resources Administration, University of KwaZulu-Natal, Private Bag X01, Scottsville, 3209, Fax. No. +27 (0) 33 260 5356 or e-mail Bhebhec@ukzn.ac.za .

Please find our Email Disclaimer here: <http://www.ukzn.ac.za/disclaimer/> brothers@ukzn.ac.za brothers@ukzn.ac.za

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## UNewSouthWales 2 EvolBiol

As part of a Strategic Initiative in Evolutionary and Behavioural Ecology, the School of Biological, Earth and Environmental Sciences intend to appoint two continu-

ing academics at the Lecturer or Senior Lecturer level. There is considerable overlap between these positions as they are intended to build on and complement existing research strengths at UNSW. Applicants wishing to apply for both positions should submit separate applications.

Position 4905 is an appointment in adaptive evolutionary biology. The appointee will be expected to build a research program in the process-based study of adaptive evolution, to teach in evolution, ecology and whole-organism biology and to supervise honours and postgraduate students with interests in adaptive evolution. Preference may be given to applicants whose research involves the experimental study of adaptation using quantitative genetics, functional genomics, physiological techniques and/or ecologically-relevant manipulative experiments. Research should involve the testing of evolutionary theory. Research programs that are mostly descriptive (e.g. restricted to phylogeography, systematics, taxonomy or population genetics) will not be favoured.

Position 4906 is an appointment in behavioural ecology and behavioural evolution. The appointee will be expected to build a research program in behavioural ecology and evolution, to teach in animal behaviour, evolution, ecology and whole-organism biology and to supervise Honours and postgraduate students with interests in behaviour, ecology and evolution. Preference may be given to applicants whose research involves the testing of theory using experimental approaches, ecologically-relevant measures of fitness, the use of quantitative genetics and/or demonstration of broad ecological consequences. Skills and experience in experimental design and data analysis or the use of molecular tools may confer a further advantage in selection.

The base salary for Lecturer is A\$68,320 - A\$80,541 per year, Senior Lecturer is A\$82,982 - A\$95,202. Membership of a University approved superannuation scheme is a condition of employment for this position.

The appointment will be full time ongoing. Women and people from EEO groups are encouraged to apply. The University reserves the right to fill the position by invitation or not to fill the position.

Enquiries may be directed to Associate Professor Paul Adam, Head, School of Biological, Earth and Environmental Sciences on (61 2) 9385 2067, [p.adam@unsw.edu.au](mailto:p.adam@unsw.edu.au) or to Associate Professor Rob Brooks ([rob.brooks@unsw.edu.au](mailto:rob.brooks@unsw.edu.au))

An information package is available by clicking [HERE](mailto:HERE), or email [seniorads@unsw.edu.au](mailto:seniorads@unsw.edu.au). Interested applicants must

obtain the information package and include a cover letter in which they address the selection criteria for the relevant position in their application. They should also submit a CV including full publication list and contact details for three referees.

School of Biological, Earth and Environmental Sciences  
The University of New South Wales Kensington, Sydney 2052 NSW, Australia PH: +61-2-9385-2587 FAX: +61-2-9385-1558 <http://www.bees.unsw.edu.au/school/staff/brooks/brooksrob.html> Australasian Evolution Society: <http://www.evolutionau.org>

[rob.brooks@unsw.edu.au](mailto:rob.brooks@unsw.edu.au) [rob.brooks@unsw.edu.au](mailto:rob.brooks@unsw.edu.au)

## UPrague ResAssist EvolOfSex

Marie Curie Early Stage Training Fellow (Fixed-term)

Institute of Vertebrate Biology, Academy of Sciences and Charles University in Prague, Czech Republic

Salary: 1,900 Euro per month plus additional allowances as per Marie Curie Early Stage fellowships

The postholder will work with Professor Jan Zima in Prague to investigate the evolutionary balance between sexual and asexual reproduction in the ostracod *Eucypris virens* using molecular genetic approaches. Applicants must have a good grounding in evolutionary biology and experience of laboratory methods in molecular ecology. Sound knowledge of English is essential. This post is available from September 2007 for a period of 9 months.

This is a component project of a Marie Curie Research Training Network (for details, see <http://www.evirens.group.shef.ac.uk/index.htm>). The official working language of the network is English.

Closing Date: June 22, 2007

Contacts: Prof. Jan Zima ([jjzima@brno.cas.cz](mailto:jjzima@brno.cas.cz)), Dr Ruza Bruvo ([r.bruvo@sheffield.ac.uk](mailto:r.bruvo@sheffield.ac.uk)).

In accordance with Marie Curie mobility regulations, this fellowship is not available to Czech nationals or to other nationals who will have resided/worked in the Czech Republic for more than 12 months in the 3 years prior to starting the fellowship. Applicants who already have a PhD are not eligible. Further details can be found in the Marie Curie Early Stage training handbook (see sections 5.4 - 5.8) and FAQs available at [http://ec.europa.eu/research/fp6/mariecurie-actions/action/stage\\_en.html](http://ec.europa.eu/research/fp6/mariecurie-actions/action/stage_en.html). Ruza Bruvo

Department of Animal and Plant Sciences The University of Sheffield Western Bank Sheffield S10 2TN  
 Tel. +44 (0)114 22 20113  
 r.bruvo @ sheffield.ac.uk r.bruvo @ sheffield.ac.uk

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### Allelic dropout

Dear EvolDir members,

I amplify macaque faecal DNA using human microsatellite primers. In addition to the risk of contamination, the chance of allelic dropout is high due to the degraded condition of the source DNA. There are many reviews that talk about many plans (e.g. Taberlet et al. 1999 and Pompanon et al. 2005 etc. ) and methods (e.g.

multiple tube approach) to tackle this problem as a subset of the whole genotyping error, but I was wondering if there is any consensus in the scientific community about the solution. Any other suggestion about paternity study in macaques also will be appreciated.

Thank you in advance.

Deb

debapriyo@ncbs.res.in

– Debapriyo Chakraborty

Research Scholar Nature Conservation Foundation  
 3076/5, 4th Cross, Gokulam Park, Mysore - 570002,

India Website: [www.ncf-india.org](http://www.ncf-india.org) – Current Address:  
 Laboratory III National Centre For Biological Sciences Tata Institute of Fundamental Research University of Agricultural Sciences Campus Bangalore - 560065, India Telephone: 91-80-23666031  
 Website: [www.ncbs.res.in](http://www.ncbs.res.in) Debapriyo Chakraborty  
 <debapriyo@ncbs.res.in>

## Allelic dropout answers

Dear EvolDir members,

Thank you very much for your suggestions. The consensus seems to be the multitube approach and a pilot survey. All the communications are given below.

original query:

I amplify macaque faecal DNA using human microsatellite primers. In addition to the risk of contamination, the chance of allelic dropout is high due to the degraded condition of the source DNA. There are many reviews that talk about many plans (e.g. Taberlet et al. 1999 and Pompanon et al. 2005 etc. ) and methods (e.g. multiple tube approach) to tackle this problem as a subset of the whole genotyping error, but I was wondering if there is any consensus in the scientific community about the solution. Any other suggestion about paternity study in macaques also will be appreciated.

Thank you in advance.

Deb

debapriyo@ncbs.res.in

– Debapriyo Chakraborty

Research Scholar Nature Conservation Foundation  
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 India Website: [www.ncf-india.org](http://www.ncf-india.org) – Current Address:

Laboratory III National Centre For Biological Sciences Tata Institute of Fundamental Research University of Agricultural Sciences Campus Bangalore - 560065, India Telephone: 91-80-23666031  
 Website: [www.ncbs.res.in](http://www.ncbs.res.in) Debapriyo Chakraborty  
 <debapriyo@ncbs.res.in>

Dear Deb,

Without simplifying too much you can categorise all microsatellite errors into two classes, stochastic (allelic dropout, false alleles) and systematic (null alleles, contamination). Given that you're using DAN from faeces

and primers from another species, you can expect to have every type of error in your data.

I don't know much about dealing with systematic errors in paternity analysis but there is a review of the effect of null alleles (Dakin & Avise, *Heredity* 93:504-9). There is also a parentage analysis program that deals with null alleles (NewPatXL, available on Bill Amos' website <http://www.zoo.cam.ac.uk/zoostaff/amos>). For general approaches to estimating null allele frequencies see last Saturday's evoldir post on null alleles and population differentiation.

Regarding stochastic errors, I'm not sure if there's a consensus, but I think the best strategy is:

1. Clean the data by repeat-genotyping. How often? You'll never make it perfect so I'd say repeat as often as possible without limiting the number of loci you type. For example, in a typical study I suspect that repeating 10 loci 4 times will give you more informative data than repeating 5 loci 8 times, even if the error rate is high (providing your analysis method uses a realistic error model - see below). There are also ways of targeting repeats on lower quality samples (qPCR: Wandeler et al. *Mol Ecol* 12,1087-1093; statistical: Miller et al. *Genetics*, 160, 357-366).
2. Estimate the residual error rate in your data. This is typically done by duplicating a subset of your genotypes. You'll get most out of your data if your analysis method (see below) can tell the difference between allelic dropouts and false alleles, in which case you need to estimate these rates separately. Dan Haydon and I have written a method (Johnson & Haydon, *Genetics* 175, 827-842) and program (<http://www.stats.gla.ac.uk/~paulj/pedant.html>) for doing this.
3. Perform the parentage analysis, incorporating your estimated error rate(s). The best approach to doing this, particularly for data with frequent errors, is Hadfield et al. *Mol Ecol* 15, 3715-3730. The program (which is a package for R) estimates and adjusts for allelic dropout and false allele rates, so you can skip step 2. There is also a sibship reconstruction method by Jinfang Wang (Colony, <http://www.zoo.cam.ac.uk/ioz/-software.htm>, *Genetics* 166,1963-1979) that uses separate error rates.

Good luck, Paul

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 Paul Johnson Robertson Centre for Biostatistics Level 11, Boyd Orr Building University of Glasgow University Avenue Glasgow G12 8QQ, UK paulj@stats.gla.ac.uk  
<http://www.stats.gla.ac.uk/~paulj/index.html> Deb,

I doubt a consensus will emerge for lcnDNA samples,



since each study is so unique. Different combinations of sample type, marker, sample size, analysis method and inference drawn will encounter unique challenges. An easy solution is to repeat all specimens 8 times, but this is not feasible, nor is it necessary, for all types of studies.

The self-critical approach advocated by Gilbert et al 2005 (TREE 20, 541-544) is on the right track.

Ken "Ken Petren" <ken.petren@uc.edu>

Woodruff-209\_NoninvasiveGenotyping.pdf – David S. Woodruff Professor of Biological Sciences Ecology, Behavior and Evolution Section Division of Biological Sciences University of California San Diego La Jolla CA 92093-0116

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

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## Asobara tabida samples

Does anyone have a stock of the wasp *Asobara tabida*. Be best if it is being raised on *Drosophila subobscura*. I need a transfer for research. Thanks, Ron Woodruff.

R. C. Woodruff Distinguished Research Professor CoEditor-in-Chief, GENETICA Department of Biological Sciences Corner Merry and N. College Life Sciences Building Bowling Green State University Bowling Green, Ohio 43403 Telephone: 419-372-0376 Fax: 419-372-2024 email: rwoodru@bgsu.edu

rwoodru@bgsu.edu

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## BotanyPictures [www botanyphotos net](http://www.botanyphotos.net)

Dear all,

Last autumn I visited the Serres d'Auteuil in Paris, which houses a nice collection of New Caledonian plants. Using my search function at <http://www.botanyphotos.net/search.php> and type Caledonia

in the search file you can see images of New Caledonian genera such as: *Acridocarpus*, *Agathis*, *Araucaria*, *Austrobuxus*, *Baeckia*, *Bocquillonia*, *Dacrydium*, *Lepidospermum*, *Loxodiscus*, *Ochrosia*, *Oxera*, *Polyscias*, *Scaevola*, *Stenocarpus*, and *Xanthostemon*.

I have also uploaded many new pictures of the families: Acanthaceae: <http://www.botanyphotos.net/thumbnails.php?album=126> Commelinaceae: <http://www.botanyphotos.net/thumbnails.php?album=126> Erythroxylaceae: <http://www.botanyphotos.net/thumbnails.php?album=268>

>From the main page it is easy to find your favorite family albums by clicking on the scientific name (some synonyms are also provided). here you can also find several external links to interesting plant sites. If you are managing a website concerning plants, I would really appreciate it if you could create a link to my site.

Welcome and thanks for visiting!

Maarten Christenhusz [www.botanyphotos.net](http://www.botanyphotos.net) PS.: sorry for cross-posting.

maachr@utu.fi

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## Commercial Fragment analysis

Would anybody know of a good high-throughput commercial or university-run (that accepts outside orders) facility that runs fragment analysis on plant samples? It's easy to find sequencing facilities, but not as easy for fragment analysis...

Thanks! Camille Barr [camille.barr@mso.umt.edu](mailto:camille.barr@mso.umt.edu)

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## Darwinian Detectives

Darwinian Detectives Revealing the Natural History of Genes and Genomes, written by Norman A. Johnson 978-0-19-530675-0

Biology is often viewed today as a bipartisan field, with molecular level genetics guiding us into the future and natural history (including ecology, evolution, and conservation biology,) chaining us to a descriptive scientific past. In *Darwinian Detectives*, Norman Johnson bridges this divide, revealing how the tried and true

tools of natural history make sense of the newest genomic discoveries. Molecular scientists exploring newly sequenced genomes have stumbled upon quite a few surprises, including that only one to ten percent of the genetic material of animals actually codes for genes. What does the remaining 90-99% of the genome do? Why do some organisms have a much lower genome size than their close relatives? What were the genetic changes that were associated with us becoming human? As molecular biologists uncover these and other new mysteries, evolutionary geneticists are searching for answers to such questions. Norman Johnson captures the excitement of the hunt for our own genetic history. Through lively anecdotes, he explores how researchers detect natural selection acting on genes and what this genetic information tells us about human origins.

Please visit our site below to learn more about this title.

<http://www.oup.com/us/catalog/general/subject/-LifeSciences/Genetics/?view=usa&ci=9780195306750>

“Vaynshteyn, Alla” <alla.vaynshteyn@oup.com>  
 “Vaynshteyn, Alla” <alla.vaynshteyn@oup.com>

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## Drosophila virilis samples

Dear Colleagues,

We are working with *Drosophila virilis* group. We would need extra samples for developing a molecular species identification method. Does anybody have spare samples from the following species: *D. virilis*, *D. a. americana*, *D. a. texana*, *D. novamexicana*, *D. lummei*, *D. montana*, *D. laticola*, *D. borealis*, *D. flavomontana*, *D. littoralis*, *D. ezoana*, *D. kanekoi*?

Flies can be alive, frozen, dried or stored in ethanol.

Thanks a lot,

Yours,

Maaria Kankare, PhD Researcher Evolutionary Genetics Department of Biological and Environmental Sciences P.O. Box 35 FIN-40014 University of Jyväskylä Finland

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[mkankare@bytl.jyu.fi](mailto:mkankare@bytl.jyu.fi)

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## DukeU Drosophila Polymorphism Summer

Hi, all, If any of you know of a grad student with computational skills looking for a summer RA or a postdoc who's looking for something to do this summer, can you please pass this along? Thanks! –Mohamed

The Noor laboratory at Duke University seeks a PhD student (or recent postdoc) looking for summer, 2007, support to perform computational analyses on polymorphism in some newly acquired *Drosophila* genome sequences and assembly of a database. Those interested should have familiarity with a scripting language (e.g., Python, PERL), familiarity with database storage/retrieval (e.g., SQL or similar), and a basic familiarity with bioinformatics. Other useful skills include experience with Java, XML, and/ or HTML and a basic foundation in evolutionary genetics. If you are interested and would like more information, please drop an e-mail (no attachments please!) to Mohamed Noor ([noor@duke.edu](mailto:noor@duke.edu)) briefly indicating your interest and experience.

Mohamed A. F. Noor [noor@duke.edu](mailto:noor@duke.edu) Associate Professor Tel: 919-613-8156 Biology Department Lab: 919-613-8193 Box 90338 FAX: 919-660-7293 Duke University Durham, NC 27708 USA <http://www.biology.duke.edu/noorlab/> [noor@duke.edu](mailto:noor@duke.edu)  
[noor@duke.edu](mailto:noor@duke.edu)

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## Excursions around the Evolution meeting 2

Dear Brian,

I am still looking for companions, so if I could post this again? Thanks! == Lev

Dear Colleagues,

A couple of fellow evolutionary biologists have already decided to join me for the Rarotonga (Cook Islands) stop-over en route to the Evolution meeting. Gerald McCormack, a local naturalist and the creator of Cook Islands Biodiversity Heritage Trust (<http://-cookislands.bishopmuseum.org>), will advise us on the

best ways to enjoy Rarotonga marine and terrestrial life. I just noticed that AirNewZealand made CI stopovers free and tickets are still available for June 10th flight from LA to Rarotonga. So if anyone is still considering joining us, it's probably a good time to decide. I am also going to decide on accommodations and other details very soon.

Also still open for suggestions on after-the-meeting hikes on South Island.

– Lev Yampolsky

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

Lev Yampolsky <yampolsk@etsu.edu>

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## GMO FieldGuide

This is to announce the publication of an inexpensive new field guide that many evolutionary biologists and geneticists may find of special interest.

Written by John C. Avise, the book is entitled "A Field Guide to Little Known Genetically Engineered Organisms (Including Revisionary Interpretations about their Impact on World History).

The author guides readers on a fascinating behind-the-scenes journey into the little-known world of genetic engineering, describing the field marks, behaviors, and geographic ranges for 35 of the world's most top-secret genetically engineered species. Also described are the historical sagas and personal dramas behind each creature's artificial manufacture. From Migratory Chickens and Marijuana-sniffing Dogs to Fire-retardant Trees, Square Tomatoes, and Oil-drinking Bacteria, the creatures described in this richly illustrated field guide give new meaning to the old adage that "fiction is stranger than truth."

The book is available from Pensoft Publishers (<http://www.pensoft.net>). Enjoy!

John Avise <javise@uci.edu> John Avise  
<javise@uci.edu>

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## GeneticDistance with indels answers

Below are the answers I received. Many thanks to everyone who kindly wrote me.

All the best,

Cristina

### MY QUESTION

Dear All, is there some genetic software to measure genetic distance between taxa taking indels into account? We are studying chloroplast DNA in a number of angiosperms, and indels appear to be useful for evolutionary comparisons. Any help and comments will be greatly appreciated.

### ANSWERS

Hi Cristina Please check out my Sys Biol paper via publication link on home page below. I also know that GapCoder may be superceded with IndelCoder in SeqState written by Kai Muller. Müller K 2006. Incorporating information from length-mutational events into phylogenetic analysis. Mol Phyl Evol, 38: 667-676. Müller K 2005. SeqState - primer design and sequence statistics for phylogenetic DNA data sets. Appl Bioinformatics, 4: 65-69. These refer to analysis tools, rather than genetic distances, but frame the indel issue well I hope? With best wishes

Si Creer Post Doctoral Research Fellow Molecular Ecology and Fisheries Genetics Group School of Biological Sciences University Wales, Bangor Bangor Gwynedd LL57 2UW UK e-mail: s.creer@bangor.ac.uk Tel: +1248 382302 Fax: +1248 371644 Home Page: <<http://biology.bangor.ac.uk/~bssa0d/>> <http://biology.bangor.ac.uk/~bssa0d/> ———

ciao, tri scrivo in italiano perchè ho visto che sei di ROMA.... puoi usare il software GAPCODER (Young ND, Healy J (2003) GapCoder automates the use of indel characters in phylogenetic analysis. BMC Bioinformatics, 4, 1-6) che ti permette di ottenere un input file che considera gli indel come presenza-assenza. Questo nuovo datafile puo poi essere utilizzato in PAUP e in mrbayes 3.1 per calcolare le distanze genetiche. Inoltre, comunque questi due ultimi programmi ti permettono di considerare gli indel come fifth base. Prova ad utilizzare tutti i due i metodi e vedi se ottieni dei risultati diversi. Ciao Federica Costantini

Federica Costantini, PhD

Laboratorio di Ecologia sperimentale

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Pagina WWW:

<<http://www.ecology.unibo.it>> [http://-  
www.ecology.unibo.it](http://www.ecology.unibo.it)

<<http://www.ecology.unibo.it/page/federica.htm>>  
<http://www.ecology.unibo.it/page/federica.htm>

Cristina, I've played with coding them as 1 (sequence present) or 0 (sequence absent) or as multi-state characters (where there are several discrete classes of the same indel), and have used AMOVA to analyze sets of indels, both along with and instead of nucleotide sequence differences for the coding sequence. There are cases where they really help, and there are cases where they work better than nucleotide substitutions (typically dominated by transitional changes) for phylogenetic reconstruction. This work is with colleagues who are "just trying things out" and is not yet published, as far as I know. The idea is free. It runs against traditional usage, but the point of the exercise is to figure out the phylogeny, not be politically correct. - Peter Smouse

From: SMOUSE@AESOP.Rutgers.edu [mailto:SMOUSE@AESOP.Rutgers.edu]  
Sent: Wednesday, March 28, 2007 8:04 AM  
Subject: other: indels

J. Peter Gogarten

gogarten@gmail.com

Many programs allow to specify indels as missing data or as a character. Parsimony in Phylip by default uses gaps as a character, PAUP by default has them as missing data. If one treats gaps as characters, larger gaps sometimes are a problem, because each individual position is counted as a character. A solution is treat the individual indel as missing data, and to

form additional (0/1) characters for the absence/presence of a gap.

Reed A. Cartwright

Do you want to include indels in the distance measure or do you want to estimate distance with an algorithm that treats indels as something other than miss-

ing data? I can do the latter with my current research project. However, if the former is what you are after, then I caution against it because it would involve nearly arbitrary choices about how to weight indels and indel lengths with respect to substitutions.

In my work I use substitutions to establish evolutionary distance and calculate the proportion of indels per substitution. I feel that this is the proper way to do it. Email me if you are interested in my approach.

— / —

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>

## Genographer software answers

Other: Genographer.software.ANSWERS

Hi, Evol-Dir,

Here is my original post...

Hi Evol-Dir, I would like to use the program Genographer to analyze fluorescent AFLP data using 5 dyes (6FAM, VIC, NED, PET, and the size standard LIZ) run on an ABI 3730 machine. The latest version of Genographer <http://hordeum.oscs.montana.edu/genographer/> <<http://hordeum.oscs.montana.edu/genographer/>> does not recognize the LIZ (orange) dye, and thus cannot be used for data with more than 4 dyes. A Google search brought up an abstract ([http://www.intl-pag.org/13/abstracts/PAG13\\_P229.html](http://www.intl-pag.org/13/abstracts/PAG13_P229.html) <[http://www.intl-pag.org/13/abstracts/PAG13\\_P229.html](http://www.intl-pag.org/13/abstracts/PAG13_P229.html)> ) regarding a modification to the software that would allow analysis of this data, however I have not had any luck with follow up emails to the abstract authors or to other colleagues.

