# EvolDir

April 6, 2007

Month in Review

## Forward

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

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

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

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# Conferences

## 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 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>

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## Edinburgh InsectParasiteEvol Jul16-18

Insect Immunity and Parasite Symposia

Royal Entomology Society, Edinburgh. 16-18th July 2007

This year's Royal Entomological Society meeting will be held in Edinburgh, and includes several symposia on host-parasite interactions. The first afternoon will include symposia on insect parasites and medical/veterinary entomology. The subsequent two days will have sessions on the evolution and mechanisms of insect immunity.

Registration and details are at: http://www.ento07.org.uk/. Tick either insect parasites or insect immunology on the registration form to be included in these sessions.

fjiggins@staffmail.ed.ac.uk fjiggins@staffmail.ed.ac.uk

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## Halifax EvolutionaryEthology Aug

Dear ethologists,

We have decided to extend the Call for Abstracts for the International Ethological Conference in Halifax, Canada, to Saturday March 24. Find below the link to the conference's web site, registration site, the list of Plenary Speakers, and the list of Symposia titles and organisers.

Hope to see you in Nova Scotia in August!

Regards,

The local organising committee

IEC 2007's web site: <http://iec2007.psychology.dal.ca/iec2007/Home.html>http://iec2007.psychology.dal.ca/iec2007/Home.html Registration and abstract submission site: <https://www.esecureshop.com/registration/iec2007/index.asp>https://www.esecureshop.com/registration/iec2007/index.asp IEC Plenary Speakers

Opening Public lecture:

Hal Whitehead, Dalhousie University, Canada. "Adventures of a marine mammalogist in the study of whale language and culture"

Plenary lectures:

Patrick Bateson, Department of Zoology, University of Cambridge, England "Developmental Plasticity and Epigenetics".

Pat Monaghan, University of Glasgow, Scotland. "Growth, lifespan and life history trade-offs"

Elisabetta Visalberghi, Istituto di Scienze e Tecnologie della Cognizione, Rome, Italy "Behavioral, cognitive and ecological factors affecting tool use in wild capuchin monkeys"

Atsushi Iriki, RIKEN Brain Science Institute, Japan. "Brain mechanism for development and evolution of monkey tool-use as a latent precursor of human intelligence"

Roger T. Hanlon, Marine Biological Laboratory, Woods Hole, USA "Masters of optical illusion: the neuroethology of rapid adaptive camouflage and communication in cephalopods"

Horst Bleckmann, Institut für Zoologie der Universität Bonn, Germany. "Neuroethology of Sensory Systems"

Rui Oliveira, Instituto Superior de Psicologia Aplicada, Lisboa, Portugal "From hormones to behavior and back: androgens, social context and competition".

Hanna Kokko, University of Helsinki, Finland "Love and hatred in a world of feedback"

Sara J. Shettleworth, University of Toronto, Canada "Cognitive ethology in the 21st century"

Marian Stamp Dawkins, Department of Zoology, University of Oxford, England "The scientific basis for assessing suffering in animals"

Robert L. Trivers, Department of Anthropology, Rutgers University, USA "Human Ethology / Genes in Conflict: The Biology of Selfish Genetic Elements"

Maydianne Andrade, Department of Life Sciences, University of Toronto, Canada. "Sexual selection and the evolution of extreme reproductive strategies"

Symposia titles and organisers

“Prospective cognition and future planning by animals” Nicola Clayton and Anthony Dickinson

“Integrative perspectives on animal contests” Ryan L. Early

“Behavioural epigenetics” Timothy Bredy

“Swarms of insects, fish, birds, and ungulates: models and empirical data” Charlotte Hemelrijk

“Does paternal care require partner preference?” Katherine E. Wynne-Edwards

“Maternal effects: evaluating maternal effects on the basis of Tinbergen’s four questions” Jeff Graves and Ton Groothuis

“Acoustic communication in noise” Peter J. B. Slater and Henrik Brumm

“Uncertainty in animal cognition” Robert Biegler

“Social and cognitive convergence in vertebrates” Isabella Scheiber, Robyn Hudson, Kurt Kotrschal