If anyone has written a modification to update Genographer and is willing to share it, or knows who to contact, please let me know.

Thanks for your help, Heidi

..And here are the two relevant emails I received in response to this (see below). The "unofficial" update to Genographer does exist (see email #1 below from Ben Sikes) however it requires yet another program that is no longer supported as an intermediary (GeneScan). The other response (see email #2 below from

Walter Durka) was a bit more promising, as it appears that Travis Blake is in fact developing a new version of Genographer that will import fluorescent AFLP profiles directly without having to use GeneScan. Genographer 2.0 can be downloaded now, but it is apparently not working on data with 5 dyes (yet).

A number of other emails suggested other programs I might try for scoring AFLPs (including PeakScanner, a new free program from ABI: [www.appliedbiosystems.com/PeakScanner](http://www.appliedbiosystems.com/PeakScanner) <<http://www.appliedbiosystems.com/PeakScanner>> ). For those interested, we have outlined a number of AFLP programs in Table 1 of a recent paper:

Meudt, HM & AC Clarke. 2007. Almost Forgotten or Latest Practice? AFLP applications, analyses and advances. Trends in Plant Science 12(3):106-117. doi:10.1016/j.tplants.2007.02.001 <<http://dx.doi.org/10.1016/j.tplants.2007.02.001>> Cheers,

Heidi

(Responses Below)

Email #1

>From Ben Sikes [bensikes@gmail.com]

I had a similar problem and did manage to get in contact with the guys who wrote that abstract. They gave me this message and the conversions worked fine on Genographer. Unfortunately the problem was that the 3730 files go straight into Genemapper and then are not usable in Genographer as it uses the Genescan data. In the end everyone in our groups has been 'pigeon-holed' into using Genemapper because ABI has monopolized how their data can be used... at least for now. Sorry for the bad news and I hope this helps.

Sincerely, Ben

On 11/18/06, Keenan Amundsen <[Keenan.Amundsen@ars.usda.gov](mailto:Keenan.Amundsen@ars.usda.gov)> <<mailto:Keenan.Amundsen@ars.usda.gov>> > wrote:

Ben,

There has not been an official update to Genographer, so we haven't made the changes available for download, but I am more than happy to send you what I have along with instructions for updating the "rusty" version. The program still relies on preprocessing data through GeneScan. ABI does not support this, but it can be done. Additionally there is a slight change in what I am sending you in that another researcher from Europe has had success in using newer versions of GeneScan to analyze her data. Also, let me know if you are working on a Mac instead of a PC and I can send those files instead.

This is an e-mail that I've sent out before:

There has been quite a bit of interest since PAG regarding the upgrades to Genographer and I'm happy to send you the modifications to update your version. There has not been an official upgrade to genographer and I'm not sure that there will be until some of the bugs are worked out, but hopefully these modification will get you by. Please open and read the file "TemporaryGenographerInstructions.doc"; it is a description of the modifications and file import process. If you would like a look at the \*.java files I am more than happy to send those as well. Let me know if you have any trouble downloading the attachments and I can resend them.

Keep in mind that we have only had success using an older

— / —

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>

## Help CreateEvol Debate thanks

Thanks to all who have forwarded suggestions, advice, encouragement and even warnings to me about my upcoming debate with Young Earth Creationist Terry Mortenson.

Many of you have offered rich and current examples of mutations that can be argued to have met the two criteria set forth in his question. Namely a) does it represent an increase in information and b) does it result in a new or novel function.

If you read the Answers in Genesis webpage (which I have extensively) you will see that they have already anticipated some of the obvious and favorite examples offered, namely that alleles that result in sickle cell anemia can offer some protection against malaria.

<http://www.answersingenesis.org/home/area/faq/dont-use.asp> <http://www.answersingenesis.org/home/area/faq/mutations.asp> None the less I now have a large number of excellent examples that I think will be effective. Yes, I am anticipating that the goal posts will be moved even as I speak, but again I think I am prepared for that. For strategic reasons (creationists read this forum) I do not intend to state which examples I plan to use but I will post a summary

of all that I have learned on my webpage shortly after the conclusion of the debate.

<http://www.uga.edu/cellbio/farmer.html> Thanks again for all your help and support. Thanks too for the warnings, they are well heeded.

-Mark Farmer

. Mark Farmer Cellular Biology University of Georgia Athens, GA 30602 USA Tel: 706 542-3383 FAX 706-542-4271

farmer@cb.uga.edu

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## Help CreateEvol debate

On Saturday May 5, 2007 I am scheduled to debate creationist Dr. Terry Mortenson of Answers in Genesis, in Loganville, GA. The topic of the debate is "Can Evolution Explain more Complex Species Arising from Simpler Life Forms? "

As part of the debate format we each have five minutes to answer a preplanned question to the other. His question for me is:

"Can you please explain (with documented research) one example of a mutation that has resulted in the addition of new genetic information for a new function in an organism?"

Since he asks for just one example I would love to present dozens, but I need your help. Please send to me concise examples (with references) of documented examples of the above. Feel free to pass this on to others as I would love to compile a huge body of examples.

Reply directly to: farmer@cb.uga.edu

Many thanks, Mark

Mark Farmer Cellular Biology University of Georgia Athens, GA 30602 USA Tel: 706 542-3383 FAX 706-542-4271

farmer@cb.uga.edu

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## Lepidoptera Evol Database

Dear All

I have already written to a number of you individually regarding a proposal we are writing to develop ButterflyBase into a genomic and organismal database for the Lepidoptera. This is a joint initiative with David Heckel in Jena and Owen McMillan and NESCent in Duke University. Over the long term we believe there is a need to establish a Lepidoptera-wide database which will process and link genomic sequences, ecological and molecular data in a fashion which will make gene-hunting easier. The establishment of a community-wide portal for accessing data comparable to FlyBase must surely be a priority for us as a community. The aim is initially to complement what is already available at SpodoBase, KaikoBase, and SilkDB, although if there is a community consensus the eventual aim would be a single web portal for lepidopteran comparative genomics and annotation. We are currently talking to EBI about hosting, but would mirror the site other areas (e.g. Asia and US) and, and the site could be given a general title (LepBase or LepGen springs to mind). Our grant proposal will develop only some of these goals, but different labs will contribute to different aspects, in a manner similar to the development of FlyBase. For our part, we have been invited to submit a proposal to the Bioinformatics and Biological Resources Fund from the BBSRC (a UK research council) to update ButterflyBase and convert it to the CHADO schema (this is the generic model organism database used by FlyBase et al see [www.gmod.org](http://www.gmod.org)). ButterflyBase ([www.gmod.org](http://www.gmod.org)) already hosts all publicly available Lepidopteran EST sequences in a clustered and annotated format. However, we believe, that it is time to move this to the next level and this requires community involvement.

If you feel able to support this proposal, would you be able to write a one page letter of support that addresses the following points:

State who you are, where you work, what sort of research you do, and who funds it Are you satisfied with the current availability of resources for Lepidopteran genomics and bioinformatics? Do you think there is a need for an international LepGen database? State in general what you think the major requirements would be If you agree with the concept behind LepGen, can you express your support for this BBSRC proposal? Would the funding of this BBSRC proposal and the establishment of LepGen stimulate additional funding opportunities for Lepidopteran and Arthropod bioinformatics in your country or community? The deadline for our proposal is 1 May.

We look forward to hearing from you

Yours sincerely,

Chris Jiggins and Alexie Papanicolaou

- contact details available at <http://heliconius.cap.ed.ac.uk/butterfly/home.php> Alexie Papanicolaou Entomology Max Planck Institute for Chemical Ecology Hans Knoell Str 8 Jena 07745 Germany Email [apapanicolaou@ice.mpg.de](mailto:apapanicolaou@ice.mpg.de) Tel +443641571561

Alexie Papanicolaou <[apapanicolaou@ice.mpg.de](mailto:apapanicolaou@ice.mpg.de)>

## MHC Cloning Artefacts answers

Hello Evoldir members, a few weeks ago I posted a question about MHC and cloning artefacts and I got a lot of really good answers which made it possible for me to solve the problem. So many thanks to you all that answered me and took your time, it was really helpful! Below my question I made a summary of most of the answers.

Please feel free to write to me if you have any more useful suggestions or any questions!

Best regards / Erik

email: [hageri@kth.se](mailto:hageri@kth.se)

My questions was:

Hello,

I read the discussion about MHC and cloning artefacts and I found it very interesting as I have a similar problem with very puzzling results. I study MHC in dogs (DLA) and to get the alleles in heterozygote individuals I use cloning (I use the GeneJET cloning kit K1221 from Fermentas). The problem is that I sometimes get more than two alleles per individual, sometimes as many as six different alleles in one single individual! This problem has occurred in around 50 % of the samples in each cloning and the incorrect ones differ every time and do not occur in specific individuals. Some of these alleles do not correspond to the diploid sequence at all (for example when the diploid ABI sequence indicates a T and G as a double peak, the cloned sequence indicates a clear C). Things that I have already done to avoid problems are the following (some are the same as the suggestions mentioned in answers in the discussion): \* HPLC purified primer. However, the differences between the alleles are not where the primers anneal but in between the annealing sites, so the artefacts can not be due to the imperfect synthesis of primers. \* I use Platinum Taq DNA polymerase from Invitrogen with high fidelity, which should generate few mis-

incorporated bases. However, the differences between the alleles are anyway far too many to be explained by mutations caused by the polymerase (at least according the ratio I know of, around 0.0006). \* The PCR product should be pure as I use a nested PCR with two different primer pairs which should enhance the purity. \* Contamination should not be a problem as I work in a special lab-room which is more or less DNA free. The diploid ABI sequences only shows two peaks at the polymorphic sites and one peak at the other sites and no indication of contamination between the samples.

So, with that said, what should I do? I read one comment where recombination between the E.coli were mentioned as a possible cause and that one should use a low or non recombinant strain to avoid this. I use a strain called RRI#61508;M15. At least one of the artefact alleles looks as a recombinant of two other alleles. Is there anyone that knows how common this problem is and if this really can cause so many artefacts as in my case? Could recombination be the problem? Or what other factor could cause this problem that I have??

And when I am writing, I will add a related question. How important is it to purify the PCR product when one is working with MHC genes and could purification improve sequence quality and reduce background signals?

I will be very grateful for all suggestions that could help me. I will put a summary of the answers on evoldir in a few weeks.

The answers were:

1.

the problems you describe are most likely PCR-errors introduced by the polymerase. Even the best proof-reading polymerase introduce enough errors that you find in clones, and the fact, that you can not reproduce the artifacts from the same sample hints to that. I had similar findings when cloning single copy genes: 1. base exchanges, normally found in only single clones ("background noise"), 2. other exchanges, that were common among clones and fitted with double peaks from direct sequencing (the real "alleles"). and 3. in very rare cases chimeric clones, that starts with sequences of one allele and ends with the other (Recombination during PCR: if in some rare cases elongation of a primer does not go over the reverse primer, the resulting fragment could in theory anneal to a template of the other allele in the next cycle and produce a mixture of both alleles).

The only chance I see to reduce such errors are: 1. Reduce the cycles in your PCRs to a minimum and 2. Do not use a nested PCR (try to design more specific

primers, if necessary).

When you try this and find that errors are reduced you can be sure, the problems were due to PCR-errors.

2.

I would hazard to guess that you might have a series of tandem duplications, although I don't know the dog genome sequence that well. But even if there is genomic sequence available, for complex regions like MHC, initial draft genomic sequence is not very reliable for inferring these type of issues, especially if not from your specific animal.

I would try using some technique to get out into the 5' or 3' genomic sequence flanking your genes to see what is happening. Also, try PCRing with a very long extension time and see if

— / —

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

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## ML DNA partitioning

Hello evoldir,

I'm looking for a phylogenetic reconstruction program implementing Maximum Likelihood which allows DNA data to be partitioned with different DNA substitution parameters (i.e. different models for different genes, in a concatenated multigene analysis).

I know Codeml can do this, but I'm looking for other programs and ones that are very fast!

thanks for your time and I'll post a summary if I get some replies,

Chris

Christopher West Wheat <cww10@psu.edu>

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## Micro HWEquilibrium

Hi all:

I am using microsatellites marker for parentage analysis, some of them are not in H-W equilibrium, this can be a problem in my analysis or in the future analysis???(eg. pedigree reconstruction)

Regards Rodrigo

rodrigo.badilla@gmail.com

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## Micro HWEquilibrium answers

Hi all:

Thanks to all who give me theirs consideration about the HWE problem. A lot of people ask me about the answers, here I send some of them... Regards Rodrigo

If you have microsat loci not showing H-W proportions you should be aware whether you have a relatively high amount of not-detected alleles ("null-alleles)giving you a surplus of homozygotes. Bo

yes, this can be a problem. It depends on why they are out of HWE, how much, and in what direction. Null alleles, Wahlund effect, (selection - unlikely on more than a very few loci)? There is quite a lot of literature on this. You might have seen the recent Evoldir posting about null alleles (question raised by Mike Ritchie) that covered a lot of it, including Selkoe & Toonen (2006). Paul

If you use software such as Cervus or Famoz for parentage analysis you can take into account the H-W disequilibrium. These softwares are able work with a level of H-W disequilibrium you can choose. I enjoy to see all the answers you will receive. Pascal

I think it will depend on which kind of parentage analysis are you doing. If you are using full exclusion I do not see why it should affect. If you are using a likelihood approach it will probably affect but it might not be to much trouble if the departure from HW is not big. Miguel

I think it depend on why they aren't in HWE. One reason might be null alleles. If this is the case, doing paternity/maternity analysis might be quite challenging. On the other hand, if some loci are out of HWE due to more biological causes (migration etc., ) then there shouldn't be much of a problem. Can you tell if you have more or fewer than the expected number of heterozygotes? Too few can be a sign of null alleles.

For other questions like estimating gene flow, many peo-



ple include a locus or two that are out of HWE. I'm not sure this is a good practice, but many of us have chosen this path, rather eliminating the locus from the data set. Jeff

Absolutely! H-W equilibrium is certainly an assumption of most parentage determination methods. While I'm not an expert on all the details of each parentage estimation method, I know for a fact that H-W genotype frequencies are assumed for exclusion analyses. Violation of H-W means that the frequency of genotypes is not just the product of the allele frequencies. Usually homozygotes are more frequent and heterozygotes less frequent than expected under H-W. I work with a tree species where individuals self about 10% of the time. Therefore mating is not random and H-W should not be met exactly. Null alleles at microsatellite loci can also lead to violation of H-W. In principle, it is possible to adjust expected genotype frequencies for increased autozygosity but I am unaware of any program that does this automatically. You should also think about the consequences of violation of the H-W assumption when interpreting your data even if you cannot adjust for it exactly. Good luck, Matt

You should probably start by reading: Hoffman JI, and Amos W (2005) Microsatellite genotyping errors: detection approaches, common sources and consequences for paternal exclusion. *Molecular Ecology* 14, 599-612. A, though it doesn't really touch on H-W equilibrium problems it is possible that there might be difficulties. Nobody has really assessed this problem in full. If your interest is paternity or genealogy construction you could look up Fernandez and Toro 2006 manuscript on a new software for genealogy construction that doesn't actually make assumptions of HW. Daniel

En el caso de que la información molecular sea "abundante" y muy informativa (valga la redundancia) no habría problema porque a lo que se reduce el análisis de paternidad es a buscar las incompatibilidades e ir excluyendo todas las parejas de padre y madre que no pueden ser y quedarnos con una sola pareja compatible. Trabajando con unos datos de dorada que se genotipaban para 11 micros encontramos casos que no tenían padres compatibles (nos confesó luego la empresa que en algún momento habían tenido unos reproductores que vendieron antes de que se pudieran tomar muestras), pero no encontramos individuos que pudieran asignarse a dos parejas diferentes. Si te salen varios padres compatibles tampoco hay problema porque a lo que se reduce es a calcular la probabilidad de que unos genotipos OBSERVADOS de los padres den unos genotipos OBSERVADOS de los hijos y así puedes ordenar las probabilidades de cada pareja. No hace falta asumir H-W, sólo asumir que no hay padres fuera de

los genotipados. Otro problema es si no te salen padres compatibles y quisieras inferir el genotipo más probable del padre fantasma (y luego buscarlo) o si quieres determinar "a priori" la probabilidad de que unos hijos vengan de una población determinada. Supongo que ahí sí que te hace falta asumir que hay equilibrio de H-W o que, si decides que no lo hay, que las frecuencias

— / —

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## Microarray of other species

Aloha Folks,

We are just about to start an expression array study using the completed genome sequence for a species that is not the focal species for our study. I would like to hear from folks who have used slides spotted with oligos derived from the sequence of a species other than the one they are studying. It seems to me that, with long enough oligos (we are going to use 60-mers), a pretty distant relative (or at least their DNA) could be hybridized against the slide but I would like to hear from people who have actually tried it including how distant their focal species was from the array'd species. How did the hybridization work across the slide. Did the annealing stringency have to be lowered so much for some spots that the higher identity genes got signal swamp-out?

Many thanks (Mahalo nui) for your help.

Cam Muir

Cam <[cmuir@big.uhh.hawaii.edu](mailto:cmuir@big.uhh.hawaii.edu)>

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## MrBayes DataPartition

Dear all,

I have encountered a problem when I tried to partition data using MrBayes. I have 60 genes and I try to partition them by genes and codon positions. When the

partitioning number was less than 150, it worked, but if I used the full 180 partitions, I got the error message said “could not find a division for character deviation 1” and crushed. I wonder if any of you have the same experiences. Does a limit exist for the total number of partitions that you can use in MrBayes? Thanks in advance.

Chenhong

Chenhong Li 316 Manter Hall School of Biological Sciences University of Nebraska - Lincoln Lincoln, NE 68588-0118 (402)472-3999 (402)436-7644

cli@unlserve.unl.edu

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## Multiple alignment software

Can anyone recommend a straightforward and free (or cheap) tool (web-based or software) for aligning multiple sequences of homologous genes (i.e., not just pairwise alignments)? Anyone have experience with Geneious? BioEdit? Thanks, Bob

Robert E. Marra, Ph.D. Plant Pathology & Ecology The Connecticut Agricultural Experiment Station 123 Huntington St New Haven CT 06511 phone: 203.974.8508 fax: 203.974.8502

Robert.Marra@po.state.ct.us

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## Multiple alignment software answers

To all:

Thanks for the many replies to my request for advice on sequence alignment software. Wow. There seems to be some agreement around BioEdit, T-Coffee, and a few others, but I think it easiest if just include a compiled list of the replies, edited for redundancy, for the most part. –Bob

—

Hi Robert, I have not used it extensively, but T-Coffee has worked nicely the times I have tried it. Both web-based <http://www.tcoffee.org/> and possible to download [http://www.tcoffee.org/Projects\\_home\\_page/-t\\_coffee\\_home\\_page.html](http://www.tcoffee.org/Projects_home_page/-t_coffee_home_page.html). Thomas Källman (PhD stu-

dent) Program in Evolutionary Functional genomics Evolutionary Biology Centre Uppsala University Norbyvägen 18D, 752 36 UPPSALA SWEDEN

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Try MEGA3 at [www.megasoftware.net](http://www.megasoftware.net). There is also a paper describing the software at that site.

Sudhir ——— Sudhir Kumar (s.kumar@asu.edu) Director, Center for Evol Func Genomics Biodesign Institute. BDA 240 Arizona State Univ Tempe, AZ 85287-5301 [www.kumarlab.net](http://www.kumarlab.net)

—

There are quite a few free packages available. I like multialign(<http://bioinfo.genopole-toulouse.prd.fr/-multalin/multalin.html>). It is web-based and allows you to view your sequences in a variety of formats. Joe Felsenstein manages a great website that contains a list of available software <http://evolution.genetics.washington.edu/phylip/-software.html#Management>

—

MAFFT, MUSCLE, and MAVID are three of the latest programs widely used for alignment. There are quite a few web servers so that you do not have to align locally on your machine. For links, see my dedicated website at <http://research.amnh.org/users/koloko/softlinks> (click “alignment”).

Best, Sergios

— Sergios-Orestis Kolokotronis Institute for Comparative Genomics American Museum of Natural History Central Park West @ 79th St. New York, NY 10024 -USA- tel +1 212 313 7648 koloko@amnh.org <http://koloko.net> Dept. of Ecology, Evolution, and Environmental Biology (E3B) Columbia University sk2059@columbia.edu

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Dear Robert,

If the alignment is difficult (many indels), we start with Clustal, which you can use on the web or download free.

We finish the alignment and check it in MacClade (not free but worth the price), where we use the nice color view to check and fine-tune the alignment by hand. MacClade will also translate the sequences, and for protein-coding genes it is best to align the amino acid sequences first. Indels due to sequencing artefacts are quickly spotted as frameshifts.

I’m guessing that there is freeware that you can use to translate, color, and align sites, although it presumably won’t do all the other things that MacClade does.

For rDNA it is best to take secondary structure into account when doing the alignment, but that is a whole different problem which others can tell you more about. We are only just getting started on it.

Good luck!

Bill C. William Birky, Jr. Professor of Ecology and Evolutionary Biology Member, Graduate Interdisciplinary Program in Genetics

Department of Ecology and Evolutionary Biology Biological Sciences West The University of Arizona Tucson, AZ

office: 520-626-6513 lab: 520-626-5108 <http://eebweb.arizona.edu/faculty/birky/home.html> —

hi Bob-

CLUSTALW, TCOFFEE, MUSCLE, KALIGN, PROBCONS, MAFFT they all have web interfaces if you google for them. <http://www.ebi.ac.uk/muscle/> <http://www.ebi.ac.uk/clustalw/> <http://www.ebi.ac.uk/t-coffee/> <http://www.ebi.ac.uk/kalign/> <http://www.ebi.ac.uk/mafft/> <http://bioperl.org/wiki/Multiple.sequence.alignment> <http://en.wikipedia.org/wiki/Multiple> Jason Stajich Miller Research Fellow University of California, Berkeley lab: 510.642.8441 <http://pmb.berkeley.edu/~taylor/people/js.html> <http://fungalgenomes.org/> —

There is a large number of free multiple sequence alignment tools:

- clustalw - well know often used, but gives not always good results (online: <http://www.ebi.ac.uk/clustalw/>)

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## NESCent CallForProposals

Call for Proposals NESCent Sabbatical Scholars, Working Groups and Catalysis Groups

The National Evolutionary Synthesis Center (NESCent) is now accepting proposals for sabbatical scholars, working groups and catalysis meetings. Proposals are accepted twice a year, with June 15 and December 1 deadlines. Proposals for post-doctoral fellowships are accepted at the December 1 deadline. Pro-

posals for short-term visitors are considered four times a year, with deadlines on January 1, April 1, July 1 and September 1. For more information, please see our website at <https://www.nescent.org/science/proposals.php>. — Karen Henry Assistant Director of Research Administration National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC 27705

email: [khenry@nescent.org](mailto:khenry@nescent.org) telephone: 919-668-4574 fax: 919-681-8444 <http://www.nescent.org/khenry@nescent.org>

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## NMNH Leiden TemminckFellowship

The Temminck-Fellowship programme for visiting senior researchers at the National Museum of Natural History 'Naturalis', Leiden, the Netherlands

Funds are available for one or more Temminck-fellows in 2007. Temminck-fellowships are intended for established, senior researchers from other countries, preferably from outside the European Union, in any of the fields that form the highlights of the Naturalis research programme (see <http://www.naturalis.nl>). Fellowships are available for periods of a minimum of three months to a maximum of twelve months, and the available budget is sufficient to cover travel and lodging for the recipient. Research costs cannot be covered. Temminck-fellows are expected to collaborate intensively with one or more Naturalis-researchers, and work on, e.g., scientific papers, books, and grant proposals, all with Naturalis as their (secondary) affiliation. Applications should be directed to [pauw@naturalis.nl](mailto:pauw@naturalis.nl), accompanied by a proposed budget, a c.v., and a detailed list of activities to be carried out during the fellowship period.

Dr. Menno Schilthuis Associate Director (Research) National Museum of Natural History 'Naturalis' P.O. Box 9517; 2300 RA Leiden; the Netherlands tel. (+31-0)-71-5687769; mobile: (+31-0)-6-22030313; home: (+31-0)-318-300380 E-mail: [schilthuis@naturalis.nl](mailto:schilthuis@naturalis.nl); [schilthuis@yahoo.com](mailto:schilthuis@yahoo.com) Second affiliation: Honorary Research Associate; Institute for Tropical Biology and Conservation; Universiti Malaysia Sabah; Locked Bag 2073; 88999 Kota Kinabalu; Malaysia

“Schilthuis, M.” <[Schilthuis@naturalis.nmm.nl](mailto:Schilthuis@naturalis.nmm.nl)>

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## Nulls and pop structure answers

Very many thanks to all those who replied to my query about null alleles and population structure. I had around 50 answers, which is testament to the extent of the problem.

Shortly before my submission Chapuis & Estoup published a simulation of the effects of various ways of estimating the frequency of “the” null allele and adjusting Fst estimates. They have also developed software to do this, which will surely become an essential resource to many:

Chapuis & Estoup 2007. Microsatellite null alleles and estimation of population differentiation. *Mol. Biol. Evol.* 24: 621-631.

<http://www.montpellier.inra.fr/URLB/> Cock van Oosterhout's MICROCHECKER (the current version is a major update from the last time I looked) applies one of these and is available here:

<http://www.microchecker.hull.ac.uk/> van Oosterhout, C., D. Weetman, and W. F. Hutchinson. 2006. Estimation and adjustment of microsatellite null alleles in nonequilibrium populations. *Mol Ecol Notes* 6:255-256.

So, if you are prepared to live with the assumptions of these (the main ones being that your problem is due to a single null, and no Wahlund effects) there is great scope for Fst-style analyses.

A nice surprise to me is that an imminent release of STRUCTURE allows treating loci as dominant markers so allowing analyses of potential sub-structure despite nulls. This is not available yet, but is to be released soon on the STRUCTURE website and Daniel Falush and colleagues have a paper (again, just out) in *MEN* on this.

<http://www.blackwell-synergy.com/doi/abs/10.1111/j.1471-8286.2007.01758.x> <http://pritch.bsd.uchicago.edu/structure.html> It may be worth mentioning here that there are also methods for relatedness and parentage:

Wagner AP, Creel S, Kalinowski ST (2006) Estimating relatedness and relationships using microsatellite loci with null alleles. *Heredity* 97:336-345.

I will not send all the responses I received out on EvolDir, as these are lengthy and the new developments bypass many of them, but I have compiled most of the

answers here:

<http://bio.st-and.ac.uk/supplemental/ritchie/-NullResponses.html> I would like to finish with two nice quotes:

My instincts are to think a lot about the data, keep your eye on the biology and total evidence, and be prepared to argue your case with editors. Sometimes they are unreasonable, but that can happen on any issue. - Paul Sunnucks

If we combine our problems, maybe there is food for an article “S.O.S. - Save Our Samples: survival guide to get the best out of the worst”. This might get a lot of citations. - Dieter Anseeuw

Best wishes & thanks again,

Mike

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

Website: <http://bio.st-andrews.ac.uk/staff/mgr.htm>  
Research website via: <http://tiree.st-and.ac.uk/cegg/-research.html> mgr@st-andrews.ac.uk

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## PAGE equipment

Dear EvolDir members Is anyone interested in PAGE equipment then let me know. We've got one power supply (EPS-3000 Series II; C.B.S. Scientific Company, Inc.) and a vertical tank for two gels on a turntable. You will only have to pay for shipping.

Anders

Anders S. Larsen Mimersgade 118, 5.tv. 2200 Copenhagen N Phone no. +4535854345 Mobile no. +4561334345Få 250 MB gratis lagerplads på MSN Hotmail

anderslarsen333@hotmail.com

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## PAUP 4 0 in OSX

I just bought a used Mac G4 PowerBook running OS

X (v. 3.9). I thought PAUP 4.0 would run in Classic mode, but when I drag the PAUP font file from my old G3 desktop to the "Classic" system folder, it disappears the minute I let go of the mouse button. This happens no matter where I try and drop the file. PAUP asks for this file as it opens, and will not run without finding it.

Has anyone figured out a work around for this?

Thanks.

PLEASE NOTE THE NEW EMAIL ADDRESS!! Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: (305) 254-3635 fax: (305) 969-6410 email: alan.meerow@ars.usda.gov

Alan.Meerow@ARS.USDA.GOV

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### PAUP 4 0 in OSX answers

Thanks to everyone who wrote me suggesting possible approaches to getting PAUP 4.0 b10 to run in classic mode on a G4 Powerbook. The fix that worked for me was to place the PAUP fontfile into the PAUP folder on my old G3 desktop Mac, then migrate that folder first to our network drive, then into the "Classic Applications" folder on my G4 Powerbook hard drive, thereby overwriting the previous installation of PAUP 4.0. Once I did that, PAUP started normally and is running fine.

Alan

PLEASE NOTE THE NEW EMAIL ADDRESS!! Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: (305) 254-3635 fax: (305) 969-6410 email: alan.meerow@ars.usda.gov

Alan.Meerow@ARS.USDA.GOV

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### Plant genomic DNA extraction Kits answers

Dear Evoldir,

I promise many of you I would post the replies to my

query about alternative DNA extraction Kits for plants. I did received some very useful replies and they are post anonymously bellow.

However, given there didn't seem to be enough evidence in direct comparisons I went ahead and order samples of a few kits to compare them myself. We tried DNEasy from Qiagen, Nucleospin from Macherey-Nagel, EZNA by Omega BioTek (sold by VWR), and the ChargeSwitch from Invitrogen (magnetic-bead based).

Bear in mind that we were using these kits in Arabidopsis which is a fairly benevolent plant to extract DNA, some of these might work quite differently in species that have lots of secondary compounds. Still, we found the same as some of the repliers told me: They all seem to work equally well.

We amplified PCR products and digest all samples with the same efficiency. The Nucleospin kit gave the highest yield but it is as expensive as the Qiagen, the EZNA is the cheapest and has comparable yields with the Qiagen. However, we were quite impressed with the ChargeSwitch. We haven't use the magnetic beads before, and they seem much easier to do, and harder to have students mess up the protocol. It also requires less centrifugation, which can be a plus in some situations. There are other companies that have magnetic beads kits now (including the EZNA) but we have not tried their kits. They might be worth giving a try.

Some repliers suggest that DNA extracted with different methods might have different shelf-life. This can be an important factor in some situations, but at the moment we can't comment on that.

Hope this is useful! And sorry it took me so long!

Paula

Replies:

"I used to work with Qiagen's kit, but recently switched to EZNA's kit for two reasons. First it was a price issue, EZNA's kit costs about 1/4 to 1/3 of Qiagen. Second, the company marketing the EZNA kit here in Sweden were pretty aggressive and directly targeted Qiagen users (they used to represent Qiagen but Qiagen decided to take over the distribution themselves). The end result is that our local chemistry store at the university now always stock the EZNA kit, meaning that we can always get a new kit within minutes without having to order and wait for a week or so to get it.

We haven't experienced any noticeable drop in DNA quality with EZNA's kit, although I think the yield for the EZNA kit might be a little lower (10-15% or so) than Qiagen's kit. We've also switched over to EZNA's

PCR purifying kit, where we also used to work with Qiagen's kit. Again the performance is about the same."

"I have compared both kits. Some of my students are able to get very good results with the EZNA kits. The other half have preferred to continue with the Qiaquick kits.

The EZNA kits do not have the same efficiency as the Qiaquick kits. So if you are working with limited DNA samples they may not be so good for you. In addition they don't seem to purify as well as the Qiaquick. However if you have lots of DNA and a robust PCR protocol the EZNA kits would be fine."

"The best method we used was after extraction perform an ethanol precipitation then the EZNA columns and that improves their purification ability enormously we did not figure a way to increase the efficiency of the recovery except to concentrate the DNA afterwards."

"Depending on the plant, you might be able to dispense with kits entirely. We do a high-throughput (2 96 well plates at a time, takes about 3 hours) CTAB/chloroform extraction with Mimulus that produces plentiful DNA of fine quality for sequencing and genotyping. It's a little fiddly and you need good equipment (a Genogrinder or some other way to grind the tissue in 96well format, a deep bucket rotor centrifuge, a Matrix 1250 extended tip pipettor – the same stuff Qiagen recommends for its 96-well plant DNEasy kits), but it is essentially free after that. We've had success with some other taxa using this protocol or variations (Silene, Solanum, leaf-eating

beetles) but some things with high secondaries (oaks, composites) yield lots of DNA but also end up with stuff coming through that inhibits PCR. Anyway, something to think about it you are looking at extracting thousands of samples on a regular basis."

"One of my friends uses the wizard kits (I can get the brand name if you need). He doesn't think the DNA comes out as clean as with Qiagen kits but he thinks he get a higher yield from them."

"Most of these kits are largely the same. If you would really like to save money, please see the attached protocol that we published this month - we compared it directly to Qiagen.

<http://www.blackwell-synergy.com/doi/pdf/10.1111/-j.1471-8286.2006.01549.x>

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

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## Prof Bruce Naylor

It is with great sadness that I convey the news of the passing of Prof. Bruce Naylor, Director of the Royal Tyrrell Museum.

Bruce succumbed to a short, unexpected illness and left behind his wife and two young children.

Bruce loved paleontology and was a good friend to those that knew him. His cowboy boots will be hard to fill (<http://www.tyrrellmuseum.com/events/-index2.php?strSection=1>).

Brian Golding

Golding@McMaster.CA Golding@McMaster.CA

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## SNP Heterozygote excess answers

Thanks to everyone who wrote me suggesting possible explanations for the heterozygote excess that I encounter within some of my SNP loci.

Some of these answers:

Original message Other: Heterozygote excess with SNP markers

Dear EvolDir members,

I'm working on the population genetics of seagrass, *Zostera marina*, using SNP loci. When I analyse the genotypic data for some natural populations I encounter high HWE departures. Some of the loci, especially some loci that are linked to each other in three different regions, have a high heterozygote excess. Some populations consist only of heterozygotes (sample size between 15-32). Based on the available msat data of these individuals, clones were excluded from SNP genotyping and subsequent data analysis. I'm not aware

of any paper that encounters similar HWE departures. Does any of you encounter similar problems or does any of you have an idea what the cause could be?

Any suggestions and tips will be greatly appreciated. Thanks

Steven Ferber

1) Natalia M. Belfiore wrote:

are you sure you're not genotyping multiple duplicated loci? When I see a locus with only hets (or nearly only), I assume the locus is duplicated and I'm amplifying 2 nearly identical copies of it. You could/should redesign the probe/genotype marker by extending it or moving it somehow to verify that you are only genotyping one copy of a locus.

Natalia M. Belfiore nmb@berkeley.edu 510 643 0986 510 666 0314

2) Jeff Dole wrote:

Steve, much of the literature going back decades show heterozygote excess/negative Fis, and the only reasonable interpretation that I know of is selection, either on the marker loci or others in linkage disequilibrium with them. Identity disequilibrium and selection against homozygotes in such disequilibrium would not produce this effect, as even if only outcrosses survive, Fis would be zero, not negative. Jeff

Jeff Dole Jepson Herbarium University of California Berkeley, CA 94720

3) Jeff Dole wrote:

Steve, to follow up; I'm not familiar with the genetics of seagrass and the interpretation of SNP's, but with gene duplication (e.g., polyploidy) it's possible to have an excess of apparent heterozygosity (ranging to fixed heterozygosity) by having two or more duplicate loci fixed for different alleles.

Jeff Dole Jepson Herbarium University of California Berkeley, CA 94720

4) Ellen M. Wijsman wrote:

Most likely you are picking up more than one locus with the same assay. Where you have only heterozygotes, you most probably have 2 monomorphic loci, each with one of the alleles. Where you have an excess of heterozygotes, you might have contamination, or more than one locus, one of which might either be monomorphic (in which case one homozygote will be missing), or both of which are polymorphic for the same alleles. These issues are well understood in SNP discovery and use in human genetics.

5) Carolien de Kovel wrote:

Beste Steven, Hoewel afwijkingen van HWE in mijn ervaring meestal technische fouten zijn, ga ik ervan uit dat je dat al hebt gecontroleerd.

Hele stukken alleen heterozygoot klinkt vreemd, maar het deed me denken aan zelf-incompatibiliteit ( a paart alleen met alpha etc.). Is dat een mogelijkheid?

Succes ermee, Carolien de Kovel

6) Anna Johansson wrote:

Hi! One explanation could be that you have duplicated genomic regions so that you actually are genotyping two loci with two different fixed alleles.

Anna Johansson Phd student, Lund university

7) Magdalena Zarowiecki wrote:

Well, usually they say things like that can be caused by migration; if two different and divergent populations come together, that would cause heterozygote excess (the Wahlund effect). But I agree your case is extreme.

Magdalena Zarowiecki

8) Monika wrote:

Hi Steven, I do not have experience with SNPs and I do not know much of the life cycle of seagrass, so I cannot give you much of advice on that. However, I used to work on trematode parasites which had complex life-cycle consisting of asexual and sexual stages, where we saw excess of heterozygotes (in terms of microsatellites) regularly, even we excluded all clonal individuals. In any case, I would be interested in responses you get. Can you please summarize them and forward to me?

cheers, Monika

9) Benoit Pujol wrote:

Dear Steven, isn't *Zostera* having some clonal reproduction which could explain your high HW departure? Regards, Ben

10) Benoit Pujol wrote:

Hi Steven, OK, but imagine one pool of clones that evolves towards fixing heterozygosity, which sounds logic. Now imagine a few differentiated clonal lineages which all fix heterozygosity but are all differentiated one from each other so that you obtain (A/B,C/D) and (E/F,G/H). Of course, I guess that a few generations of crosses among them will put all that at Hardy Weinberg unless mating isn't allowed between specific lineages.

Another, maybe more 'naturally realistic' explanation

— / —

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

363 2261 E-mail: S.Ferber@rug.nl Website: <http://marbee.fmns.rug.nl> S.Ferber@rug.nl S.Ferber@rug.nl

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## SNP analysis

Hi everyone,

I am in the process of genotyping SNPs as an alternative marker for the population genetic analysis of abalone. Could someone advise me on how the raw data should be processed in Excel (1& 3 for homozygotes, 2 for heterozygotes???) and then what population genetic software are currently favoured for SNPs analysis.

Thank you in advance Aletta Bester Genetics University of Stellenbosch South Africa

aeb@sun.ac.za

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## SNP heterozygote excess

Other: Heterozygote excess with SNP markers

Dear EvolDir members,

I'm working on the population genetics of seagrass, *Zostera marina*, using SNP loci. When I analyse the genotypic data for some natural populations I encounter high HWE departures. Some of the loci, especially some loci that are linked to each other in three different regions, have a high heterozygote excess. Some populations consist only of heterozygotes (sample size between 15-32). Based on the available msat data of these individuals, clones were excluded from SNP genotyping and subsequent data analysis. I'm not aware of any paper that encounters similar HWE departures. Does any of you encounter similar problems or does any of you have an idea what the cause could be?

Any suggestions and tips will be greatly appreciated. Thanks

Steven Ferber Ph.D student Department of Marine Benthic Ecology and Evolution Center for Ecological and Evolutionary Studies University of Groningen Biological Center Postbus 14 9751 NN Haren The Netherlands

Telephone : +31 (050) 363 2258 FAX : +31 (050)

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## Silene nutans samples

Dear all,

I am working on a research project concerning the study of the phylogeography of *Silene nutans* (Caryophyllaceae) in Europe, in collaboration with Pascal Touzet and Solenn Le Cadre of the Lab. of Genetics and Evolution of Plant Populations (University of Lille1, France). During the last 15 years, I have been collecting leaf material or seeds in more than 100 populations from Belgium, France, Sweden (and northern Finland), which can now be used for DNA analysis. This year we plan to collect (or we will receive material) from British populations. *Silene nutans* has a quite wide continental distribution in Europe, so we would like to extend your sampling area, especially to the east (and to complete the northern distribution). Anyone who could help us by collecting seeds and capsules (for 5-10 maternal plants) in wild populations of *Silene nutans* is welcome and can contact me for more information.

Best regards,

Fabienne Van Rossum

Department of Vascular Plants National Botanic Garden of Belgium Domein van Bouchout, BE-1860 Meise, Belgium e-mail: [fabienne.vanrossum@br.fgov.be](mailto:fabienne.vanrossum@br.fgov.be)

[fabienne@br.fgov.be](mailto:fabienne@br.fgov.be)

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## Software DAMBE

Dear All,

I have just uploaded a new version of DAMBE that fixed a few bugs in a few phylogenetic functions and also included the functions for RNA folding from the Vienna package. A sample file (CowtRNA.FAS) is included for you to learn the new functions.

1. To explore RNA folding, read in CowtRNA.FAS and click "Graphics|Plot RNA secondary structure". The first sequence folded with the default parameters is displayed. The available options are self-explanatory, es-



pecially for those who have already used the Vienna package. Click another sequence on the list will plot the secondary structure of that sequence.

To paste the structure into PowerPoint or any other software supporting graphics, you have two options (BMP file or Windows enhanced metafile). To paste the BMP image, first click "Edit|Copy image as BMP file" when the structure is displayed, and then click Paste when you are in PowerPoint. Transfer windows enhanced metafile needs one extra step. First you click "Edit|copy image as Windows enhanced metafile" when the structure is displayed, then then click 'Paste' in PowerPoint. At this point you will only see four small circular dots on the slide. Just click "Draw|ungroup" will plot the secondary structure in PowerPoint. Windows metafile allows you to produce graphics of any resolution and you can ungroup the graphic elements and do whatever modifications you wish.

2. The functions in the Vienna package also improved the previous function for predicting tRNA anticodon loop under the menu 'Seq.Analysis|tRNA anticodon and AC loop'.

3. Sometimes one may want to build a tree based on structural similarities. This is done by clicking "Phylogenetics|Tree with unaligned sequences|distance based on RNA secondary structure". Everything follows is self-explanatory. THIS FUNCTION IS VERY SLOW WITH LONG SEQUENCES BECAUSE IT NEEDS TO DO THE FOLDING, ALIGN THE STRUCTURES, AND COMPUTE THE EDIT DISTANCES WHICH ARE THEN MODIFIED TO GENERATE A TREE.

The release site of DAMBE is at:

<http://dambe.bio.uottawa.ca/dambe.asp> Best Xuhua

Dr. Xuhua Xia CAREG and Biology Department University of Ottawa 30 Marie Curie, P.O. Box 450, Station A Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 Fax: (613) 562-5486 URL: <http://dambe.bio.uottawa.ca> Xuhua Xia <Xuhua.Xia@uottawa.ca>

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## Software SeqVis 1 2

Dear All,

SeqVis is a program that allows users to visualize compositional heterogeneity in sequence alignments and to

determine whether the sequences can be assumed to have evolved under stationary, reversible and homogeneous conditions.

The latest version of the program, which allows data to be entered from a table, is now available for PCs and Linux. It can be obtained from:

<http://www.bio.usyd.edu.au/jermiin/SeqVis/-index.htm> . All the best,

Lars

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## Teaching Evol with animations

Dear friends,

I am looking for computer animations (applets, animated gifs, etc...) of natural selection, genetic drift, variation and gene flow. Does anyone know if there is an online library with teaching material like this ?????

Thanks for any help !!!

Voltolini

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamíferos (ECOMAM) Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: [jcvoltol@uol.com.br](mailto:jcvoltol@uol.com.br) Website do ECOMAM: <http://jcvoltol.sites.uol.com.br/> Fotos de Cursos: <http://jcvoltol.fotoblog.uol.com.br/> Currículo Lattes: <http://lattes.cnpq.br/8137155809735635> Fotos Artísticas: <http://voltolini.fotos.net.br/texturas> "Siamo tutti angeli con un'ala e possiamo volare soltanto se ciabbracciamo"

[jcvoltol@uol.com.br](mailto:jcvoltol@uol.com.br)

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## US passports

I just learned that if you are a US citizen attending a scientific meeting outside the US (now including

Canada and Mexico) and your passport needs to be renewed, there is a 10-week backlog because of the new regulations requiring passports for trips to Canada and Mexico; so apply as early as possible.

If you are organizing a symposium it would be a good idea to warn your US participants.

(Apparently it is not difficult to get into Canada and Mexico without a passport but it is much for difficult to return.)

– Chris Simon Professor, Ecology & Evolutionary Biology 75 North Eagleville Road, University of Connecticut Storrs, CT 06269-3043

chris.simon@uconn.edu (Please note that my old uconnvm address no longer works) Office (860) 486-4640; Lab (860) 486-3947; Fax (860) 486-6364, Biopharm 305D, 323,325

June-August: Victoria University of Wellington, School of Biological Sciences, Wellington, New Zealand Office: Kirk 611; Office phone: +64-4-463-5026; Fax: +64 4 463 5331; email: as above Home phone 64-4-970-0265

Home page: <http://hydrodictyon.eeb.uconn.edu/people/simon/Simon.htm> Reprints: <http://hydrodictyon.eeb.uconn.edu/projects/cicada/Resources/reprints.html> chris.simon@uconn.edu  
chris.simon@uconn.edu

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## VisitingGradStu Spain

Dear All,

I am conducting a comparative study of lifespan and mitochondrial evolution in parrots. Some critical samples for our underlying phylogeny are held at a zoo in the Canary Islands. My colleagues there have suggested that the easiest way to obtain the necessary data would be to do the extraction, PCR and sequencing at a suitable lab in the Canary Islands or elsewhere in Spain. I am writing to inquire whether anyone might be willing to host my graduate student as a short-term (3-4 weeks) visitor to collect these data. I have ample funds from NIH to cover any associated costs, and would be very happy to reciprocally host students in my own lab.