“Social networks: Patterns” Jens Krause

“Social networks: Processes” David Lusseau

“Allonursing: an adaptive behavior in mammals?” Beatriz Zapata and Luis Ebensperger

“Avian social cognition: Do birds think about other minds?” Nathan J. Emery and Shige Watanabe

“Developmental influences on behavioural phenotypes: implications for animal welfare” Georgia Mason

“Physiology, Ethology, and Wildlife Conservation” Christina Buesching

“Welfare assessment: new ideas” Donald Broom

Dr Richard E. Brown Killam Research Professor and Chairman Department of Psychology Dalhousie University Halifax, Nova Scotia CANADA B3H 4J1

email: rebrown@dal.ca

tel: 902-494-3647 fax: 902-494-6585 http://myweb.dal.ca/rebrown/ International Ethological Congress. Halifax 15-23 August 2007 http://iec2007.psychology.dal.ca/ Richard Brown <rebrown@dal.ca>

## Halifax SMBE Jun24-28 3

The 2007 annual meeting of the Society for Molecular Biology and Evolution (SMBE) is being held JUNE 24-28 at Dalhousie University in Halifax, Nova Scotia, Canada. The meeting is being co-hosted by the Canadian Institute for Advanced Research.

Conference registration is now open:

http://www.smbe.org/ The deadline for submission of conference presentation abstracts and titles is MAY 15. Please note that registration fees will increase after APRIL 15. We encourage you to register early and to become a member of SMBE:

http://www.smbe.org/membership.php IMPORTANT: Halifax is a busy tourist destination in summertime. We STRONGLY ADVISE you to reserve your hotel or dorm rooms early at the following website:

https://smbe2007.dal.ca/Accommodation/ Please refer to the SMBE website for more information on conference registration, abstract submission, symposium topics, preliminary schedule, awards, travel, and more.

Plenary Speakers

MAY BERENBAUM–Department of Entomology, University of Illinois at Urbana-Champaign DEBORAH CHARLESWORTH–School of Biological Sciences, University of Edinburgh MARCUS FELDMAN–Department of Biological Sciences, Stanford University NICK LANE–University College London, author of “Oxygen: The Molecule that made the World” and “Power, Sex, Suicide: Mitochondria and the Meaning of Life” TRUDY MACKAY–Department of Genetics, North Carolina State University BRIAN SPRATT–Molecular Microbiology, Imperial College London

SymposiA and invited SPEAKERS (*indicates chair)

Bayesian phylogenetic inference

Robert Beiko*, Dalhousie University John Huelsenbeck, University of California-Berkeley Bret Larget, University of Wisconsin Nicolas Lartillot, LIRMM Marc Suchard*, UCLA

Towards more realistic models of protein evolution

Cecile Ané, University of Wisconsin Christian Blouin*, Dalhousie University Nick Goldman, European Bioinformatics Institute Richard Goldstein, National Institute for Medical Research Andrew Roger*, Dalhousie University Ed Susko*, Dalhousie University Ziheng Yang, University College London Eukaryotic and prokaryotic genome beginnings

Eukaryotic and prokaryotic genome beginnings

Siv Andersson, Uppsala University Martin Embley, University of Newcastle Doug Erwin, Smithsonian

Institution Peter Gogarten, University of Connecticut Jim Lake*, UCLA William Martin, Universität Düsseldorf J. William Schopf, UCLA

Evolutionary genomics of domestication

Carlos Bustamante*, Cornell University Brandon Gaut*, UC-Irvine Elaine Ostrander, NIH Francesco Salamini, Max-Planck-Institute für Züchtungsforschung Tao Sang, Michigan State University Scott Williamson, Cornell University

Evolution and function of non-protein-coding sequences in complex organisms

Jürgen Brosius, University of Münster Elliott Margulies, NHGRI (NIH) John Mattick*, University of Queensland

Extreme genomes

Jean-Michel Claverie, CNRS Patrick Keeling*, University of British Columbia Atsushi Nakabachi, University of Arizona Jeffrey Palmer, Indiana University

Gene / genome duplication

Keith Adams*, University of British Columbia Matthew Hahn, Indiana University Claude de Pamphilis, Penn State University Yves van de Peer, University of Ghent Shin Han Shiu, Michigan State University Todd Vision, University of North Carolina