Sincerely, Tim Wright

Assistant Professor Department of Biology MSC 3AF New Mexico State University Las Cruces, NM 88003 Phone: 505-646-1136 E-mail: [wright@nmsu.edu](mailto:wright@nmsu.edu) New office: 375 Foster Hall New lab: 301 Foster Hall <http://biology-web.nmsu.edu/twright> “Timothy F. Wright”

[/biology-web.nmsu.edu/twright](http://biology-web.nmsu.edu/twright) “Timothy F. Wright” [<wright@nmsu.edu>](mailto:wright@nmsu.edu)

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## VisitingGradStu Spain 2

I apologize for re-posting the message below, but our e-mail server suffered a catastrophic failure Sunday night and many incoming messages were lost, including my own version of the original message from evoldir. If you happened to have responded to the original and have not heard back from me could I ask that you please resend you message to me at [wright@nmsu.edu](mailto:wright@nmsu.edu)? I want to be sure I respond to all messages.

Thank you, Tim Wright

Dear All,

I am conducting a comparative study of lifespan and mitochondrial evolution in parrots. Some critical samples for our underlying phylogeny are held at a zoo in the Canary Islands. My colleagues there have suggested that the easiest way to obtain the necessary data would be to do the extraction, PCR and sequencing at a suitable lab in the Canary Islands or elsewhere in Spain. I am writing to inquire whether anyone might be willing to host my graduate student as a short-term (3-4 weeks) visitor to collect these data. I have ample funds from NIH to cover any associated costs, and would be very happy to reciprocally host students in my own lab.

Sincerely, Tim Wright

Assistant Professor Department of Biology MSC 3AF New Mexico State University Las Cruces, NM 88003 Phone: 505-646-1136 E-mail: [wright@nmsu.edu](mailto:wright@nmsu.edu) New office: 375 Foster Hall New lab: 301 Foster Hall <http://biology-web.nmsu.edu/twright> “Timothy F. Wright” [<wright@nmsu.edu>](mailto:wright@nmsu.edu)

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## Working with multiple copy genes answers

Dear Evoldir members

Thanks to all of you that have answered my question about working with multiple copy genes for population genetics. Below I have compiled the mails I got in re-

sponse. In short, it seems that the conclusion is that even low-copy genes are a pain in the neck, and the best way is to try to develop locus-specific primers to amplify just one of the paralogs. The problem of false recombinants appearing during PCR amplification further complicates the issue. There are useful references in the answers.

Best regards

Xavier

The original question:

Hi everyone

We have been working in population genetics with several invertebrate groups. In an effort to develop new sequence-based markers, not just the usual mitochondrial genes, we have been doing sequencing work on nuclear genes (both introns and exons). We are finding in many cases that our target genes are multiple copy genes. Although the number of copies is low (nothing to do with rRNA genes, for instance) and probably there is some concerted evolution, when we clone the amplification products we end up with several alleles in most individuals.

My question is, what can we do with these data? cloning represents a lot of effort and I wonder if it is worth it. This kind of data violates assumptions for most analyses for phylogeny, phylogeography or population genetics. The concept of homogygosis or heterozygosis breaks down. They cannot be treated as polyploid, either, as the different copies are paralogous. Hence, different copies may follow different evolutionary models. To further complicate the issue, often the different copies are close together in chromosomes, so recombination is possible both intragene and intergene.

We can calculate some sort of "haplotype frequency" based on the different sequence types found in the clones but then, can we legitimately use these estimates in popgen programs? are there any program that can handle this information, or any published reference?

Any hint will be appreciated. I will of course compile and post the answers to the whole list.

Best regards

The answers:

Hi Xavier, Depending on whether you can distinguish (at the sequence level) different alleles per locus and different loci in each pcr, my suggestion would be to run the primers you have already designed on a few individuals, clone and sequence all alleles/loci from each and from there design gene specific primers. then use these in all your individuals. good luck! -mark

Mark A. Chapman [mchapman@plantbio.uga.edu](mailto:mchapman@plantbio.uga.edu)  
[www.theburkelab.org](http://www.theburkelab.org) University of Georgia Department of Plant Biology Miller Plant Sciences Bldg. Athens, GA 30602

<http://darwinawards.com/> [www.bbc.co.uk/littlebritain](http://www.bbc.co.uk/littlebritain) Dear Xavier, Are you sure the loci are in multiple copy? Or are you simply getting more than just the expected 2 loci per individual? That also happens due to cloning artifacts. Chimeras between alleles can be created during amplification and then isolated during cloning and sequencing. Are you using a PCR+1 protocol for cloning? In my experience, and I too have cloned non-rDNA nuclear loci, cloning artifacts are extremely common - they happened everytime until I started using PCR+1. Once I did that the number of alleles became 2. The drawback is that PCR+1 is a lot of work. But for pop. gen. it is a must.

Briefly, in PCR+1 you start-up by using a lot of one of the primers and 1/10 as much of the other (by the way, you have to use a proof reading polymerase - we use Easy-A because it also generates T overhangs and then we use TOPO-TA kit). You then do 1 last PCR cycle in which you add the primer that was in short supply but that primer has been modified so it has a RE cut site (a 10 bp tail is added with a restriction site).

After that last cycle, you clone the PCR products, amp a bunch of clones (using primers in the vector), clean them, and cut them with the restriction enzyme. Only sequence the ones that do cut. That means they were generated in that last cycle using the new primer and are not the result of priming by unfinished fragments (which generates the chimeras).

Dina - Dina M. Fonseca, PhD Associate Professor

Center for Vector Biology Rutgers University 180 Jones Avenue New Brunswick, NJ 08901 Phone:(732) 932 3146 Fax: (732) 932 9257 email: [dina-fons@rci.rutgers.edu](mailto:dina-fons@rci.rutgers.edu)

Why don't you try to make gene-trees for each gene, using the inferred haplotypes? The pseudogenes should form a cluster separate from the real genes, and you should be able to, at least for the exons, figure out which ones are real and pseudo, by looking for indels and stop-codons. If the pseudo ones are distant enough, you will probably not have to do much cloning, just enough to confirm your findings.

— / —

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>

## mtDNA ambiguous sites answers

Thanks to everyone who wrote me suggesting possible approaches to mtDNA ambiguous sequences (heteroplasmy or other). Some of these answers:

1) Have you considered the possibility that you have amplified Numts (nuclear copies of mitochondrial DNA fragments) along with your mitochondrial DNA? I have found Numts in beetle genomic DNA before. One way to get around the problem is to amplify a larger mtDNA fragment (for example, half of the mitochondrial genome). Most (but not all!) Numts consist in relatively short fragments. Therefore, amplifying a larger fragment often allows to get rid of the nuclear copies. Patrick

2) Hi, most probably you're not facing heteroplasmy (which is extremely rare in animals) but rather co-amplification of nuclear pseudogenes (numts). It's a pretty nasty job to get rid of them, mainly playing around with primers, PCR conditions or doing long-PCR reactions making advantage that nuclear insertions are rather short. You should really consider cloning at least a few samples to get clean seqs; a sequence analysis checking nonsynonymous substitutions, indels, damaged ORFs, GC content, ... should guide you to the authentic mtDNA seq and may help in primer development. See the refs below, mainly that one of Thalman et al, for some hints.

Which beetle are you working on and which primers did you use? regards, Wolfgang Bensasson D., Zhang D.X., Hartl D.L., and Hewitt G.M. (2001) Mitochondrial pseudogenes: evolution's misplaced witnesses. *Trends in Ecology and Evolution* 16, 314-321. \*Thalman O., Hebler J., Poinar H.N., Pääbo S., and Vigilant L. (2004) Unreliable mtDNA data due to nuclear insertions: a cautionary tale from analysis of humans and other great apes. *Molecular Ecology* 13, 321-335. \*Arctander P. (1995) Comparison of a mitochondrial gene and a corresponding nuclear pseudogene. *Proceedings of the Royal Society of London, B* 262, 13-19. Pons J., and Vogler A.P. (2005) Complex Pattern of Coalescence and Fast Evolution of a Mitochondrial rRNA Pseudogene in a Recent Radiation of Tiger Beetles. *Molecular Biology and Evolution* 22, 991-1000. Sunnucks P., and Hales D.F. (1996) Numerous Transposed Sequences of Mitochondrial Cytochrome Oxidase I-II in Aphids of the Genus *Sitobion*/

(Hemiptera: Aphididae). *Molecular Biology and Evolution* 13, 510-524. Zhang D.X. and Hewitt G.M. (1996) Nuclear integrations: challenges for mitochondrial DNA markers. *Trends in Ecology and Evolution* 11, 247-251. Dr. Wolfgang Arthofer Universität für Bodenkultur, Wien Institut für Forstentomologie, Forstpathologie und Forstschutz Hasenauerstrasse 38, A-1190 Wien, Austria wolfgang.arthofer@boku.ac.at <mailto:wolfgang.arthofer@boku.ac.at> <http://iff.boku.ac.at>

3) Hi, Fotini Are you sure that the results are not caused by the presence of pseudogenes in the nucleus? Are the problems present in both genes or only one of them and in cases where there is only a single difference have you checked that it does not result in a stop codon which could clearly indicate that it was pseudogenes. Kind regards, Søren  
4) Answer: Your problem may be with nuclear copies of the mtDNA rather than with mtDNA heteroplasmy. If you can determine the nuclear sequence, you may be able to "subtract" it from the hetero sequence. There are also other possible solutions. See: Sorenson, M.D. & T.W. Quinn. 1998. Numts: A challenge for avian systematics and population biology. *The Auk* 115: 214-221. Sorenson, M.D. & R.C. Fleischer. 1996. Multiple independent transpositions of mitochondrial DNA control region sequences to the nucleus. *Proceedings of the National Academy of Science USA* 93:15239-15243. Question: Thank you very much for your response. I already read your papers but I don't think that I have amplified Numts. When I checked for amino acid changes in these sites I only found synonymous mutations and no stop codons. Additionally DNA was extracted for tissue very rich in muscle (beetle legs).

What do you think about it? Is it enough to exclude Numts case? Answer: In general, I'd say that the above is not sufficient evidence. The example highlighted in our 1998 paper is one where a numt was amplified from muscle tissue. Even if you have a very high ratio of mtDNA to nuclear copies, you can still amplify the nuclear copy if the primers you are using match the nuclear sequence better. As for the patterns of change, I would expect most substitutions between mtDNA and a recently evolved numt to be 3rd position transitions. The reason is that the numt evolves more slowly (given better DNA repair mechanisms in the nucleus), such that most of the change represent subsequent substitutions in the mtDNA copy. As a next step, I would first ask about your primers. Are they "universal" primers developed from other species? Do the primers incorporate degenerate sites to accommodate likely variation at 3rd

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To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

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## mtDNA data analysis

Other: mtDNA data analysese

Dear EvolDir members, based on mtDNA sequence data, I found very high levels of haplotype diversity ( $h > 0.8$ ) and very low nucleotidic diversity in local samples of a sea urchin and no clear geographic patterns are evident. I am wondering whether it is possible to apply a Bayesian assignment test to mtDNA sequence data in order to give insight on population genetic structuring. At my knowledge, the only program handling sequence data for this purpose is STRUCTURE, but its use for sequence data is not recommended by the authors. It can be used only for purely exploratory analyses. Any suggestions and tips will be greatly appreciated. Thanks ciao

Michele Barbieri Ph.D. student Università di Pisa Dipartimento di Biologia Unità di Biologia Marina ed Ecologia Via A. Volta 6, 56126, Pisa Italy (I)

fax: +39 050 2211410

mbarbieri@biologia.unipi.it mbarbieri@biologia.unipi.it

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## mtDNA extraction

Dear all,

It has been a while I asked on EvolDir some help with my problems of ambiguous sites on mitochondrial DNA sequences.

In order to verify the origin of these ambiguities (nuclear or mitochondrial) I search for a simple and quick method or even better a kit extracting only mtDNA from specimens or from whole genomic DNA (already extracted from insects).

Any help would be appreciated.

Best regards,

Fotini Koutroumpa

Fotini KOUTROUMPA Porte 128 Laboratoire de Biologie des Ligneux et des Grandes Cultures UPRES EA 1207 Université d'Orléans Rue de Chartres BP 6759 45 067 ORLEANS Cedex 2 FRANCE Tel.: 02 38 49 43 32

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Fotini KOUTROUMPA <fotini.koutroumpa@univ-orleans.fr>

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## PostDocs

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### CNRS Gif sur Yvette DrosophilaSystematics

CNRS POST DOCTORAL POSITION IN EVOLUTIONARY SYSTEMATICS OF DROSOPHILIDAE IN THE AFROTROPICAL REGION Gif-sur-Yvette (LEGS, France)

We seek one enthusiastic researcher to join our lab for a collaborative study supported by an ANR project. The post-doc is for one year (possible renewal once) starting by september-october 2007 but not later than January 1st, 2008.

Drosophilidae (Diptera) represent a unique study model in evolutionary biology understood in its widest sense. Recent work highlights the need to combine both morphological and molecular approaches even for a relatively well-known group like drosophila. Besides the value of the taxonomy itself, biosystematics also involves an understanding of the phylogenetic relationships between species in order to propose evolutionary scenarios retracing their history. Obtaining reliable phylogenies is central in comparative studies, where the aim is to understand, for instance, the origin and nature of adaptations and the moment they occurred during species diversification. Such an approach, developed over many years in the laboratory, particularly by Daniel Lachaise, is at the heart of a series of ongoing research programmes involving several researchers in the lab. The research project is centered around evaluating the role of insularity and fragmentation of continental habitats in the distribution of certain groups of species especially in the southwestern Indian Ocean.

The candidate must be experienced in morphological and molecular systematics (any kind of organisms). This means a knowledge and the capability of having a

critical approach of all the tools required for morphological and molecular analyses and especially those used for phylogenetical reconstruction. The candidate must also be interested in bio- and phylogeography. Moreover, he/she must have the capacity and willingness to conduct field work especially in Madagascar.

Informal inquiries as well as applications (letter detailing your experience, a full CV, PDF's of your most significant publications and references) should be mailed to : Marie-Louise CARIOU ([marie-louise.cariou@legs.cnrs-gif.fr](mailto:marie-louise.cariou@legs.cnrs-gif.fr)) Pierre CAPY ([pierre.capy@legs.cnrs-gif.fr](mailto:pierre.capy@legs.cnrs-gif.fr)) Dominique JOLY ([dominique.joly@legs.cnrs-gif.fr](mailto:dominique.joly@legs.cnrs-gif.fr)) Jean-François SILVAIN ([jean-francois.silvain@legs.cnrs-gif.fr](mailto:jean-francois.silvain@legs.cnrs-gif.fr))

Dominique JOLY Laboratoire Evolution, Genomes et Speciation CNRS - UPR 9034 - bat 13 Avenue de la Terrasse F-91198 Gif sur Yvette Cedex France Tel: (33) 1 69 82 37 34 Fax: (33) 1 69 82 37 36 E-mail: [joly@legs.cnrs-gif.fr](mailto:joly@legs.cnrs-gif.fr) Web: <http://www.legs.cnrs-gif.fr/> Dominique Joly <[Dominique.Joly@legs.cnrs-gif.fr](mailto:Dominique.Joly@legs.cnrs-gif.fr)>

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### CNRS Lyon EvoDevo

CNRS postdoc position available

<https://www2.cnrs.fr/DRH/post-docs07/?pid=-1&action=view&idx9&lang=en>

Diversity of sex determination in fish: functional genetic analysis of sex chromosomes in the platyfish *Xiphophorus maculatus*.

- Description of the project In contrast to the situation observed in mammals and birds, sex determination is hypervariable and evolves extremely rapidly in fish. This variability is potentially associated with the for-

mation of new master sex-determining genes and new sex chromosomes. Hence, fish represent an outstanding model for the study of the evolution of sex determination, sex chromosomes and sex-linked traits. Understanding the molecular and evolutionary mechanisms involved in the diversity of sex determination requires the identification of master genes controlling the sex of individuals. The only gene of this type identified so far in fish, *dmrt1bY* in the medaka, is present in only a restricted number of species. Due to the absence of recognizable sex chromosomes and sex-linked molecular markers, zebrafish and both pufferfishes *Fugu* and *Tetraodon*, with almost completely sequenced genomes, are not suitable for this type of analysis. Hence, new models are required to study sex determination in fish. The platyfish *Xiphophorus maculatus* is an aquarium fish reputed for its use in cancer research. Due to the availability of numerous molecular markers delimiting the sex-determining region, this species is particularly suitable to study the control of sexual dimorphism. Our major goal is to identify through positional cloning and to characterize at both functional and evolutionary levels the master sex-determining gene of the platyfish, as well as other sex chromosomal genes involved in pigmentation, sexual development and melanoma formation. Bacterial artificial chromosome contigs from both X and Y chromosomes have been already constructed and are being sequenced to completion in collaboration with the Genoscope sequencing center. The expression, function, genomic localization and evolution of the identified genes will be studied in platyfish and other fish models including killifish, medaka and zebrafish, as well as in guppies and mollies, which are important biological models closely related to the platyfish. This study has implications for cancer research through the identification of genes involved in the formation of melanoma, as well as for aquaculture, for which molecular sexing and manipulation of sex determination are important economical challenges.

- Candidat profil The candidate will analyse at the functional level the genes identified on the sex chromosomes of the platyfish. He/she should be highly motivated by research in the field of "Evo/devo" and be experienced in methods used in fish developmental biology. Knowledge in bioinformatics and molecular evolution would be of advantage. The candidate should be able to work autonomously and demonstrate interest in pluridisciplinary scientific interactions inside as well as outside of the institute. - Duration of project 1 year - Laboratory of project UMR 5242 Rhône Auvergne (07) Institut de Génomique Fonctionnelle de Lyon Lyon - Contact Prof. Jean-Nicolas VOLFF jean-nicolas.volff@ens-lyon.fr

Frederic.Brunet@ens-lyon.fr

Frederic.Brunet@ens-lyon.fr

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## CNRS Paris HumanPopGenet

POST-DOCTORAL POSITION Human Population Genetics and Immunity, CNRS-INSTITUT PASTEUR, Paris

Population genomics of human innate immunity receptors : genetic diversity and natural selection

\* Description of the project Infectious diseases have played a major role in the evolution of modern humans because they have been paramount among the threats to health and survival for most of human evolutionary history. Natural selection is a major force behind the shaping of patterns of human genome variability. Inferences concerning the action of natural selection in the human genome provide a powerful tool for predicting regions of the genome potentially associated with disease. Genetic variants influencing human susceptibility to disease are likely to affect the fitness of the organism, unless the disease concerned begins late in the life. There is therefore an intimate relationship between disease and selection that can be exploited for the identification of candidate disease loci. As infectious diseases have exerted, and exert, strong selection pressures, the identification of selected loci or variants of immunity-related genes may provide insight into immunological defense mechanisms and highlight host pathways playing an important role in pathogen resistance. To date, some of the strongest evidence for selection in the human genome has been obtained for human genes involved in the immune response or host-pathogen interactions (MHC, G6PD, CCR5), but few studies have investigated the extent to which pathogens have exerted selective pressure on the innate immune system.

The major goal of our research is to investigate the extent to which natural selection has shaped the patterns of genetic variability of human genes involved in innate immunity. The innate immune system governs the initial detection of pathogens and stimulates the first line of host defense. In this context, we have recently identified distinctive patterns of selection in two closely related innate immunity genes (DC-SIGN and L-SIGN) (Barreiro et al. 2005. *Am J Hum Genet*). We have further identified two variants in the DC-SIGN promoter region associated with stronger protection against the

development of TB (Barreiro et al. 2006. PLoS Med). These population genetic approaches have allowed us to show that the patterns of genetic diversity of another innate immunity gene, MBL2, are compatible with neutrality, suggesting a largely redundant role for this lectin in immune responses (Verdu et al. 2006. Hum Mol Genet). In the context of the present project, we aim to investigate the selective pressures imposed by the presence of pathogens on genes and gene families encoding pattern-recognition receptors (PRRs), such as Toll-like receptors, C-type lectin receptors and scavenger receptors. These PRRs have been shown to recognize pathogen-derived molecular patterns or to play key roles in the initial steps of the immune response. This study, which integrates molecular and population genetics and bioinformatics approaches, will allow us to determine the extent to which natural selection has shaped the patterns of variation of these genes, and to identify those genes or gene families, variations in which may affect susceptibility to infectious diseases.

The successful candidate will work in the CNRS Unit URA3012 at Institut Pasteur in Paris. The main research lines of this Unit are the study of human, vectorial and microbial diversity, the interactions among these populations, and the molecular mechanisms involved in host protection against pathogens. In this context, the candidate will interact with scientists in France (Institut Pasteur, Necker Medical School, Muséum National d'Histoire Naturelle, IRD Montpellier) working in population genetics or other different but highly complementary disciplines (Immunology, Evolutionary Biology, Microbiology, Anthropology, Epidemiology). In addition, core facilities for genomic studies (sequencing, genotyping) are available in Institut Pasteur Campus. This, together with our international collaborations (Universities of Cambridge, Oxford, Yale, Chicago, Barcelona), will provide an excellent framework to carry out this research project.

\* Candidate profile The successful candidate will be expected to hold a Ph.D. in the field of population genetics or genomics and have a number of international publications in the relevant field. Applicants are required to have research experience in basic molecular biology techniques (sequencing, genotyping, Real-Time PCR), training in human genetics or population genetics, and bioinformatics skills in genetic data analyses. In addition, strong background in theoretical population genetics, statistics, and computer modeling by simulation would be an advantage. A willingness to engage in inter-disciplinary research in population genetics and evolution, or

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

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## CSIRO Perth EvolEpigenetics

POSTDOCTORAL FELLOW (EPIGENETICS) -  
CSIRO ENTOMOLOGY (Perth, Australia)

We are seeking a highly motivated postdoctoral fellow to investigate the molecular mechanisms underlying trans-generational inheritance of epigenetically-regulated detoxification and developmental gene expression in an animal model system, the aphid *Myzus persicae*. Aphids are an ideal model for studying epigenetic inheritance because of their capacity for clonal reproduction. The project will focus initially on a detoxification gene locus known to be regulated epigenetically via DNA methylation, which is often associated with epigenetic inheritance of traits in plants and animals. The change in methylation pattern of this gene and the associated insecticide resistance phenotype is maintained for several generations in the absence of the insecticide trigger, and a PCR test is available to assess the methylation status of the gene. It was once thought that DNA methylation was rare in insects but it now appears that the low levels of DNA methylation observed in *Drosophila* is an exception rather than the rule. Interestingly, it appears that the same genes regulate DNA methylation in aphids and vertebrates: We have already identified in the currently-unassembled aphid genome orthologues for three vertebrate DNA methyltransferases.

One might expect that asexually-reproducing species like aphids would rely heavily on epigenetic mechanisms. It is known that polyphagous aphids, such as *M. persicae*, take 2-3 generations to achieve maximum reproductive performance after being transferred to a new host plant. Epigenetic regulation of detoxification genes could be the mechanism enabling these species to adapt quickly to different host plants. This project will take maximum advantage of aphid genomics tools now becoming available, including a full genome sequence.

APPLICATIONS (until 31 May, 2007)

More information about the CSIRO can be found at [www.csiro.au](http://www.csiro.au) <<http://www.csiro.au>> . A full description of the position can be found under the sub-heading Careers. CSIRO prefers applications be lodged



online via this careers site.

You are required to include two documents

- (1) "Covering Letter Addressing the Selection Criteria" and
- (2) "Resume or CV" including the names of at least two referees.

Note: Applications that do not address the selection criteria will not be considered.

If you experience difficulties applying online call 1300 301 509 and someone will be able to assist you. Outside business hours please email: [csiro-careers@csiro.au](mailto:csiro-careers@csiro.au) <<mailto:csiro-careers@csiro.au>>

If you are unable to lodge your application online you can post your application to:

CSIRO Careers Online PO Box 225 DICKSON ACT 2602 or fax your application (quoting reference number 2007/240 to (02) 6246 4068.)

If after reading the selection documentation you require further information please contact Dr Owain Edwards via email [Owain.Edwards@csiro.au](mailto:Owain.Edwards@csiro.au) or phone +61 8 9333 6401.

Do not email your application to Dr Edwards, any applications received by this method will not be accepted.

Owain Edwards, Principal Research Scientist Stream Leader, Applied Genomics CSIRO Entomology Centre for Environment and Life Sciences (CELS) Floreat Park, WA 6014 AUSTRALIA

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### CollegeWilliamMary Biomath

The Department of Biology at the College of William and Mary seeks applications for a two year Visiting Assistant Professor postdoctoral position in biomathematics. The candidate should be trained in modeling approaches to population ecology and evolution and exhibit a sincere commitment to undergraduate education and research. Specifically, the biomath postdoc will mentor undergraduates in quantitative and modeling projects, related to population ecology and evolution, and collaborate with faculty in the biology, mathematics, and applied science departments on new and existing research projects. The postdoc will also help develop lab activities associated with an introductory biomathematical modeling class. Therefore, some experience of empirical systems is strongly

desired. More information about recent biomathematics projects and faculty involved with this group can be found at <http://jpswad.people.wm.edu/iibbs/-home.htm> Please forward this information to anyone you think may be interested.

Informal enquiries and requests for more information should be directed to Dan Cristol ([dacris@wm.edu](mailto:dacris@wm.edu)) or John Swaddle ([jpswad@wm.edu](mailto:jpswad@wm.edu)) in the Biology department, and Sebastian Schreiber ([sjschr@wm.edu](mailto:sjschr@wm.edu)) in the Mathematics department. Review begins April 20, 2007 and will continue until an appointment is made. Submit a letter of application, curriculum vitae, statements of research plans and teaching philosophy, and three letters of reference to Biomathematics Search Committee, Department of Biology, The College of William and Mary, P.O. Box 8795, Williamsburg, VA 23187-8795. The College is an EEO/AA employer.

Dr. John Swaddle Director of Environmental Science and Policy Associate Professor Biology Department College of William and Mary Williamsburg, VA 23185 <http://jpswad.people.wm.edu/> Tel. 757.221.2231

John Swaddle <[jpswad@wm.edu](mailto:jpswad@wm.edu)>

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### CollegeWilliamMary EvolutionaryPhysiology

EVOLUTIONARY PHYSIOLOGY Postdoctoral Position, College of William and Mary. A postdoctoral position will be available beginning August of 2007, renewable through May 2009, to investigate the evolution of complex neuroendocrine pathways. Applicants should have a PhD prior to August 2007 and experience in one or more of these areas: physiological ecology, neuroendocrinology, behavior, evolutionary biology, physiology, or cell and molecular biology. The research focus is on the contribution of genetic variation and phenotypic plasticity to the evolution of the photoneuroendocrine pathway in mammals. This pathway integrates photoperiod and other environmental information to regulate reproductive, physiological and behavioral responses to seasons. The model system is a wild-derived laboratory colony of white-footed mice (*Peromyscus leucopus*). The successful candidate will conduct collaborative research, help supervise students in the research laboratory, and teach a one semester course in animal physiology during the spring. More details on the research are available at: <http://faculty.wm.edu/-pdheid>. The College of William and Mary is a <sup>3</sup>Public

Ivy<sup>2</sup> with 5500 undergraduate enrollment, an excellent undergraduate program, and a strong research tradition. Starting salary is \$39,000 plus benefits. Contact information is available for the previous postdoctoral fellows (both in or about to begin permanent positions). Please send curriculum vita, a brief description of research interests/experience, and the names and contact information of three references to: Dr. Paul Heideman, Chair, Department of Biology, P.O. Box 8795, College of William and Mary, Williamsburg, VA 23187-8795; e-mail: pdheid@wm.edu. Review of applications begins immediately and continues until the position is filled. The College of William and Mary is an Affirmative Action/Equal Opportunity Employer.

Paul D. Heideman, Professor and Chair Department of Biology email: pdheid@wm.edu College of William and Mary P.O. Box 8795 FAX: 757-221-6483 Williamsburg, VA 23187-8795 Ph: 757-221-2239

<http://pdheid.people.wm.edu/> Paul Heideman <pdheid@wm.edu>

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## CornellU GenetSpeciation

A postdoctoral position in behavioral genetics and speciation is available in the laboratory of Dr. Kerry Shaw, Department of Neurobiology and Behavior, Cornell University, Ithaca, NY.

Research Project: A postdoctoral position is available to examine the genetics of behavior and speciation among closely related species of the Hawaiian cricket genus *Laupala*. We seek to examine the genetic basis of male signal and female preference for song-related traits that differ within and between species of *Laupala*. The successful candidate will participate in marker-assisted hybrid introgression studies of behavior, marker development with the assistance of BAC libraries, and the testing of hypotheses about the nature of the genetic basis of behavior and speciation. The development of additional independent projects is encouraged.

Background: While ecologically and morphologically similar, species of *Laupala* are easily distinguished by the pulse rates of the male calling song. The evolution of this behavior has played a large role in the rapid and extensive diversification of *Laupala*. Quantitative trait locus mapping studies have shown that male song is under the genetic control of many loci. QTL mapping also shows that female preference is under genetic control. A comparative phylogenetic framework exists

with which to understand behavioral evolution in *Laupala*. This genus is part of a larger radiation of endemic Hawaiian trigonidiine crickets that is conspicuously characterized by frequent speciation and acoustic signaling evolution. In *Laupala*, DNA data suggest that the current radiation began on the oldest island where the genus is presently found (Kauai, 5 mya), and radiated into younger island habitats as those islands appeared within the last 5 million years. These data also show that speciation has occurred both within and between islands and that species ranges are limited to single islands. Communities of *Laupala* occur on all the major Hawaiian Islands and convergent patterns of song evolution among islands, and divergent evolutionary patterns within islands, are evident. This phylogenetic structure provides a recent evolutionary context in which to study the evolution of genes, behavior and speciation. The focal species of the genetic work are endemic to the Big Island of Hawaii and are very closely related.

Requirements: The desired candidate will possess experience with a number of molecular bench skills (such as DNA/RNA extraction, PCR, AFLP analysis, cDNA synthesis, cloning). Some knowledge and/or prior experience studying behavior, evolution, and/or speciation or the strong desire to study in these areas would be highly beneficial.

Cornell University provides a highly stimulating environment with a cross-disciplinary approach to the study of evolutionary biology, providing a rich academic environment for those interested in proximate and ultimate causes of behavior, evolution and/or speciation. State of the art genomic facilities are available to assist with the current research.

The position can be filled immediately and at least two years of funding are available. To apply, please send a c.v., statement of research interests, and the email addresses of three references to Dr. Kerry Shaw (kerryshaw@umd.edu).

Kerry Shaw Dept. of Biology University of Maryland College Park, MD 20742

ph: 301-405-7503 fax: 301-314-9358

kerryshaw@umd.edu kerryshaw@umd.edu

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## CornellU TheoPopGenet

A post-doctoral position is available in the laboratory

of Carlos D. Bustamante, Department of Biological Statistics and Computational Biology, Cornell University. The focus of the group is on development of statistical methods for inference in population genetics/genomics and on analysis of genome-wide data sets in a diverse array of taxa (current research interest include: humans and other primates, HIV/SIV and their hosts, the domestic dog and its relatives, and domesticated Asian rice). Potential research areas for this position include: population genetic theory, primate population genetics/genomics, evolutionary genetics of domesticated plant and animals species, and methods development for association mapping in natural populations and domesticated species.

Please see the following web page for more information on our research:

<http://bustamantelab.cb.bscb.cornell.edu/index.php>

Interested applicants should send a PDF with CV and research statement to CDB28@CORNELL.EDU (Do not send me MS Word documents as these will be not be opened and, thus, not read). The starting date for the position is flexible.

Carlos

“Carlos D. Bustamante” <cdb28@cornell.edu>

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## EAWAG Switzerland AlpineBiodiversity

Eawag is the Swiss Federal Institute for Aquatic Science and Technology, a Swiss-based and internationally operating aquatic research institute within the ETH domain.

The Department Aquatic Ecology (prof. Jukka Jokela, ETH-Zurich) and Department of Fish Ecology and Evolution (prof. Ole Seehausen, University of Bern) have an opening for a

PostDoc in Evolutionary Ecology with an emphasis on alpine biodiversity

The position is funded for three years by the Competence Centre of Environmental Sustainability (under the ETH-Domain, where Eawag and ETH-Zurich are partners). The PostDoc will participate in the project CCES-BioChange, which focuses on evolutionary ecology of alpine biodiversity change. In this project seven research groups of ETH-domain collaborate to develop concepts, collect data and conduct experiments to de-

rive predictive models of biodiversity change in response to environmental, ecological and evolutionary processes affecting alpine habitats. The PostDoc would be one of several post-docs working in BioChange. Here, the focus would be on the population genetic structure, ecological divergence and local adaptation of aquatic alpine invertebrates and fish, with either empirical or theoretical approach. We have the opportunity to work with molecular markers, but experience with molecular techniques is not the primary consideration. Creative mind, good team skills, broad knowledge in evolutionary ecology, and scientific curiosity are important.

We offer a very stimulating and interactive research environment encompassing a lively population of researchers working with evolution, environmental sciences and ecology in Eawag, ETH-Zurich and University of Bern. Facilities for research are excellent and the project has a solid funding. The position will start as soon as possible (1 June 2007 or soon thereafter). PhD degree is required. The ideal candidate has a proven record of research experience, preferentially few years of post-doc experience, but fresh PhDs will be considered if their skill profile and experience matches the search.

Applications should include a letter of interest with a description of relevant experience, curriculum vitae, a list of publications, the names (with e-mail address) of three potential reviewers, and copies of the certificates of academic qualifications. These should be compiled to a single PDF file. In the letter of interest please describe the relevance of your experience and career goals with respect to evolutionary ecology, biodiversity research, and environmental change of the alpine habitats. Here, a broad definition of biodiversity is sufficient.

Please submit your application by 13 May 2007 in electronic form to Sandra Isenring, Eawag, Human Resources : [sandra.isenring@eawag.ch](mailto:sandra.isenring@eawag.ch). For further information, consult [www.eawag.ch](http://www.eawag.ch) or contact Jukka Jokela [jukka.jokela@eawag.ch](mailto:jukka.jokela@eawag.ch).

[Jukka.Jokela@eawag.ch](mailto:Jukka.Jokela@eawag.ch) [Jukka.Jokela@eawag.ch](mailto:Jukka.Jokela@eawag.ch)

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## EAWAG Switzerland DaphniaEvolution

Eawag is the Swiss Federal Institute for Aquatic Science and Technology, a Swiss-based and internationally op-

erating aquatic research institute within the ETH domain.

The Department Aquatic Ecology (group of Piet Spaak) seeks for a

PostDoc in Evolutionary Ecology to study rapid evolution in *Daphnia* (80-100%)

The PostDoc will participate in a collaborative research project with the Environmental Chemistry and Ecotoxicology department to investigate the adaptation of a natural *Daphnia* population to recently (past 30 - 40 years) introduced chemicals.

Within this project advantage will be taken from the fact that *Daphnia* resting eggs can be hatched from old sediment layers. The project will have a molecular (genotyping past and recent populations using microsatellites) as well as an experimental component (exposing old and recent clones to different chemicals). Project duration is two years.

We offer a stimulating research environment in a lively and social institute in Dübendorf (near Zürich). In a department with several other evolutionary and ecological research groups. The position will be for a period of two years, and should start as soon as possible (1 June 2007 or soon thereafter). Candidates should have a strong background in evolutionary biology typically acquired during their Ph.D. studies. The ideal candidate has a proven record of research experience with experimental work, statistical and writing skills, as well as molecular skills (PCR, sequencing, genotyping).

Applications should include a letter of interest with a description of pertinent experience, curriculum vitae, a list of publications, the names (with e-mail address) of three potential reviewers, and copies of the certificates of academic qualifications.

Please submit your application by 22 April 2007 in electronic form to Sandra Isenring, Eawag, Human Resources Department: [sandra.isenring@eawag.ch](mailto:sandra.isenring@eawag.ch). For further information, consult [www.eawag.ch](http://www.eawag.ch) or contact Piet Spaak (Tel. +41 44 823 5617) [spaak@eawag.ch](mailto:spaak@eawag.ch).

Piet Spaak Eawag Limnologie Department  
Überlandstrasse 133 P.O. Box 611 8600 Dübendorf  
Switzerland Phone: +41 (0)44 823 56 17 Fax:  
+41 (0)44 823 58 17 [spaak@eawag.ch](mailto:spaak@eawag.ch) <http://www.eawag.ch/~spaak> <<http://www.eawag.ch/>>

[Piet.Spaak@eawag.ch](mailto:Piet.Spaak@eawag.ch) [Piet.Spaak@eawag.ch](mailto:Piet.Spaak@eawag.ch)

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## EmoryU ModelingInfectiousDisease

POSITION ANNOUNCEMENT: Mathematical Modeling of Infectious Disease Post-doctoral position Center for Disease Ecology Emory University Atlanta, GA

Consideration of applications begins immediately and will continue until the position is filled. The desired start date is June 1, 2007.

The Center for Disease Ecology (CDE) invites applications for a postdoctoral position. The applicant will be responsible for developing theoretical models for host-pathogen interactions stressing transmission dynamics within explicit seasonal and spatial contexts. The applicant will have access to established databases from a variety of infectious diseases including (but not restricted to) rabies, Ebola, classic swine fever, and malaria. The Center for Disease Ecology is a cross-disciplinary initiative involving the Emory College, Graduate School, Medical School, School of Public Health, Yerkes National Vaccine Center, and the Centers for Disease Control and Prevention. The Director of the CDE is Leslie A. Real of the Department of Biology, Emory University, Atlanta, GA.

The position is funded for a two-year period (with a possible extension) and all work will be conducted at Emory. The successful applicant should have a Ph.D. or related research experience. The applicant should be familiar with mathematical modeling, computer programming, and data visualization and management. Responsibilities will include extending and analyzing retrospective data sets and integration of data into models of disease dynamics.

To apply, please send a letter of application with a statement of research interest, select copies of publications, CV, and the names (with email addresses) of three referees. Applications should have "CDE Post-doc" as the subject field and should be directed to [lreal@emory.edu](mailto:lreal@emory.edu) or by mail to:

Dr. Leslie A Real Center for Disease Ecology Department of Biology 1510 Clifton Road Emory University Atlanta, GA 30322

Emory University is an Equal Opportunity/Affirmative Action Employer.

Leslie Real <[lreal@emory.edu](mailto:lreal@emory.edu)>

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## Gif-sur-Yvette MetabolicSystemEvol

A CNRS postdoctoral position is available in the group Fundamental Quantitative Genetics (INRA-University Paris Sud-CNRS-AgroParisTech) in Gif-sur-Yvette, France, on the following topic: "Genetics and evolution of metabolic systems: heuristic modelling for flux prediction and optimization". All details about the project are given at the address: <https://www2.cnrs.fr/DRH/post-docs07/index.php?pid=-1&action=view&idW7&lang=en> Dominique de Vienne Professeur, Université Paris-Sud Directeur de l'UMR de Génétique Végétale INRA-UPS-CNRS-AgroParisTech Ferme du Moulon 91190 Gif-sur-Yvette, France Tel : 01 69 33 23 60 Fax : 01 69 33 23 40

devienne@moulon.inra.fr

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## INRA Lusignan PlantGenetics

Post-doctoral position - 16 months from September 2007

Title : Genetic determinism of the dynamics of stem elongation in alfalfa : towards an association study

Supervisor : Bernadette Julier (Dr, HDR) Site : I.N.R.A., Unité de Génétique et d'Amélioration des Plantes Fourragères, BP 6, 86600 Lusignan, France Contact : email : [bjulier@lusignan.inra.fr](mailto:bjulier@lusignan.inra.fr), tel : (33) +5 49 55 60 38, fax : (33)+5 49 55 60 44

Conditions for recruitment : the candidate must have a foreign nationality (non French)

The young scientist will have the task to initiate an analysis of the genetic basis of stem elongation with a strategy of association genetics, on the main forage legume, alfalfa (*Medicago sativa*). Data of neutral polymorphism (microsatellite markers) as well as the phenotypic data, collected on a population of 400 genotypes, sampled in 10 European varieties (40 individuals per variety) will be available. This set of molecular and phenotypic data will be used to write a publication describing the structuration, within and between-varieties, of the diversity.

A second objective will be to quantify the linkage disequilibrium on the chromosome 7 (in a region involved in stem elongation and flowering date in the legume model species *Medicago truncatula*, Julier et al., TAG, 2007). To achieve this task, markers will be defined in the region, and polymorphism will be studied on the 400 individuals. The scientist will analyse allelic polymorphism available for candidate genes mapped in this region. All data will be used to propose a strategy for an association study, that could start during the period of the contract, depending on the time availability. More precisely, he will test the possibility to have an association study on the population of 400 individuals sampled in 10 synthetic varieties, taking into account the structuration of this population (preliminary results showed that the structuration among varieties is very low).

Please send CV, covering letter, references or contacts.

– Bernadette Julier INRA Unité de Génétique et d'Amélioration des Plantes Fourragères 86600 Lusignan France

Tel: 33 (0)5 49 55 60 38 Fax: 33 (0)5 49 55 60 44

Bernadette Julier <[Bernadette.Julier@lusignan.inra.fr](mailto:Bernadette.Julier@lusignan.inra.fr)>

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## INRA Versailles TE Bioinformatics

Transposable Elements and tobacco genes

A 6 months (postdoc level) position is open at the Laboratoire de Biologie Cellulaire, Institut Jean-Pierre Bourgin, INRA-Versailles, France (<http://www-ijpb.versailles.inra.fr/>), in the team "Host-Transposon Interactions and Plant biodiversity". The projet will focus on the bioinformatic analysis of Transposable Elements (TEs) sequences found in tobacco databases, notably EST databases, and on the evaluation of genes/TEs associations. Previous knowledge of the various ET types (structure and molecular diversity) will be highly appreciated.

Starting date: no later than June 1st, 2007 Send CV and two recommandations contacts to: Dr Marie-Angèle GRANDBASTIEN Laboratoire de Biologie Cellulaire Institut Jean-Pierre Bourgin INRA-Centre de Versailles 78026 Versailles cedex, France [gbastien@versailles.inra.fr](mailto:gbastien@versailles.inra.fr) tel: 33 1 30 83 30 24 fax: 33 1 30 83 30 99

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Marie-Angèle GRANDBASTIEN Laboratoire de Biologie Cellulaire Institut Jean-Pierre Bourgin INRA - Centre de Versailles 78026 Versailles, France Tel: 33 (1) 30 83 30 24 Fax: 33 (1) 30 83 30 99 Email: gbastien@versailles.inra.fr

Marie-Angèle.Grandbastien@versailles.inra.fr

/www.bio.indiana.edu/> Daphnia Genomics Consortium: daphnia.cgb.indiana.edu <<http://daphnia.cgb.indiana.edu/>> NSF Training Grant: Evolution, Development, & Genomics: evodevo.uoregon.edu

milynch@indiana.edu

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## IndianaU EvolGenomics

### POSTDOCTORAL POSITION: EVOLUTIONARY GENOMICS / MUTATION RATE

A postdoctoral position is available in the laboratory of Michael Lynch, Department of Biology, Indiana University, Bloomington, Indiana to estimate the genome-wide mutation rate and molecular spectrum in four model systems. This work will take advantage of long-term mutation-accumulation lines in four model organisms: the nematode *C. elegans*, the microcrustacean *Daphnia pulex*, the ciliate *Paramecium tetraurelia*, and the yeast *S. cerevisiae*. The project relies on new high-throughput techniques for genome sequencing, with a long-term goal of establishing generalities across eukaryotes. Candidates should have an interest in molecular/genomic evolution, good molecular skills, and be comfortable dealing with very large data sets. The position is available immediately and will remain open until suitable candidates are located. For immediate consideration, please send applications via email with 'Lynch Application' in the subject line (include a cover letter outlining your interests, complete CV, and contact information for three individuals willing to provide references) to Dee Verostko at [dverostk@indiana.edu](mailto:dverostk@indiana.edu) or 1001 E. Third Street, Bloomington, IN 47405. Indiana University is an Equal Opportunity/Affirmative Action employer.

Michael Lynch [milynch](mailto:milynch) at [indiana.edu](http://indiana.edu)

Distinguished Professor Dept. of Biology Phone: 812-855-7384 Indiana University FAX: 812-855-6705 Bloomington, IN 47405

Lab: [www.bio.indiana.edu/facultyresearch/faculty/Lynch.html](http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html) <<http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html>>

2007 AGA Genome Evolution Symposium:

[www.theaga.org/agasymposium/index.html](http://www.theaga.org/agasymposium/index.html) <<http://www.theaga.org/agasymposium/index.html>>

IU Biology: [www.bio.indiana.edu](http://www.bio.indiana.edu) <<http://www.bio.indiana.edu>>

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## LIRMM Montpellier Bioinformatics

Post-doctoral position, LIRMM, Montpellier, France

A Post-doctoral position is available for up to 3 years in the "Method and Algorithm for Bioinformatic" group (MAB) to join the PlasmoExplore project. This project involves teams from CEA Grenoble (Eric Marechal), the Museum d'Histoire Naturelle Paris (Isabelle Florent) and the LIRMM, and is funded by the french National Research Agency.

MAB web page: <http://www.lirmm.fr/mab/>  
 PlasmoExplore web page: <http://www.lirmm.fr/~brehelin/PlasmoExplore> Contact: Olivier Gascuel ([gascuel@lirmm.fr](mailto:gascuel@lirmm.fr)) or Laurent Bréhélin ([brehelin@lirmm.fr](mailto:brehelin@lirmm.fr)).

The candidate will work on functional prediction and gene annotation of *Plasmodium falciparum*. He/She should have PhD in bioinformatics, with special interest in statistical machine learning, algorithmics, genomics, and(or) gene annotation. Please submit a summary of research interests, CV, reprints of the main publications, and reference contacts.