Genomics of speciation

Dan Hartl*, Harvard University Hopi Hoekstra, University of California-San Diego Rob Kulathinal*, Harvard University John Willis, Duke University

Introns early, introns late: the sequel

Ford Doolittle*, Dalhousie University Eugene Koonin, NIH Michael Lynch, Indiana University Scott Roy, Harvard University Arlin Stoltzfus, CARB

Lateral gene transfer, the tree, ring, web or network of Life

Ford Doolittle, Dalhousie University Peter Gogarten, University of Connecticut James McInerney*, National University of Ireland Christos Ouzounis, Institute of Agrobiotechnology Mark Ragan*, University of Queensland

Molecular and developmental approaches to speciation

Ehab Abouheif, McGill University Paul Brakefield, University of Leiden Brian Hall*, Dalhousie University Axel Meyer, University Konstanz Michael Shapiro, University of Utah

Plant population genomics

Brandon Gaut, UC-Irvine Thomas Mitchell-Olds, Duke University Brian Morton*, Columbia University Magnus Nordborg, University of Southern California Kermit Ritland, University of British Columbia Stephen Wright*, York University

Recombination (emphasis on molecular mechanisms)

Sir Alec Jeffreys, University of Leicester Jeff Lawrence, University of Pittsburgh John Logsdon, University of Iowa Rosie Redfield*, University of British Columbia

Resolution and dating of the eukaryotic tree

Debashish Bhattacharya, University of Iowa B. Franz Lang*, Université de Montréal Jan Pawlowski, University of Geneva Hervé Philippe*, Université de Montréal

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## Halifax SMBE Jun24-28 4

SMBE Undergraduate Diversity Mentoring Program Awards

2007 Annual meeting of the society for molecular biology and evolution?

June 24-28, Halifax, Nova Scotia, CANADA

CONFERENCE WEBSITE

https://smbe2007.dal.ca DEADLINE FOR RECEIPT OF NOMINATIONS/APPLICATIONS: APRIL 15

Program outline

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students from underrepresented groups to participate in a Diversity Mentoring Program. The goals of this program are: (1) to promote diversity at the SMBE annual meeting, (2) to provide students with the opportunity to experience the excitement of attending and presenting at an international scientific conference, and (3) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field.

To achieve these goals, each recipient of an SMBE Undergraduate Diversity Mentoring Program Award will be paired with two mentors, one a senior graduate student and the other a postdoctoral fellow or faculty member (who may or may not be the student?s current advisor). Specific mentoring activities will include:

? Attending conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the ?goings-on? at a multi-day scientific conference.

? Interacting with the student during some mealtimes, coffee breaks and other social gatherings.

? Introducing the student to other undergraduates, graduate students, postdoctoral fellows and faculty members as a way of facilitating connections with potential future graduate supervisors and colleagues.

? Attending the poster session and SBME Undergraduate Diversity Program Award reception with the student in order to minimize/overcome the anxiety often felt by first-time conference attendees.

? Serving as a contact point for the student to help resolve any issues surrounding conference registration, travel and accommodation.

Eligibility

Candidates must currently be enrolled as undergraduate students (Bachelor's level degree) or have graduated within the last 6 months at the time of application and be from groups underrepresented in our scientific discipline (e.g., minority groups and/or women).

Conference participation

Recipients of an SMBE Undergraduate Diversity Mentoring Program Award will be invited to present their research at a special reception / poster session on Tuesday, JUNE 25, attended by their mentors, supervisors and other interested conference participants.

Award

Award recipients will receive US $1,000 to be used to help cover the cost of airfare, accommodations, and meeting registration. Each participant will also receive an online student membership to the Society journal, Molecular Biology and Evolution, for the year of 2008.

Application

1. Faculty members may nominate undergraduates by sending a brief letter/email of recommendation to Laura Katz (Lkatz[at]email.smith.edu) and John Archibald (jmarchib[at]dal.ca). The letter should outline the student?s eligibility for the award and confirm their current academic status. Also indicate if your student would be able to present a poster.

OR

2. Students may apply for the award themselves by providing information on their background, academic status and an email address for their current supervisor. Students should also indicate whether they are able to present a poster.

The deadline for receipt of nominations/applications is APRIL 15.

John M. Archibald, Ph.D. Assistant Professor and Scholar, CIAR Program in Evolutionary Biology Department of Biochemistry and Molecular Biology Dalhousie University Sir Charles Tupper Medical Building 5850 College Street, Halifax, Nova Scotia B3H 1X5, Canada

Phone: (902) 494-2536 Fax: (902) 494-1355 Webpage: <http://myweb.dal.ca/jmarchib/> John Archibald <jmarchib@dal.ca>

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## Halifax SMBE Jun24-28 UndergraduateDiversity 5

CALL FOR MENTORS?SMBE UNDERGRADUATE DIVERSITY MENTORING PROGRAM AWARDS

2007 Annual meeting of the society for molecular biology and evolution

June 24-28, Halifax, Nova Scotia, CANADA

https://smbe2007.dal.ca Program outline

The Society for Molecular Biology and Evolution (SMBE) is offering 10 awards to undergraduate students from underrepresented groups to participate in a Diversity Mentoring Program. The goals of this program are: (1) to promote diversity at the SMBE annual meeting, (2) to provide students with the opportunity to experience the excitement of attending and presenting at an international scientific conference, and (3) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field.

To achieve these goals, each recipient of an SMBE Undergraduate Diversity Mentoring Program Award will be paired with two mentors, one a senior graduate student and the other a postdoctoral fellow or faculty member (who may or may not be the student?s current advisor). WE ARE SEEKING INDIVIDUALS INTERESTED IN BEING A MENTOR. Specific activities will include:

? Attending conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the ?goings-on? at a multi-day scientific conference.

? Interacting with the student during some mealtimes, coffee breaks and other social gatherings.

? Introducing the student to other undergraduates, graduate students, postdoctoral fellows and faculty members as a way of facilitating connections with potential future graduate supervisors and colleagues.

? Attending the poster session and SBME Undergraduate Diversity Program Award reception with the student in order to minimize/overcome the anxiety often felt by first-time conference attendees.

? Serving as a contact point for the student to help resolve any issues surrounding conference registration, travel and accommodation.

Conference participation

In addition to the activities outlined above, mentors will be invited to attend a special reception / poster session on Tuesday, JUNE 25, along with undergraduates, supervisors and other interested conference attendees.

If you are interested in mentoring an undergraduate at this year?s SMBE meeting please email Laura Katz (Lkatz[at]email.smith.edu) and John Archibald (jmarchib[at]dal.ca).

John Archibald <jmarchib@dal.ca>

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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

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

Bruce Weir

Bruce Weir <bsweir@u.washington.edu>

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## Marseilles 11thEvolBiol Sep19-21 Deadlines

Daer all the eraly dead lines of the 11th evolutionary biology meeting at marseilles is March 31st. Information concerning the program, housing.....is available at http://www.up.univ-mrs.fr/evol-cgr/ all the best

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

Pierre.Pontarotti@up.univ-mrs.fr

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## Montreal CSZ ComparativeMorphology May21-25

The Comparative Morphology & Development section of the Canadian Society of Zoologists is pleased to announce the following symposium and two satellite symposia that may be of interest. These will all be part of the Canadian Society of Zoologists annual meeting in Montreal, May 21-25. For full details and abstracts, visit the Comparative Morphology & Development web site:

http://www.biology.ualberta.ca/CMD/home.htm For information about the annual meeting, or to register to attend, please visit the CSZ meeting web site:

http://martin.parasitology.mcgill.ca/csz2007/ ———————- MAIN SYMPOSIUM Wed. May 23 ————————

Appendages & Body Plans: Development, Morphology and Evolution

Nipam Patel (Berkeley) The evolution of segmentation and body patterning: Insights from the crustacean Parhyale

Jarmila Kukalova-Peck (Carleton) Arthropods are all legs: Evolution of arthropod appendages

Bob Shadwick (UBC) Evolution of a unique morphology for locomotion in high-performance fishes

———————- SATELLITE SYMPOSIUM #1 Tue. May 22 ——————

Craniofacial Development and Evolution

R. Craig Albertson (Syracuse) The genetic and developmental basis of cichlid trophic diversity

Kyle Martin, A. Maurya, S. Kuraku, S. Kuratani, M. Ekker (Ottawa) Regulation of agnathan Dlx genes

Tamara Franz-Odendaal (Mount Saint Vincent) Are all vertebrate scleral ossicles homologous to one another?