The PlasmoExplore project aims at predicting the function of orphan genes of *P.falciparum*, by exploiting the rapidly growing mass of genomic and post-genomic data of the organism. This characterisation should allow identifying new therapeutic targets for new treatments. The proposed approach will combine: (1) the ontologies of the Gene Ontology (GO) consortium, which define the function of genes; (2) efficient methods of sequence alignment that take into account the high A/T content of the malarial genome; these methods will be used to exploit genomic data and establish new homologies, at the gene level but also at the chromosome or the entire genome levels; (3) supervised statistical learning methods, that will exploit post-genomic data and build predictors associated with each GO class; (4) classifier combination methods to synthesize the information extracted from each data source; and finally (5) visualisation and interaction adapted methods, allowing a

multi-scale exploration of the predictions by end users. The project will elaborate a free-access database on the web, which will provide to the international scientific community the best available predictions.

brehelin@lirmm.fr

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## LeipzigU Bioinformatics

The Leipzig University, Fakultät für Biowissenschaften, Pharmazie und Psychologie, Institut für Biologie II, are seeking to fill a Postdoc position in bioinformatics.

Applications are sought from researchers for a postdoctoral position in the group for Molecular Evolution and Systematics with Prof. Dr. Schlegel. The position will be for a period of three years.

We are looking for a person who can demonstrate research experience in the field of bioinformatics. A focus on molecular phylogenetics would be desirable, but is not necessary. The research of this position should focus on bioinformatics and molecular phylogenetics and the post also includes teaching duties in Zoology and Molecular Systematics.

The ideal candidate will have a PhD in bioinformatics, molecular phylogenetics, zoology, theoretical biology or a related subject.

The deadline is April the 30th 2007, but applications maybe considered until the post is filled.

Applications of women are encouraged and given comparable qualifications; applications of handicapped persons will be given preference.

Applications, including curriculum vitae and bibliography, summary of past accomplishments, and the names and email addresses of three references, should be sent to:

Prof. Dr. Martin Schlegel Universität Leipzig Fakultät für Biowissenschaften, Pharmazie und Psychologie Institut für Biologie II, Molekulare Evolution & Systematik der Tiere Talstr. 33 04103 Leipzig Tel.: 0341/9736725 Fax: 0341/9736848 e-mail: schlegel@rz.uni-leipzig.de

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Dr. Thomas U. Berendonk

Universität Leipzig, Institut für Biologie II Molekulare Evolution und Systematik der Tiere Talstr. 33 D-04103 Leipzig, Tel.: +49-(0)341-9736742 Fax: +49-(0)341-

9736789

e-Mail: tberendonk@rz.uni-leipzig.de

tberendonk@rz.uni-leipzig.de

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## Milan 2 RotiferEvolution

1) two year Post-Doc position available at the Department of Biology in Milan, Italy, in the lab of Claudia Ricci, claudia.ricci@unimi.it. Deadline: 27 April 2007

Analysis of the nervous system of bdelloid rotifers and its role in anhydrobiosis.

Almost all 380 species of Bdelloidea (phylum Rotifera) live in freshwater (Segers, 2002), but most of them are able to survive lack of water entering a form of dormancy known as anhydrobiosis (Ricci et al., 1987; Ricci, 1998, 2001). Anhydrobiotic animals undergo a series of adaptations at morphological, metabolic, and biochemical level (Crowe, 1971).

In detail, due to evaporation of water, the bdelloids contract in a characteristic tun shape, which slows down water lost, compacting tissues and organs in ordered and rigorous ways (Dickson & Mercer, 1967; Schramm & Becker, 1987).

Plausibly, the nervous system, together with the cytoskeleton, is highly involved in activating the events leading the rotifer to its dormant state. Nevertheless, few studies dealt with functional and morphological aspects of the nervous system in rotifers (see Hochberg, 2006), and almost nothing is known in bdelloid rotifers.

Aims of the projects are: - describing the structure and ultra-structure of the nervous system in hydrated and dormant bdelloids, - elaborating a model to understand how the nervous system is involved in anhydrobiotic response, - disentangling the role of the cytoskeleton in the mechanisms involved in anhydrobiosis.

For details, look at the application form (in Italian only): [http://www.unimi.it/ricerca/assegni\\_ricerca/-7550.htm](http://www.unimi.it/ricerca/assegni_ricerca/-7550.htm) 2) Another post-doc position will be opened soon. This will involve the analysis of DNA damage in bdelloid rotifers after stressful events (eg dehydration, radiation, freezing), and of the subsequent repair mechanisms after recovering.

Experience with microscopic organisms is preferred, together with knowledge of techniques of DNA double strand breakage (tunnel assay, comet assay, markers, etc).

If you are interested, please contact prof. Claudia Ricci, Department of Biology, Università' di Milano, [claudia.ricci@unimi.it](mailto:claudia.ricci@unimi.it) <http://users.unimi.it/ricci> [diego.fontaneto@unimi.it](mailto:diego.fontaneto@unimi.it)

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## Milan EvolGenomics

Postdoctoral Fellowship in Evolutionary Genomics and Bioinformatics

A postdoctoral position is available in the group of Bioinformatics and Evolutionary Genomics of Cancer at the European Institute of Oncology in Milan (Italy).

The group is interested in detecting the genotypic determinants of human cancer through the study different features of human genes, proteins and of the entire genome. A number of projects are currently going on in the lab. Therefore, a certain flexibility in the choice of the project is allowed. In all cases, the successful candidate will deal with well-assessed procedures for data analysis as well as with the development of tools for solving specific problems. A tight collaboration with the many wet labs in the campus is a major trait of the job.

Qualifications: A PhD in bioinformatics, theoretical biology, genetics or equivalent is required. Computational skills (Perl, Python, C++) are mandatory. A background in evolution and developmental biology would be favourable.

To apply: send, via email, a CV, a statement of research interests, and the names and contact information for two references. Applications and inquiries should be addressed to Francesca Ciccarelli [francesca.ciccarelli@ifom-ieo-campus.it](mailto:francesca.ciccarelli@ifom-ieo-campus.it)

Francesca D. Ciccarelli, PhD IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303-053 fax +39-02574303-231 web: <http://ciccarelli.group.ifom-ieo-campus.it/fcwiki/> francesca.ciccarelli –

Francesca D. Ciccarelli, PhD Biocomputing IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303-053 fax +39-02574303-231 web: <http://ciccarelli.group.ifom-ieo-campus.it/fcwiki/> francesca.ciccarelli@ifom-ieo-campus.it

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## NewYorkU PlantEvolGenomics

JOB OPENING: Postdoctoral Fellow in Plant Evolutionary Genomics

We have an opening for a postdoctoral fellow at the Purugganan Laboratory in the Department of Biology/Center for Comparative Functional Genomics at New York University, subject to final approval of funds. The postdoc will join a project on identifying domestication genes in rice, and utilize techniques in population genetics and plant genomics. This project provides an opportunity to gain experience in project management of a plant evolutionary genomics project. Experience in molecular evolutionary techniques, including population genetics and computational biology, are desirable. Salary is commensurate with experience, and will start at \$40,000/year plus full benefits.

If you are interested, please send me a CV at [mp132@nyu.edu](mailto:mp132@nyu.edu). If you want to know more about our laboratory, check out our website at <http://www.nyu.edu/fas/dept/biology/faculty/purugganan/-index.html> The position will be in NYU's main campus in Washington Square Park at the heart of Greenwich Village in downtown Manhattan. The Center is an exciting group that includes researchers working on systems biology, evolutionary genomics and bioinformatics.

Michael Purugganan Dorothy Schiff Professor of Genomics

Department of Biology Center for Comparative Functional Genomics 100 Washington Square East New York University New York, NY 10003

Tel. (212) 992 9628

Michael Purugganan <[mp132@nyu.edu](mailto:mp132@nyu.edu)>

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## Perpignan France EvolEpigenetics

Employer: CNRS/Université de Perpignan

Location: Perpignan, France

Posting Date: 2007-04-17



Description: Call for Applications to PostDoc Position (deadline April 30, 2007)

<https://www2.cnrs.fr/DRH/post-docs07/?pid=1&action=view&idX2&lang=en> A CNRS funded position for a PostDoc is open at the Laboratory for Tropical and Mediterranean Ecology in Perpignan (Southern France). The goal of the project is to investigate the role of epigenetic mechanisms in evolutionary processes. Our model is the human blood fluke *Schistosoma mansoni* and its hosts. Further details on the project may be found at:

<https://www2.cnrs.fr/DRH/post-docs07/?pid=1&action=view&idX2&lang=en>

The postdoc position is open for 12 months starting September/October 2007. Starting date can be postponed if needed. A 12 month extension can be possible. Gross salary 2500 Euros/month (roughly 2000 Euros after insurance and taxes). Administrative aid in organizing accommodation, insurance etc. will be provided.

Subject:

The successful applicant will investigate the epigenetic basis of phenotypic plasticity. Phenotypic plasticity is the basis of adaptive evolution. In particular, in rapidly evolving organisms like those belonging to host-parasite systems, epigenetic mechanisms are likely to play an important role since they enable a given genotype to generate a larger variety of different phenotypes. The candidate will study the interrelation of epigenetic variability, phenotypic plasticity and fitness (infection success) using both a whole genome approach and investigation of candidate genes that play a key role in host-parasite compatibility. These genes have recently been identified in our laboratory. The expected results will be of benefit not only for the understanding host-parasite systems, but will shed light on the role of epigenetics in evolution in general.

Conditions of the PostDoc:

The successful candidate will be physically located in Perpignan, with the Evolutionary and Functional Parasitology team (<http://cbetm.univ-perp.fr/>). Perpignan is a lively town at the Mediterranean coast of Southern France, close to the Spanish border. The candidate will work with Christoph Grunau (<http://www.methdb.net>) but will be interacting with all other partners of the project, and with the partner lab at the Pasteur Institute in Lille (<http://www.pasteur-lille.fr/fr/accueil/index.htm>). The laboratory is well-equipped, has its own animal facilities, and has an acknowledged expertise in the field (WHO Collaborating Center for Biological Control and Snail/Parasite rela-

tionships). Working language are French or English.

The candidate should preferably have a PhD in Biology, Biochemistry, Genetics, Epigenetics or Parasitology with an interest in new aspects of population genetics and evolution. He or she should also have good communicating skills and a facility and taste for interacting with other people, including Master and PhD students with different scientific backgrounds. Knowledge in techniques in epigenetics like ChIP and ChIP-on-chip will be an advantage but are not a prerequisite.

Submitting the application:

The application is in two steps. First, interested candidates must send a CV to Guillaume Mitta ([mitta@univ-perp.fr](mailto:mitta@univ-perp.fr)). The deadline for this initial application is April 30, 2007. The candidates selected at the end of this first step will then be invited by email to a telephone interview or videoconference.

Person to contact for further information:

Mitta Guillaume Biologie et Ecologie Tropicale et Méditerranéenne UMR 5244 CNRS/EPHE/Université de Perpignan Equipe "Parasitologie Fonctionnelle et Evolutive" 52, Avenue Paul Alduy 66860 Perpignan Tel 33 (0)468662185 Fax 33 (0)468662281 – Ce message a été vérifié par MailScanner pour des virus ou des polluriels et rien de suspect n'a été trouvé. CRI UPVD <http://www.univ-perp.fr> Guillaume Mitta <[mitta@univ-perp.fr](mailto:mitta@univ-perp.fr)>

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## PurdueU SalmonidGenomics

POST-DOCTORAL RESEARCH ASSOCIATE  
Salmonid developmental genomics Purdue University

A post-doctoral research associate is sought for work on the functional genomics of alternative developmental phenotypes in rainbow and steelhead trout at Purdue University. The project is supported by an USDA-NRI Animal Genome grant, and will utilize expression technologies with linkage and QTL mapping to efficiently identify candidate genes for development rate, growth, and age at sexual maturity in rainbow and steelhead trout. Postdoctoral research will provide training in the area of microarray expression experiments and statistical analyses (in collaboration with Dr. Lauren McIntyre, University of Florida), QTL mapping, and molecular evolution. Our lab is a part of the Ecology, Evolution, and Population Biology group in the Department of Biological Sciences, Purdue University. Purdue Uni-

versity is an excellent place for the study of genetics and genomics, with numerous statistical, quantitative, and population genetic faculty in multiple colleges and departments.

**QUALIFICATIONS:** Applicants should have a PhD in Biology, Genetics, or related field. Applicants should also have considerable experience with molecular tools and a background in statistical analyses of molecular data. Strong quantitative and statistical skills are desirable.

**APPLICATION:** Interested persons should contact Dr. Krista Nichols, kmnichol@purdue.edu with a curriculum vita which includes the names of and contact information for at least three references. The position is available immediately but will begin no later than August 2007. Postdoctoral funding is available for up to 2 years, contingent upon satisfactory progress.

Krista M. Nichols Assistant Professor Purdue University Departments of Biological Sciences & Forestry and Natural Resources 915 W State Street West Lafayette, IN 47907 765.496.6848 (phone) 765.494.0876 (fax) <http://bilbo.bio.purdue.edu/www-ecology/faculty/-nichols/index.html>

kmnichol@purdue.edu

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## QueensU ModelingInfluenzaEvol

Two Postdoctoral Fellowships in the Mathematical Evolutionary Epidemiology of Influenza.

Applications are sought from outstanding researchers for two postdoctoral positions in the mathematical evolutionary epidemiology of influenza, in the labs of Drs. Troy Day (Queen's University, Canada), Jonathan Dushoff (McMaster University, Canada), David Earn (McMaster University, Canada), and Junling Ma (University of Victoria, Canada). Both positions will be for a period of two years, and will involve developing and analyzing mathematical and simulation models of influenza evolution. Positions should be taken up by Sept. 1, 2007. Duties will also include the teaching of two one-semester courses per year. Salary will begin at C\$40,000 per year.

For more information on research in our labs see: [www.mast.queensu.ca/~tday](http://www.mast.queensu.ca/~tday), <http://www.eeb.princeton.edu/~dushoff/>, <http://www.eeb.princeton.edu/~dushoff/>, [www.math.mcmaster.ca/earn/](http://www.math.mcmaster.ca/earn/), and

[www.math.mcmaster.ca/earn/](http://www.math.mcmaster.ca/earn/), To apply, send a current curriculum vitae and arrange to have two letters of reference sent to Dr. Troy Day at tday@mast.queensu.ca.

Alternatively, materials can be sent by post to: Troy Day Dept. of Mathematics and Statistics Jeffery Hall, Queen's University Kingston, ON, K7L 3N6 CANADA

Deadline for applications is May 15, 2007.

tday@mast.queensu.ca tday@mast.queensu.ca

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## SangerInst StatBiology

Postdoctoral Doctoral Training Fellows - Statistician/Mathematical Biologist (Ref: SW1267-1268)

The Wellcome Trust Sanger Institute leads the world in genomic research, with an expanding scientific programme dedicated to understanding gene function in health & disease.

DNA Copy Number Variation and Disease

Now is an extremely exciting time for the study of human genetic variation. The Wellcome Trust Sanger Institute (WTSI) is a world leader in human genomics and genome informatics. We are consolidating and expanding an ambitious programme of research characterising Copy Number Variation in the human genome (Redon et al., Nature, 444:444-454 (2006)) and integrating this knowledge into disease association studies. This programme combines large-scale experimental data generation, on a variety of platforms, with sophisticated data analyses.

Statistician/Mathematical Biologist Ref 1267

We are seeking a highly talented and motivated postdoctoral researcher with a background in Mathematical Biology or Statistics who may have a proven track record or who has demonstrated exceptional potential during a recently-completed PhD. A biological background is not strictly necessary. Experience with analysing microarray data and/or association studies would be an advantage. The successful applicant will be involved in the design and analysis of genetic association studies to assess the functional impact of copy number variation, and would interact with a multi-disciplinary group of mathematical biologists.

Informal enquiries to Matthew Hurles (meh@sanger.ac.uk) and Nigel Carter (npc@sanger.ac.uk).

Statistician/Mathematical Biologist Ref 1268

We are seeking a highly talented and motivated post-doctoral researcher with a background in Mathematical Biology, Mathematics, Computer Science or other relevant Physical Science who may have a proven track record or who has demonstrated exceptional potential during a recently-completed PhD. A biological background is not strictly necessary. Experience with DNA sequence analysis would be an advantage. The successful applicant will be involved in the development and application of novel algorithms for identifying DNA copy number variation from data generated by the latest generation of DNA sequencing technologies, and would interact with a multi-disciplinary group of mathematical biologists.

Informal enquiries to Matthew Hurles (meh@sanger.ac.uk) and Richard Durbin (rd@sanger.ac.uk).

PDTFs will be seeking a period of early career research training or be changing fields/scientific direction necessitating the acquisition of new research skills. Typically, PDTFs will be carrying out original research within a defined scientific area in a Faculty team.

Salary range £26,650 to £35,875 per annum dependant upon experience and both posts are available for 3 years in the first instance. Benefits include 25 days annual leave, final salary pension scheme, optional private healthcare (on successful completion of a qualifying period), permanent disability insurance, life assurance, childcare voucher scheme, campus bus services from Cambridge and Saffron Walden, car-share scheme, on-site restaurant, café and gym.

To apply for this position please email your CV (including 2 referees) and current salary details, quoting reference number SW1267 or 1268 to: recruit@sanger.ac.uk

Or post to: Human Resources, The Wellcome Trust Sanger Institute, Genome Campus, Hinxton, Cambridge, CB10 1SA

The closing date for applications is 20th April 2007.

Internal applicants must complete an internal application form and provide an up-to-date curriculum vitae

<http://www.sanger.ac.uk/humgen/cnv> <http://www.sanger.ac.uk/Teams/Team29/> Matthew Hurles  
Genome Dynamics and Evolution Group The Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Tel +44 (0)1223 495377; Fax +44 (0)1223 494919  
<http://www.sanger.ac.uk/Teams/Team29/> <http://www.sanger.ac.uk/humgen/cnv> meh@sanger.ac.uk  
meh@sanger.ac.uk

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## Shanghai Computational Biol

Wanted

PostDocs

The Comparative Biology group is looking for postdocs with background in Biology, Bioinformatics or Computer Science.

The successful applicants will work on projects involving human genome and transcriptome evolution, transcriptional regulation, aging, and the evolution of human cognitive abilities. The applicant will be expected to be able to analyze large amounts of DNA sequence, microarray expression data, as well as protein expression data from the mass spectroscopy experiments.

We offer competitive salary and excellent academic environment within the group, as well as collaboration with leading research institutes in Europe and the United States. Successful applicant should be able to communicate, read and write in English fluently.

Dr. Philipp Khaitovich's (Group PI) current publication list can be found at:

<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=pubmed&cmd=search&term=Khaitovich+P>

Submit your current CV with a letter detailing your interest in the position to:

fxue@sibs.ac.cn or send to: CAS-MPG Partner institute for Computational Biology, 320 Yue Yang Road, Shanghai, 200031

Please quote the position on envelope or email

Detail information is also available on our website: <http://www.picb.ac.cn> sqli <sqli@sibs.ac.cn>

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## UAarhus 2 Bioinformatics

Postdoctoral Positions in Statistical and Computational Bioinformatics

UNIVERSITY OF AARHUS, FACULTY OF HEALTH SCIENCES, BIOINFORMATICS RESEARCH CENTER (BIRC)

Bioinformatics Research Center (BiRC), University of Aarhus, Denmark invites applications for two postdoctoral positions in statistical and computational biology from May 2007 (starting date negotiable). The positions are initially available for one year but with possible extension to a maximum of three years.

The two positions are related to two different projects.

A. The project of the first position seeks to develop statistical methods for analysis of biological network data; in particular Protein Interaction Networks, preferably integrated with other relevant data. The exact topic of the work is open, but should focus somewhat on the development of MCMC, likelihood-free, or Bayesian methods for analysis of network data. Currently, one PhD student and Professor Wiuf are working on the project. We have a strong collaboration with researchers at Imperial College, London and the candidate is expected to spend some time in London. Relevant Refs: [1], [2]; see also <<http://www.birc.au.dk/~wiuf/group.htm>> <http://www.birc.au.dk/~wiuf/gr...> . B. The project of the second position seeks to develop statistical methods for validation of methylation arrays and for their further analysis in relation to different cancers and cancer subtypes. Currently, several PhD students, one postdoc and Professor Wiuf are working on similar issues using various array types (SNP, gene, CGH, miRNA). The successful candidate will work with experimental researchers at the Institute of Human Genetics, as well as with researchers at BiRC. Relevant Refs: [3], [4] (though none on methylation arrays yet); see also <<http://www.birc.au.dk/~wiuf/group.htm>>

Scientific qualifications corresponding to a PhD-degree are required.

The conditions of employment are based on the agreement between The Ministry of Finance and The Federation of Graduate Employee Unions. Remuneration will include an additional pension-based bonus of DKK 44,899.51 per year (April-2006 level).

The application should include a curriculum vitae, a full list of the applicant's scientific publications showing which publications the applicant wishes to be included in the assessment. Three copies of each of these publications should be included with the application. The assessment committee can decide to include material which has not been in the evaluation. In this event, the applicant will be informed and asked to send the material, or else to withdraw the application.

The guidelines of the Faculty for the assessment committee and guidelines concerning writing an application may be found on <<http://www.health.au.dk/fakultet/>

stillingsopslag> <http://www.health.au.dk/fakultet/> or can be requested from the Faculty Secretariat on tel. +45 8942 4105 (Liselotte Westerby).

When the assessment committee has made its evaluation, applicants will receive the part of the evaluation which concerns them.

Applications are encouraged regardless of age, gender, race, religion or ethnic background.

Further information about the position can be requested from Professor Carsten Wiuf; e-mail; [wiuf@birc.au.dk](mailto:wiuf@birc.au.dk)

Four copies of the application, together with three copies of the publications to be assessed, should be sent to The Faculty of Health Sciences, Vennelyst Boulevard 9, DK-8000 Aarhus C. Applications must reach the Faculty Secretariat before 12.00 noon, April 30, 2007.

The application should be marked 2007-212/2-218

Kind Regards

Enette Berndt Knudsen, Administrative Organizer  
BiRC - Bioinformatics Research Center University of Aarhus Høegh-Guldbergs Gade 10, Building 1090 DK-8000 Aarhus C, Denmark Phone +45 8942 3123 E-mail: [enette@birc.au.dk](mailto:enette@birc.au.dk)

[enette@birc.au.dk](mailto:enette@birc.au.dk)

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## UAdelaide AncientDNA DNABarcoding

The position is responsible for developing an ancient DNA and DNA bar-coding programme for the State Herbarium in conjunction with the Australian Centre for Ancient DNA analysis, entailing: establishing a DNA processing facility within the Herbarium precinct, developing ongoing linkages and joint projects with the ancient DNA labs of the Australian Centre for Ancient DNA with Professor Alan Cooper, aimed at producing molecular plant identification tools for historic (100s to 10000s of years old), degraded and diminutive material, from a range of sources, including river and lake sediments, stick nest rat nests and cave deposits. developing a targeted DNA barcoding initiative on a taxonomically complex group to facilitate identification (e.g. seaweeds and grasses), together with key personnel within the Herbarium and at Adelaide University providing ongoing and active research linkage with other systematics and paleoecological research at

the combined laboratory of the University of Adelaide, and South Australian Museums Evolutionary Biology Unit. helping to develop systematics and paleoecological projects with and providing phylogenetic analytical advice to staff of the State Herbarium

Eligibility: Open

Experience required: 1. Comprehensive knowledge of plant phylogenetics, systematics and ancient DNA; 2. A critical knowledge of molecular biology principles necessary to undertake targeted loci development for species distinction and probing of degraded target tissue (e.g. ancient DNA) 3. Demonstrable experience in undertaking DNA extraction and molecular analysis for a range of preserved plant material, utilising a range of genomic loci 4. Demonstrable experience in the phylogenetic analysis and advanced data interpretation for a range of plant groups.