David Evans (Toronto) Cranial crest growth in lambeosaurine dinosaurs

(co-sponsored by the journal Developmental Dynamics)

———————- SATELLITE SYMPOSIUM #2 Wed. May 23 ——————

Developmental Biology and Evolutionary Transformations

Robert Carroll, Nadia Frölisch, and Rainer Schoch (McGill) Evolutionary developmental biology and the ancestry of modern amphibians

Basile Tarchini, Denis Duboule and Marie Kmita (Montreal) >From ancestral appendages to tetrapod limbs: A Hox story

Luke Harrison, Hans Larsson (McGill) Molecular evolution and correlation of Hoxa11 and Hoxa13 genes to skeletal patterning changes across the fin to limb transition

Marcos Nahmad, Leon Glass, Ehab Abouheif (McGill) A model for the developmental genetic origin of the wing polyphenism in ants

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A. Richard Palmer Systematics and Evolution Group Department of Biological Sciences University of Alberta Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234

http://www2.biology.ualberta.ca/palmer/palmer.html (biological asymmetries, software, course notes) Chair, Comparative Morphology & Development section, Canadian Society of Zoologists. For info. see: http://www.biology.ualberta.ca/CMD/home.htm rich.palmer@ualberta.ca

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## Montreal GeneticsSocietyCanada Jun18-22

The 50th Annual Conference of The Genetics Society of Canada will take place in Montreal from June 18-22 2007. This meeting will be held jointly with the Canadian Drosophila Research Conference.

To register, to submit an abstract and to view a preliminary schedule please go to the website http://life.mcmaster.ca/GSC . Paul Lasko

“paul.lasko” <paul.lasko@mcgill.ca>

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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

dewoody@purdue.edu dewoody@purdue.edu

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## RoccadeiPapi Italy ProblemSpecies Jun8-9

INTERNATIONAL CONGRESS

Problematic species: Conservation and management

Rocca dei Papi, Montefiascone (Viterbo), Italy June 8 - 9, 2007

The University of Tuscia, in collaboration with the Provincial Authority of Viterbo (Department of Agriculture, Hunting and Fishery), has scheduled an International Congress, in Montefiascone, Viterbo (Latium, Central Italy) on June 8-9, 2007. The title of the meeting is “Problematic species: Conservation and management”, in which several international specialist contributors will be participating. These two days are an opportunity to compare different experiences about this crucial aspect of Wildlife management and conservation, in particular concerning the relationship with the human activities and the environments. The congress concerns different levels, from local problems (i.e. Central Italy) to National and International cases.

Argument of the meeting will be only birds and mammals

The congress is articulated in four symposia:

a) Alien species: habitat impact and interaction with native species; b) Fauna-Agriculture interactions; c) Wildlife conservation and management, and hunting; d) Vanishing species and spreading species.

The official languages will be English and Italian.

Scientific Committee:

Francesco M. Angelici (Università degli Studi della Tuscia, Viterbo); Marco Apollonio (Università degli Studi di Sassari); Nicola Baccetti (Istituto Nazionale per la Fauna Selvatica, Bologna); Natale E. Baldaccini (Università degli Studi di Pisa e Unione Zoologica Italiana); Sandro Bertolino (Università degli Studi di Torino); Luigi Boitani (Università degli Studi di Roma “La Sapienza”); Stephen J. Browne (Fauna and Flora International, London, UK); Paolo Ciucci (Università degli Studi di Roma “La Sapienza”); Anna Maria Fausto (Università degli Studi della Tuscia, Viterbo); Romolo Fochetti (Università degli Studi della Tuscia, Viterbo); Philippe Gaubert (Muséum National d’Histoire Naturelle, Paris, France) ; Petr Genov (Bulgarian Science Academy, Sofia, Bulgaria); Piero Genovesi (Istituto Nazionale per la Fauna Selvatica, Bologna); Vittorio Guberti (Istituto Nazionale per la Fauna Selvatica, Bologna); Juan Herrero (Alcala University, Spain) Alessandro La Posta (Italian Ministry of the Environment); Massimo Mazzini (Università degli Studi della Tuscia, Viterbo); Alberto Meriggi (Università degli Studi di Pavia); Fabio Perco (Stazione Biologica Isola della Cona); Claudio Prigioni (Università degli Studi di Pavia); Mario Spagnesi (Ekoclub Italia); Guido Tosi (Università degli Studi dell’Insubria, Varese)