Application Information: Applicants must address the criteria listed in the Person Specification available from Department website <http://www.environment.sa.gov.au/vacancies> or from our Recruitment and Selection Team by email [deh.jobs@saugov.sa.gov.au](mailto:deh.jobs@saugov.sa.gov.au) or telephone 08 8204 1898. Applications Close:- 5PM FRIDAY 4 MAY 2007.

Enquiries to: Professor Andrew Lowe, e-mail [lowe.andrew@saugov.sa.gov.au](mailto:lowe.andrew@saugov.sa.gov.au) or Ph: 08 8222 9326.

[peter.prentis@adelaide.edu.au](mailto:peter.prentis@adelaide.edu.au) peter.prentis@adelaide.edu.au

programming at the scripting level or higher, experience with Linux/Unix computing environments, familiarity with open source databases such as MySQL, and a commitment to developing software tools and web accessible database resources. Salary range is \$45-50,000 depending on experience. Applicants should apply for the position electronically on the University's Human Resources website (<https://www.uacareertrack.com>; look for posting #37706). Please include CV, statement of research and programming interests and experience, and arrange to have two letters of recommendation sent directly to Mike Sanderson at the Department of Ecology and Evolutionary Biology, University of Arizona, Tucson AZ 85721 ([sanderm@email.arizona.edu](mailto:sanderm@email.arizona.edu)). Application review will begin immediately.

Michael J. Sanderson

New Address: Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

New Email: [sanderm@email.arizona.edu](mailto:sanderm@email.arizona.edu)

Phone: 520-626-6848

lab web site: <http://loco.biosci.arizona.edu> Phylota project: <http://loco.biosci.arizona.edu/phylota> r8s software: <http://loco.biosci.arizona.edu/r8s> [sanderm@email.arizona.edu](mailto:sanderm@email.arizona.edu) [sanderm@email.arizona.edu](mailto:sanderm@email.arizona.edu)

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## UArizona PrionEvol

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## UArizona Biodiversity Informatics

Postdoctoral Research Position - Biodiversity Informatics, University of Arizona

A two-year postdoctoral research position is open in biodiversity informatics at the University of Arizona. The position is associated with a new initiative on campus aimed at leveraging the university's extensive natural history collections and their databases to develop new integrative tools and research programs involving (but not necessarily limited to) phylogenetics, genomics, ecology and evolution. The postdoc position will be in Dr. Mike Sanderson's research group. Responsibilities will include working with existing collections databases on campus, as well as other biodiversity informatics resources, to construct new software tools and address biological questions enabled by these developments. The candidate must have good skills pro-

gramming at the scripting level or higher, experience with Linux/Unix computing environments, familiarity with open source databases such as MySQL, and a commitment to developing software tools and web accessible database resources. Salary range is \$45-50,000 depending on experience. Applicants should apply for the position electronically on the University's Human Resources website (<https://www.uacareertrack.com>; look for posting #37706). Please include CV, statement of research and programming interests and experience, and arrange to have two letters of recommendation sent directly to Mike Sanderson at the Department of Ecology and Evolutionary Biology, University of Arizona, Tucson AZ 85721 ([sanderm@email.arizona.edu](mailto:sanderm@email.arizona.edu)). Application review will begin immediately.

Evolutionary capacitor mechanisms such as the PSI prion and the heat shock protein Hsp90 store variation in a latent form and reveal it later. Adaptations revealed by a capacitor remain dependent on the continued expression of that capacitor for some time, until genetic assimilation is complete. During this period, "cheater" lineages that do not bear the costs of the capacitor are unable to usurp the benefits through recombination. This limited effect of recombination, together with the reversibility of the capacitor, which unlike a mutation is easily able to switch off at any time, distinguish evolvability mediated by capacitors from evolvability stemming from other mechanisms such as elevated mutation rates. The postdoc will design and implement mathematical models and/or simulations to capture these two effects. The postdoc may also initiate other projects that model evolutionary capacitance and/or test their predictions using a bioinformatic / comparative genomic approach.

The postdoc will work with PI Joanna Masel (<http://eebweb.arizona.edu/Faculty/bios/masel.html>) at the University of Arizona in Tucson. NIH funding is secured, the position is renewable over multiple years, and is available immediately. Ph.D. with strong quantitative background and computational and/or modeling experience is required. A background in evolutionary theory is strongly preferred. Other potential assets are experience in computational methods based on linear algebra, other algorithm experience, finite Markov chains, other computational or mathematical biology, bioinformatics, comparative genomics, PERL, MySQL. Contact Joanna Masel at [masel@u.arizona.edu](mailto:masel@u.arizona.edu) for more information and to apply.

[masel@U.Arizona.EDU](mailto:masel@U.Arizona.EDU) [masel@U.Arizona.EDU](mailto:masel@U.Arizona.EDU)

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## UArizona SystemsBiology

The postdoc will implement a computational model of transcriptional networks that is both realistic enough to be related to yeast data and simple enough for experimental evolution to be rapidly simulated. The model will then be used to study a range of questions, including network topology and the evolution of robustness/canalization to mutation, to the environment, and to the stochasticity associated with small numbers of molecules in cells.

The postdoc will work closely with PI Joanna Masel (<http://eebweb.arizona.edu/Faculty/bios/masel.html>) at the University of Arizona in Tucson, and will also interact with collaborator Mark Siegal ([www.nyu.edu/fas/dept/biology/faculty/siegal](http://www.nyu.edu/fas/dept/biology/faculty/siegal)) at NYU. The position is renewable over multiple years, and is available immediately. Ph.D. with modeling and/or scientific programming experience is required. Experience in systems biology, genomics, evolutionary biology and/or the biology of transcription factors and their binding sites is preferred.

Contact Joanna Masel at [masel@u.arizona.edu](mailto:masel@u.arizona.edu) for more information and to apply.

[masel@U.Arizona.EDU](mailto:masel@U.Arizona.EDU) [masel@U.Arizona.EDU](mailto:masel@U.Arizona.EDU)

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## UCC Cork Ireland MicrobialPopGenetics

Post-doctoral position, Microbial Population Genetics

Fixed Term Contract Post from 01.10.2007-31.05.2012

Applications are invited for a post-doctoral position in the newly created SFI research group on Microbial Population Genetics and Genomics (MPGG), led by Prof. Mark Achtman at University College Cork, Ireland. The successful applicant will be responsible for building on prior high-impact projects on *Salmonella enterica* Typhi. In particular, the applicant will initiate, conduct and supervise comparative genomic analyses of Typhi isolates from healthy carriers and acute phase disease to test the hypothesis that the healthy carriage state represents a protected niche in the population dynamics of these bacteria. The applicant will also be responsible for supervising additional ongoing projects on MLST and fine typing of *Salmonella*. With time, it is expected that the applicant will also write and submit grant applications for independent research.

The MPGG group will begin at UCC in June, 2007 and operate in parallel till 30.09.2008 with Mark Achtman's currently existing group at the MPI for Infection Biology, Berlin, whose publication record can be found at <http://web.mpiib-berlin.mpg.de/mlst/AGroup/team/marksRef.html> In addition to the post-doctoral fellow, the MPGG group will initially consist of Mark Achtman, Daniel Falush (currently Oxford University), a bioinformatician for genomics analyses, an informatics specialist/program manager and two doctoral students. Over the next three years, the MPGG group is anticipated to grow to a total size of 15-20 individuals. The successful candidate will be expected to participate in organization as well as the supervision and instruction of new members of the group.

The successful candidate will have a proven, track record of success in population genetics, microbiology, molecular biology and/or bioinformatics. Prior experience with medium to high throughput genetic typing and/or genomics is desirable but not absolutely necessary. Preference will be given to candidates with excellent communication and organizational skills.

A salary up to an initial gross salary of 41,553 (plus 10.75% Employer's PRSI and 13.5% Employer's pension costs) will be offered to the successful candi-

date, commensurate with experience and qualifications. Closing Date for informal discussions: 1 June, 2007. Starting date: 1 Oct, 2007

For informal discussions on this post, please contact Mark Achtman. [achtman@mpiib-berlin.mpg.de](mailto:achtman@mpiib-berlin.mpg.de).

Mark Achtman Max-Planck Institut für Infektionsbiologie Schumannstr. 21/22 10117 Berlin, Germany Tel: +4930 28460751 Fax: +4930 28460750 e-mail: [achtman@mpiib-berlin.mpg.de](mailto:achtman@mpiib-berlin.mpg.de)

Mark Achtman <[achtman@mpiib-berlin.mpg.de](mailto:achtman@mpiib-berlin.mpg.de)>

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## UCambridge ButterflyEvoDevo

Applicants are invited for two five-year Leverhulme-funded postdoctoral positions in the Zoology Department at the University of Cambridge. This is an exciting opportunity to study the developmental and genetic basis of dramatic phenotypic adaptations, namely the mimetic colour patterns of *Heliconius* butterflies. These butterflies are an excellent model system for studying the genetic basis of natural adaptation and diversity, in part because mimicry between species means that adaptive peaks are well defined, and that the same phenotypic adaptations have arisen multiple times. We have recently shown that the same regions of the genome are involved in mimicry in three different species, *H. melpomene*, *H. erato* and *H. numata*. In addition these same genes are also responsible for species level divergence and contribute directly to speciation. This project aims to develop our understanding of phenotypic adaptation and developmental evolution in *Heliconius*.

Position 1. EVO-DEVO: Gene regions controlling major phenotypic switches in colour pattern are being cloned and sequenced. This now offers an opportunity to study the function of natural allelic variants that have major phenotypic effects in development of pattern and colour. This position will develop functional assays for candidate genes and study their expression in different races of *Heliconius melpomene*. The postholder will need to develop techniques for RNAi knockdown experiments and perhaps also germline transformation in these butterflies in order to carry out functional assays. In addition the postholder will study expression patterns of candidate loci by rt-PCR, in situ hybridisation and/or antibody stains. The candidate should have a keen interest in evolutionary developmental biology and adaptation, and should have experience

in relevant experimental techniques such as antibody staining, rt-PCR and genetic transformation of insects.

Position 2. EVOLUTIONARY GENETICS: *Heliconius* offer a unique opportunity to study sequence variation around genes under strong selection in natural populations. The second position will study natural variation in *Heliconius melpomene* populations around the genes controlling colour pattern. The position will also involve fine scale linkage mapping of further patterning genes in mapping families that have already been obtained, and the identification of quantitative trait loci responsible for modifying the expression of major pattern elements. The successful applicant should have experience in the study of molecular evolution and a keen interest in the genetics of adaptation.

The two postdocs will join a dynamic group working on *Heliconius* butterflies at the Department of Zoology in the University of Cambridge. The department also includes other labs that offer opportunities for collaboration, including that of Prof. Michael Akam and Prof. Pat Simpson working on insect evo-devo, and Dr Nick Mundy and Dr Bill Amos working on evolutionary genetics. A new insect rearing facility is due to be built by the end of 2008 and will provide state of the art facilities to replace existing greenhouses for stock maintenance. The project is funded by Leverhulme and forms part of a collaboration between the University of Cambridge, Prof. Richard French-Constant at the University of Exeter (Cornwall Campus), Dr Jane Rogers and Dr Sean Humphray at the Sanger Institute, Dr Owen McMillan at NC State, who is carrying out a parallel project on *H. erato*.

Selected recent publications: Joron, M, et al. 2006 A Conserved Supergene Locus Controls Colour Pattern Diversity in *Heliconius* Butterflies *Plos Biology*. Vol. 4, No. 10, e303 Mavárez, J., Salazar, C., Bermingham, E., Salcedo, C., Jiggins, CD., Linares, M. 2006 Speciation by hybridization in *Heliconius* butterflies *Nature*. 441: 868-871. Joron, M. Jiggins, CD., Papanicolaou, A. McMillan, WO. 2006 *Heliconius* wing patterns: an evo-devo model for understanding phenotypic diversity *Heredity*. 97: 157-167..

In the first instance please contact me ([c.jiggins@zoo.cam.ac.uk](mailto:c.jiggins@zoo.cam.ac.uk)) for further details.

One of these posts will become a Senior Research Associate position which, subject to SRA status being established, an agreed salary would be backdated from the start of the appointment. For a standard application form and further details please see our website: <http://www.zoo.cam.ac.uk/zoone/-administration/vacancy.html> where the standard application form and Further Particulars can be obtained.

Completed application forms (Form PD18) together with a CV should be returned by the deadline, 30 June 2007 to The Departmental Administrator at: The Department of Zoology, Downing Street, Cambridge CB2 3EJ or via email: Reception@zoo.cam.ac.uk

Salary: £24,402-£31,840

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

## UChicago EvolYeastGeneRegulation

My lab has been pursuing research in the evolution of gene regulation in yeasts using both computational and experimental approaches. I am looking for an experimentalist with good molecular biology and genetics skills, some knowledge of yeast genetics and genomics, and a strong background in molecular evolution. The position is available now.

Applicants should send a CV and three references (email addresses and phone numbers) to Wen-Hsiung Li, Dept of Ecology and Evolution. Email: whli@uchicago.edu

Wen-Hsiung Li <whli@uchicago.edu>

## UCollegeLondon DrosophilaAdaptation

UNIVERSITY COLLEGE LONDON Department of Biology Centre for Evolutionary Genomics

Post-doctoral position in genetics and genomics of geographic adaptation in *Drosophila*

Applications are invited for a 3-year, post-doctoral position funded by the Natural Environment Research Council. The project will be conducted in close collaboration with the University of Melbourne, Australia.

The fruit fly *Drosophila*, show repeated, latitudinal, genetic clines in different continents, with body size increasing with distance from the equator. The clinal

patterns can evolve rapidly, within a decade, indicating that natural selection is involved. The aim of this collaborative programme of work is to reach a better understanding of the selective forces involved and the target of selection. This will in part be achieved by the mapping, identification and experimental manipulation of the genetic variants that underlie the latitudinal trend in body size.

The project will involve gene mapping, screening of candidate molecular variants, whole-genome RNA-expression profiling, genetic manipulation including homologous recombination, and phenotyping of flies. The appointee will have excellent skills in genetics and molecular biology of *Drosophila* and an ability to work collaboratively and in a busy laboratory. The post-holder will be responsible, in discussion with the Principal Investigators, for experimental design, day-to-day running of the project, data analysis and write-up and public presentation of the work. The post-holder will also be responsible for directing and supervising the day-to-day activities of the dedicated technician on the grant. The starting salary will be at spine point 31 on the Grade 7, ?27,465 plus ?2,497 London Allowance.

Application Process: It is essential that candidates first read the Job Description and Person Specification. Please do not apply for this post unless you fit the criteria outlined. To apply, visit <http://www.ucl.ac.uk/~ucbtcee/flies/positions.html>, where you can download the Job Description, Person Specification, and the UCL application form. This form must be completed, accompanied by a covering letter, a current CV and details of three referees and sent to: Professor L. Partridge FRS, c/o Judith James, Centre for Research on Ageing, Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT. Or email to [judith.james@ucl.ac.uk](mailto:judith.james@ucl.ac.uk)

If there are any difficulties in downloading the forms, please contact Judith James ([judith.james@ucl.ac.uk](mailto:judith.james@ucl.ac.uk)), Tel: 0207 679 4380.

Applications will be accepted until a suitable candidate has been identified.

UCL Taking Action for Equality

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Judith James PA to Linda Partridge UCL Centre for Research on Ageing Department of Biology University College London Darwin Building Gower Street London WC1E 6BT

Telephone: 020 7 679 4380 Fax: 020 7 679 2662 Email: [judith.james@ucl.ac.uk](mailto:judith.james@ucl.ac.uk) or [ucbhlof@ucl.ac.uk](mailto:ucbhlof@ucl.ac.uk)

PA to Linda Partridge/CEE Secretary



<ucbhlof@ucl.ac.uk>

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## UDublin TrinityCollege BarcodingBees

Dear Members,

I have a 3-year postdoctoral position (funded by Science Foundation Ireland) available to study the value of the DNA barcoding approach to species identification, cryptic species and species boundaries in solitary bees, a group of conservation importance. A further aim of this project is to integrate DNA-based and GIS-based approaches to produce a spatially explicit conservation tool.

Candidates must have experience in mtDNA sequencing and analysis, and in morphological identification of bees. Skills in GIS and an active interest in conservation, as well as evidence for publication in international journals would be advantageous. Applicants must have a valid driving licence as the study will involve field collecting.

For further details, or to apply, please contact me by email: [mabrown@tcd.ie](mailto:mabrown@tcd.ie) or go to <http://www.tcd.ie/Zoology/research/insects/opportunities.php> There is no closing date, but the position will filled as soon as a suitable candidate applies.

Yours,

Mark

Mark JF Brown, MA (Oxon), PhD Lecturer in Zoology Department of Zoology School of Natural Sciences University of Dublin Trinity College Dublin 2 Ireland

tel: +353 (0)1 896 1627 fax: +353 (0)1 677 8094  
email: [mabrown@tcd.ie](mailto:mabrown@tcd.ie) web: <http://www.tcd.ie/Zoology> [mabrown@tcd.ie](mailto:mabrown@tcd.ie)

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## UEdinburgh PlantGenomics

Postdoc position, EDINBURGH

UNIVERSITY of EDINBURGH Faculty of Biomedical & Life Sciences Division of Environmental and Evolutionary Biology

POST-DOCTORAL RESEARCH ASSISTANT IN  
PLANT GENOMICS AND ADAPTATION

SALARY £26,666 - £31,840 per annum

Ref: 3007265

A Post-Doctoral Research Assistant position is available for 2 years to work on a project entitled "Leveraging the genome sequences of two Arabidopsis relatives for evolutionary and ecological genomics", funded by a grant from the Biotechnology and Biological Sciences Research Council, as part of an international consortium assembled under the ERA-plant genomics initiative.

The specific aims of the consortium are to: 1) Detect genomic regions responsible for species-specific adaptation 2) Identify genetic variation affecting a model adaptive trait in Arabidopsis and Capsella 3) Compare evolution of self-incompatibility (SI) in Arabidopsis and Capsella

The Edinburgh contribution to the project will be to study DNA sequence diversity within and between natural populations of Arabidopsis lyrata, and will involve molecular laboratory work and population genetics analyses. The goals will be to provide reference loci to aid the analyses of selection which will be done in other laboratories in the consortium, and to provide expertise in population genetics analyses.

The applicant must have a PhD or equivalent, and must have molecular laboratory experience, including sequencing experience, and should also have previous experience in software for sequence analyses, such as sequence alignment, and, ideally, in population genetics analyses.

Further particulars about the post and the research environment, and online application forms can be found at: <http://www.jobs.ed.ac.uk/>. A CV will be required, and the names, postal and e-mail addresses and fax numbers of two academic referees.

Closing Date: 11 April, 2007.

Informal enquiries by email can be sent to Deborah Charlesworth <[deborah.charlesworth@ed.ac.uk](mailto:deborah.charlesworth@ed.ac.uk)>. – Professor Deborah Charlesworth Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Ashworth Lab., King's Buildings, West Mains Rd., Edinburgh EH9 3JT, UK

phone 131-650-5751 Fax: 131-650-6564

Deborah Charlesworth <[deborah.charlesworth@ed.ac.uk](mailto:deborah.charlesworth@ed.ac.uk)>

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## ULausanne FishEvolBioinformatics

A postdoc position is open to study the molecular evolution of teleost fishes, particularly in relation to whole genome duplication.

The position is funded for two years. Freedom will be given to the person to explore any aspects which s/he might find interesting, within the limitations of a bioinformatic approach.

Our laboratory has a double affiliation to the Department of Ecology and Evolution of Lausanne University (<http://www.unil.ch/dee>) and to the Swiss Institute of Bioinformatics (<http://www.isb-sib.ch>). We investigate the relation between genome evolution and evolution of development, using or developing bioinformatic tools. We are situated on the beautiful campus of Lausanne, with view on the Geneva lake and Mont Blanc. Public transportation is excellent, and the atmosphere in the Department is friendly. The working language of the lab and the Department is English. For further information, see our webpage: <http://www.unil.ch/dee/page22707.html>

Candidates should have a PhD, preferably in evolutionary biology. Salary starts at 58 kCHF/year (approx 35.5 kEuros/year), depending on experience. An estimation of the cost of life in Lausanne can be found here: <http://www.unil.ch/bienvenue/page8184.en.html> Interested candidates should send a CV, a one page research project, and the contact information of two references, to [marc.robinson-rechavi@unil.ch](mailto:marc.robinson-rechavi@unil.ch)

--- Marc Robinson-Rechavi <http://www.unil.ch/dee/-page22707.html> Department of Ecology and Evolution Biophore, University of Lausanne, 1015 Lausanne, Switzerland. tel: +41 21 692 4220 fax: +41 21 692 4165

Swiss Institute of Bioinformatics <http://www.isb-sib.ch/> La liberte ne s'use que quand on ne s'en sert pas

Marc Robinson-Rechavi <[Marc.Robinson-Rechavi@unil.ch](mailto:Marc.Robinson-Rechavi@unil.ch)>

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## ULaval QTLAssociationMapping

- Arborea is a Canadian large-scale research project, which involves about fifty people from universities and governmental institutions. We want to hire a post-doctoral fellow for QTL and association mapping study. The research agenda of the project is the following : Discovery of genomic tools for the conservation and sustainable use of natural genetic resources, including the identification of novel varieties to improve productivity and value in spruces by integrating functional genomics and association studies.

Description: \*QTL data analyses to detect genes and or genomic regions involved in growth related-traits and adaptation in eastern white spruce (*Picea glauca*) \*Conduct association study in natural populations to look for alleles/genes involved in growth and adaptation \*Conduct association study in structured populations to look for alleles/genes involved in wood formation \*Supervision of students and technical staff in related areas \*Redaction and presentation of scientific papers and reports in referree journals and scientific conferences \*The successful candidate will be expected to develop strong lines of communication and coordination of activities with group members at the Canadian Forest Service in Québec City, as well as with other participants in the project, principally at Université Laval and the University of Alberta

Qualifications: \*Doctoral degree (Ph. D.) in population genetics or related field, or statistics applied to genetics, or QTL data analysis, and or related areas \*Experience with computation methods \*Experience in analysis of mixed-models \*Very good verbal and written communication skills. \*Demonstrated aptitudes for teamwork \*Ability to work independently and to supervise

Compensation and conditions: \*Duration of contract: one year (renewable) \*Salary range: NSERC (Visiting Fellowships in Canadian Government Laboratories) \*Location of employment: Natural Resources Canada, Canadian Forest Service-Quebec (Quebec City)

Please send a resume, a description of research experience, and contact information of three references to:

M. Pascal Poulin Pavillon Charles-Eugène-Marchand Université Laval Sainte-Foy, Québec, Qué G1K 7P4 E-mail : [info@arborea.ulaval.ca](mailto:info@arborea.ulaval.ca)

pascal.poulin@rsvs.ulaval.ca

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## URennes EvolEcol

A one year post-doc position (eventually 2 years) is available from September 1, 2007 at the University of Rennes, France.

Title: "Climatic change and the evolution of life-history and foraging behaviour in parasitoids" Candidate profile: The post-doc will develop models to investigate phenotypic and long term evolutionary consequences of climate change on life-history trade-offs and foraging behaviour of parasitoids. The ideal candidate will work in close collaboration with the empirical researchers and with the local expert in stochastic modeling (Prof. JS Pierre). She/he has a strong interest in the evolution of life history traits and insect behaviour and preferably has previous experience in state-dependent stochastic dynamic modeling. The post-doc will participate in the project COMPAREVOL of the Marie Curie Excellence Chair, held for three years by Prof. Jacques van Alphen in the ECOBIO group (UMR) at the University of Rennes1 and financed by the EU and the region of Brittany. He (she) will be integrated in the team Impact of Climate Changes of the UMR ECOBIO. The UMR ECOBIO, led by Dr. P. Marmonier, includes 55 research scientists, 25 engineers and technicians, 30 Post-doc and PhDs in 2006. The research area of the UMR concerns Ecology in the broadest sense, from genetic expression, life-history traits evolution and adaptation to landscape ecology.

The deadline for applications is April 30, 2007.

Salary: 2500 per month

For more details in french: <https://www2.cnrs.fr/-DRH/post-docs07/?pid=1&action=view&idW5> <<https://www2.cnrs.fr/DRH/post-docs07/?pid=1&action=view&idW5>> in english: <https://www2.cnrs.fr/DRH/postdocs07/?pid=1&action=view&idW5&lang=en> <<https://www2.cnrs.fr/DRH/postdocs07/?pid=1&action=view&idW5&lang=en>>

postdocs07/?pid=1&action=view&idW5&lang=en>

Contacts: J.J.M.van.Alphen@biology.leidenuniv.nl  
<<mailto:J.J.M.van.Alphen@biology.leidenuniv.nl>> ,  
joan.van-baaren@univ-rennes1.fr

t.j.m.van.dooren@biology.leidenuniv.nl

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## URochester EvolGenetics

Postdoctoral Position, Evolutionary Genetics University of Rochester, Rochester, NY, U.S.A.

A three-year NIH-funded postdoctoral position is available in the laboratory of Dr. James Fry to study the genetic basis of adaptation to dietary ethanol in *Drosophila*. Ethanol is a natural component of *Drosophila* breeding sites, and ethanol resistance shows substantial and apparently adaptive variation among wild *D. melanogaster* populations. The powerful genetic tools available in *D. melanogaster* make this an excellent system for studying the genetic basis of adaptive variation in a trait that has both ecological and medical relevance. Preference will be given to applicants with demonstrated experience in some or all of the following: basic molecular methods, *Drosophila* genetics, bioinformatics, and population/quantitative genetics.

Applicants should send C.V., 1-2 page statement of research accomplishments and interests, names and contact information for three references, and up to four reprints or preprints, by email to [jfry@mail.rochester.edu](mailto:jfry@mail.rochester.edu) . More information on the Fry laboratory, and on the Evolutionary Biology group at the University of Rochester, may be found at the following links:

<<http://www.rochester.edu/College/BIO/professors/fry.html>><http://www.rochester.edu/College/BIO/professors/fry.html> <http://www.rochester.edu/College/BIO/professors/dept/Ecology+and+Evolutionary+Biology.html>  
[jfry@mail.rochester.edu](mailto:jfry@mail.rochester.edu)

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### Berlin CompSsystemsBiol Aug27-Sep5

Dear colleague,

we are happy to announce the

Otto Warburg International Summer School and Workshop on Computational Systems Biology

August 27 to September 5, 2007

Harnack House, Berlin, Germany

The aim of this program is to bring together researchers and students from different backgrounds (including molecular biology, bioinformatics, biological physics) to discuss a topic of high current interest. We plan an integrated program, which is focused on high-level training during the first days and leads to topical research seminars in the second part. The schedule will leave sufficient time for discussion and interaction among students and lecturers.

Invited speakers:

Alexander Bockmayr - Berlin Hamid Bolouri - Seattle Hanspeter Herzel - Berlin Thomas Höfer - Heidelberg Steffen Klamt - Magdeburg Florian Markowitz - Princeton Pedro Mendes - Manchester Balasz Papp - Manchester John Tyson - Blacksburg Ralf Zimmer - München

Scientific Coordinators:

Peter Arndt - Edda Klipp - Martin Vingron Max Planck Intitute for Molecular Genetics, Berlin

The deadline for applications is June 17, 2007. The registration fee of 600 EUR includes costs for accommodation, social events and meals.

The application form is available online on the workshop's website at

<http://ows.molgen.mpg.de> The announcement as a

printable poster is available from

<http://ows.molgen.mpg.de/2007/poster07.pdf> For further questions please contact

Hannes Luz c/o Max Planck Institute for Molecular Genetics Computational Molecular Biology Ihnestrasse 73 D-14195 Berlin, Germany Tel: +49 30 8413 - 1154 Fax: +49 30 8413 - 1152 Email: [luz@molgen.mpg.de](mailto:luz@molgen.mpg.de)

Best regards,

the Otto Warburg Summer School team

Hannes Luz Max Planck Institute for Molecular Genetics | Tel: +49 30 8413 - 1154 Computational Molecular Biology | Fax: +49 30 8413 - 1152 Ihnestrasse 73 | Email: [luz@molgen.mpg.de](mailto:luz@molgen.mpg.de) D-14195 Berlin, Germany | [www.imprs-cbsc.mpg.de](http://www.imprs-cbsc.mpg.de) hannes luz <[luz@molgen.mpg.de](mailto:luz@molgen.mpg.de)>

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### Cancun CompBiol Aug20-26

Dear Colleagues,

We are pleased to inform you about the upcoming workshop:

“Computational biology: From genomes to cells & ecosystem”

in Cancun (Mexico) sponsored by EMBO World Practical Course program.

The 7-day workshop (August 20-26th 2007 at the Oasis Hotel in Cancun) introduces advanced methods and applications in computational biology ranging from molecules to ecosystems with a particular focus on metagenomics.

Participation is restricted to 20 graduate students and postdocs, who will work on biological problems that could even lead to scientific discoveries made during the course. For all participants, fellowships will be made

available covering housing, subsistence and registration.

Further information and registration:  
at <http://cwp.embo.org/wpc08-01> Email:  
genomes2ecosystems@googlegroups.com

Sincerely Yours

francesca ciccarelli, for the organizers\*

\* Organizing Committee of the EMBO Workshop on Computational biology: "From genomes to cells & ecosystems" Cancun (Mexico), August 20-26, 2007:

Dr. Peer Bork, EMBL Heidelberg , Germany Dr. Francesca D. Ciccarelli, EIO Milan, Italy Dr. Jan Korb, Yale University, New Haven, CT USA Dr. Roland Krause, Max-Planck-Institute Berlin, Germany Dr. Enrique Morett, UNAM, Cuernavaca, Mexico

– Francesca D. Ciccarelli, PhD Biocomputing IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303-053 fax +39-02574303-231 web: <http://ciccarelli.group.ifom-ieo-campus.it/fewiki/> Upcoming EMBO Workshop on "Computational Biology: From genomes to cells & ecosystems / Cancun 2007" More info at <http://cwp.embo.org/wpc08-01> francesca.ciccarelli@ifom-ieo-campus.it francesca.ciccarelli@ifom-ieo-campus.it

themes\_polyploidy.htm> you might like to join us at the Kaikoura field station - 2.5 hours drive north of Christchurch in Kaikoura - 13th -15th June (and if there is sufficient interest, at the Cass field station - 1.5 hrs drive from Christchurch near Arthur's Pass in the southern Alps - 11<sup>th</sup> and 12<sup>th</sup> June) .

These occasions will provide an opportunity to meet with some of the New Zealand plant research community, discuss research, and at the same time see a bit more of New Zealand. There is no charge for attending, and free Hostel style bunk-bed accommodation is available at the field stations, but you need to bring a sleeping bag. Food can be bought in Kaikoura (there is a supermarket, many restaurants and cafes). At Cass, food needs to be brought in. Because there are a limited number of beds available, bookings in advance are necessary.

If you are interested in attending please email Mort Piripi (m.m.piripi@massey.ac.nz) as soon as possible and before May 30<sup>th</sup> .

Best wishes

Pete Lockhart

Professor of Molecular Evolution Allan Wilson Centre for Molecular Ecology and Evolution Massey University, New Zealand

M.M.Piripi@massey.ac.nz M.M.Piripi@massey.ac.nz

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## Christchurch PlantEvol Jun11-15

NZ Plant Evolution Workshop

If you are arriving early for the June 16-20 Evolution meeting in Christchurch, New Zealand <http://www.evolution2007.com/> and are interested in talking informally about plants, and in particular about the research themes that are described on the New Zealand Plant Radiation Network website <http://awcmee.massey.ac.nz/NZPRN/themes.htm>

\* Delimitation of Species Boundaries <[http://awcmee.massey.ac.nz/NZPRN/themes\\_species.htm](http://awcmee.massey.ac.nz/NZPRN/themes_species.htm)>

\* Evolutionary drivers of radiation <[http://awcmee.massey.ac.nz/NZPRN/themes\\_radiation.htm](http://awcmee.massey.ac.nz/NZPRN/themes_radiation.htm)>

\* Impact of climate change on distribution and diversity <[http://awcmee.massey.ac.nz/NZPRN/themes\\_climate.htm](http://awcmee.massey.ac.nz/NZPRN/themes_climate.htm)>

\* Reconstructing the evolutionary history of species radiations <[http://awcmee.massey.ac.nz/NZPRN/themes\\_history.htm](http://awcmee.massey.ac.nz/NZPRN/themes_history.htm)>

\* The genetic basis of diversification <[http://awcmee.massey.ac.nz/NZPRN/themes\\_genetics.htm](http://awcmee.massey.ac.nz/NZPRN/themes_genetics.htm)>

\* Evolutionary significance of hybridisation and polyploidy <<http://awcmee.massey.ac.nz/NZPRN/>

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## Hawaii GenomeScalePhylogenies Jan4-8

Call for Papers and Posters

Beyond gap models: reconstructing alignments and phylogenies under genomic-scale events

A Pacific Symposium on Biocomputing 2008 Session January 4-8, 2008 Fairmont Orchid, The Big Island of Hawaii Hawaii, U.S.A.

Multiple sequence alignment (MSA) has long been a mainstay of bioinformatics and has proved quite useful in the alignment of well conserved protein and DNA sequences; some of these sequences have also been used with great success in phylogenetic reconstruction. Sequences with low percentage identity, on the other hand, typically yield poor alignments. Now that researchers want to produce alignments among widely divergent genomes, including both coding and noncoding sequences we need to revisit both multiple alignment

and phylogenetic reconstruction under more ambitious models, ones that take into account the plethora of genomic events rather than just substitutions and insertions/deletions (indels). We also need to revisit multiple sequence alignment and phylogeny reconstruction for datasets currently beyond the capability of existing methods, due to high rates of site substitution, high indel rates, and large numbers of taxa or sites. Most current methods postulate only two types of events: substitutions (modeled with a transition matrix, such as PAM or BLOSUM matrices for protein data) and indels (rarely modelled beyond a simple affine cost function for the size of the gaps). While these two events can indeed transform any sequence into any other, their model of genomic events is far too simplistic: substitutions are not location- or neighbor-independent and indels can be caused by a variety of complex events, such as uneven recombination, insertion of transposable elements, gene duplication/loss, lateral transfer, etc. Moreover, genomic rearrangement events can completely mislead procedures based on most current models, resulting in a total loss of alignment when a homologous element has undergone an inversion or a duplication. Computational biologists have been studying genome rearrangements for 20 years and have started work on duplication and loss events. Taking these events into account in a multiple alignment will require the simultaneous construction of the alignment and of the phylogenetic tree – an approach also known as phylogenetic alignment. Up to very recently, the computational complexity of phylogenetic alignment was widely viewed as too high, but the state of the art in phylogenetic reconstruction has advanced significantly over the last 10 years, both in terms of accuracy and in terms of computational efficiency, so that what was then impossible is now merely difficult.

#### Session Topics

We would like to invite contributions presenting new methods for multiple sequence alignment, new simulation software for evolving sequences under complex models of evolution, or evaluations of existing methods for multiple sequence alignment or phylogenetic reconstruction under such models. Papers presenting new methods should provide experimental or empirical evidence of the performance of the new methods. In addition, papers that present novel empirical evidence of complex evolutionary processes operating on molecular sequences are welcome. In this context, submission topics can include, but are not limited to: - Methods for simultaneous alignment and phylogeny reconstruction under site substitutions and indels that demonstrate clear benefits over independent MSA and phylogeny reconstruction. - Methods and models for

genomic-scale alignment and phylogenetic reconstruction, including the handling of gene families. - Comparisons of existing MSA and phylogeny reconstruction methods under complex models. - Molecular evolution relevant to the above topics. Other topics within the subject area are welcome. Note that all submitted papers should demonstrate the relevance to this topic. If unsure whether your paper fits the session theme, please contact one of the co-chairs.

See <http://www.cs.utexas.edu/users/tandy/cfp.html> for submission instructions

#### Session Co-chairs

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## KansasStateU ArthropodGenomics Apr20

KSU Arthropod Genomics <[dmerrill@KSU.EDU](mailto:dmerrill@KSU.EDU)>

Just a reminder that the 1st Annual Arthropod Genomics Symposium is scheduled for Friday, April 20, 2007, in the Big 12 Room of the Kansas State University Student Union in Manhattan, Kansas. A Poster Session is planned during lunch from 12:30 to 2:00. You are invited to set-up your poster between 7:30 and 8:00 a.m. during registration check-in.

Registration is FREE but is required to obtain a count of attendees for lunch. Please register online at: <<http://www.ksu.edu/agc/RegisterOnline.shtml>> [www.ksu.edu/agc/RegisterOnline.shtml](http://www.ksu.edu/agc/RegisterOnline.shtml), and provide us with information about your poster title and authors.

Featured speakers at the Symposium include: <<http://www.nd.edu/%7Ebiology/romero-severson.shtml>>  
 Dr. Jeanne Romero-Severson, University of Notre

Dame; and Dr. Stephen Richards, Human Genome Sequencing Center, Baylor College of Medicine. K-State faculty will also provide information about their Arthropod Genomics research projects including: Srinu Kambhampati, Entomology; Anna Whitfield, Plant Pathology; Kun Yan Zhu, Entomology; Christopher Culbertson, Chemistry; and Gerald Reeck, Biochemistry.

The Symposium will begin with refreshments at 7:30 am and conclude by 2:00 pm. A poster session will be held in the Union Concourse on the 2nd Floor. A brochure with the symposium schedule is attached and is also available at our website, <<http://www.k-state.edu/agc/symposium.shtml>> <http://www.k-state.edu/agc/symposium.shtml>. Please register TODAY and plan to attend! We will appreciate your sharing this invitation with colleagues and students.

If you have already registered, THANK YOU.

Funded by Targeted Excellence at Kansas State University

Doris Merrill, Program Coordinator K-State Arthropod Genomics Center Division of Biology, Kansas State University 116 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, [dmerrill@ksu.edu](mailto:dmerrill@ksu.edu)

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### LakeheadU AncientDNA May22-Jun9

#### Ancient DNA Training Program

A training program focused on training participants in the analysis of degraded, difficult, ancient or low copy number DNA.

The ancient DNA training program is a three week intensive course in DNA. This year we are delivering the program from May 22nd to June 9th, 2007 at the Paleo-DNA laboratory Lakehead University.

During the program, participants will work in small groups (one instructor to 4 participants) and are given a project depending upon their interests. This may be genetic analysis of museum specimens, genetic analysis of degraded samples, disease in ancient mummified tissue, genetic analysis of archived specimens or forensic profiling of a remains or many other such projects. As a participant, you will learn a variety of different extraction methods to compare and contrast on both your

own DNA and other samples. You will generate your own DNA profile, determine your own mitochondrial haplogroup/haplotype, your own STR profile, confirm your own sex genetically and learn numerous techniques for the analysis of DNA.

The lectures will include the history of various types of analytical techniques, detailed mechanisms of each method and an large array of techniques that can be used in a genetic project. Participants will learn about the different types of DNA that can be analyzed: mitochondrial, nuclear, chloroplast and pathogenic DNA. You will be taught different methods of analysis PCR-RFLP, multiplex PCR, sequencing, regular PCR and electrophoresis. You will learn different methods of sample preparation from a number of different tissue types like bone, teeth, hair, archived specimens, museum specimens, blood residues and mummified tissue.

You will understand the use of genetic analysis and its potential in archaeozoology, palaeopathology, archaeology, forensic science, palaeobotany and palaeontology. Lectures by professors and senior analysts in the fields of archeology, genetics, ancient DNA, forensic science, palaeopathology and more are integrated with the laboratory sessions.

If you would like further information, please visit our website at <http://www.ancientdna.com/> or feel free to contact me at [cjaspers@lakeheadu.ca](mailto:cjaspers@lakeheadu.ca).

With many thanks,

Cheryl Jaspers Administrator Ancient DNA Training Program Paleo-DNA Laboratory Lakehead University Thunder Bay, ON 1-807-343-8862 [cjaspers@lakeheadu.ca](mailto:cjaspers@lakeheadu.ca)

Carney Matheson <[cmatheso@lakeheadu.ca](mailto:cmatheso@lakeheadu.ca)>

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### Leksand Sweden EcolGenomics Nov4-7

We announce a workshop in ECOLOGICAL GENOMICS that will address evolutionary and ecological genetics issues in natural populations using the new technologies and methods provided by genomics studies. The major obstacle is to apply methods arrived in model species to rare and threatened species where genomic information is scarce.

The following major topics will be addressed by keynote speakers (Roger Butlin, Scott Edwards, Volker

Loeschcke, Stuart Piertney, Jon Slate) - Review of the use of "candidate genes" in ecology and conservation. - The use of AFLP based genome wide scans in studies of speciation and identification of genes promoting the speciation process. - The use of transcriptome profiling in ecology - QTL mapping and SNP analysis in the post-genomics era - Genomic synteny and evolution

The workshop will be held in the centre of Sweden (Leksand, <http://www.langbers.se/>) from the 4-7.11.2007 (arrival Sunday 4.11., departure Wednesday 7.11.)

We here Call for Applications Please provide a title and an abstract of at most one page and add also a short list of your three most relevant publications. Note that the workshop is limited to 25 participants, and a final selection will be done at the beginning of May. Grant applications will be chosen based on scientific quality, and priority will be given to applicants who come from countries supporting the programme (Austria, Belgium, Croatia, Czech Republic, Denmark, Finland, France, Hungary, Netherlands, Norway, Spain, Sweden, Turkey). Funding will cover all local costs (accommodation, meals) and part of the travel costs.

Deadline for registration is April 21th 2007

Send applications by e-mail to:

Dr. Gernot Segelbacher  
gernot.segelbacher@wildlife.uni-freiburg.de

Organizers: Gernot Segelbacher Jacob Hoeglund Dept. Wildlife Ecology Dept. Population Biology University of Freiburg Uppsala University

<http://www.esf.org/congen/> -

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segelbac@orn.mpg.de

<http://www.wildlife.uni-freiburg.de/team/segelbacher>  
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## UCopenhagen PlantMolMarkers May21-25

Some time ago, I posted the following course on evoldir. There are still empty seats, so you or your students still have a chance to sign up.

Invitation for Ph.D. course "Molecular marker analy-

sis of plant population structure and processes", 21-05-2007 - 25-05-2007 at Faculty of Life Sciences, University of Copenhagen (formerly the Royal Veterinary and Agricultural University).

This course provides the participants with advanced knowledge of the analysis of genetic structure, mating patterns, and population processes in plant populations, using molecular marker data. The course includes theoretical lectures, discussions of student projects, and exercises with various computer programs. This course is Module 3 of the course package: "Molecular plant breeding and genetic resources", <http://www.kursus.kvl.dk/shares/-phdmarker/index.htm>. Course content: Estimation of diversity, inbreeding level, restricted gene flow, population admixture, hybridization, selfing rate, paternity assignment, and allocation to parental populations and hybrids. Assumptions and limitations behind diverse procedures used in relevant computer programmes, such as: GenAlEx, Spagedi, Structure, MLTR, Two-gener, Population Graph, Split tree, New Hybrids, AFLPOP, Famos, Cervus, etc. Discussion of student projects (use this opportunity to discuss your Ph.D. research!). Practical computer analysis with various software.

Course credit: 3 ECTS points. Requirement for obtaining credit: approval of a written synopsis of the course content. Course material: All course material, such as discussion articles, presentations and software, will be available through a restricted web site. All software to be used is freely available.

Practicals: Maximum number of participants is twenty. Ph.D. students have preference until 15/4; after that, remaining seats' are open to interested non-PhD students. Final deadline for registration is May 1st. The course will take place at the Faculty of Life Sciences, University of Copenhagen, 1958 Frederiksberg C (part of Copenhagen). Computers will be available for all; if you prefer to bring your own laptop computer, do that. Coffee and tea will be served. Travel, lodging, and accommodation are to be organised and paid by the participants on their own; suggestions for hostels and hotels will be posted on the web. Course fee: none.. Organisers and teachers: Gunter Backes, Associate Professor in Plant Breeding, guba@life.ku.dk; Ole Kim Hansen, Ph.D. in Forest Genetics, okh@life.ku.dk; Thure Hauser, Associate Professor in Plant Ecology, tpha@life.ku.dk; Erik D. Kjær, Professor in Forest Genetics, edk@life.ku.dk.

Registration and questions: Write an e-mail to Thure Hauser, tpha@kvl.dk, containing the following information: Full name, sex, e-mail address, mobile phone no.,



institution, full mailing address, country, whether you are a Ph.D. student, title of present research project, whether you would like to present your project during the course; in that order and on separate lines. tpha@life.ku.dk

Thure Hauser, Ph.D., Associate Professor Depart-

ment of Ecology Faculty of Life Sciences University of Copenhagen Rolighedsvej 21 DK-1958 Frederiksberg C. Phone: 3528 2818 or 3528 2800 Mobile: +45 2011 4469 Fax: 3528 2821 E-mail: tpha@kv1.dk

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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 the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

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

## Afterward

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