Under the Patronage of: Italian Ministry of the Environment; Italian Ministry of the Agricolture and the Forestry; Montefiascone Town Administration; Latium Regional Authority; Italian Zoological Society -Unione Zoologica Italiana (UZI)- Italian Mammal Society - Associazione Teriologica Italiana (A.T.It.)-; Italian Centre of Ornithological Studies - Centro Italiano Studi Ornitologici (C.I.S.O.)-; National Institute of Wildlife -Istituto Nazionale per la Fauna Selvatica (INFS)-; Italian Society of Wildlife Ecopathology -Società Italiana di Ecopatologia della Fauna (SIEF)- Italian League for Bird Protection -Lega Italiana Protezione Uccelli (LIPU)-; Legambiente; World Wildlife Fund (WWF), Italy.

At this meeting will participate both national and international exponents with oral invited relations, concerning animal ecology and, more generally, applied environmental studies. This happening wants to investigate the problems created by the environmental changes and the following fauna adaptability. In fact, several species can represent a problem with the agriculture and other human activities. In particular, the following issues will be discussed: Wildlife management in protected areas, hunting pressure on wildlife, wildlife interaction with agriculture and livestock, species urbanization.

The Organizer Committee establishes the special prize “Fauna Etrusca” of 750,00 euros, for the more interesting and innovative contribution (oral relation or poster) presented by young researcher/s, included in one of these proved categories:

q Young graduated, with any grant; q MSc or PhD students; q Young researchers unsalaried;

Call for abstracts

All participants are invited to give their scientific contributions as oral communication, strictly belonging to the subjects of the symposia, 15'+5' for the discussion, or poster (high 120 cm and width 70 cm).

The registration (with the payment receipt), the contribution title/s, the abstract including author/s, address, phone number, e-mail address must be sent via e-mail to: info@ecologiaapplicataitalia.it within APRIL 15th, 2007.

For every information, please, contact at one of these following addresses:

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## Roscoff EnvironmentalGenomics Jun9-13

Registration deadline soon (1 March 2007) for the CONFERENCE JACQUES MONOD Environmental genomics : from individual genomes to genomes of complex communities

Génomique environnementale : du génome individuel aux génomes de communautés complexes d'organismes

Roscoff (Brittany, France), 9-13 juin 2007, June 9-13 2007

Further information at the following web sites / Sites web à consulter

http://www.cnrs.fr/sdv/cjm/cjmyoung_e.html http://environmental-genomics.univ-rennes1.fr/Roscoff_2007/accueil_fr.asp http://www.sb-roscoff.fr/ M. L. AINOUCHE Evolution des Genomes et Speciation, Dpt Ecologie Evolutive UMR CNRS 6553 Ecobio, Universite de Rennes 1 Campus Scientifique de Beaulieu, Bat. 14A 35 042 Rennes Cedex France Ph. 33 (0)2 23 23 51 11 Fax 33 (0)2 23 23 50 47

malika.ainouche@univ-rennes1.fr

## RoyalSoc London AnimalEvol Jun18-19

Dear Colleague,

We are delighted to announce a meeting entitled:

The evolution of the animals: a Linnean tercentenary celebration

which takes place in the meeting rooms of the Royal Society, London, 18-19 June 2007. A full two days of presentations by leading scientists in the field of animal evolution is planned. The meeting is free to attend but pre-registration online is essential.

http://www.royalsoc.ac.uk/event.asp?id=4163&month=6,2006

We expect the meeting to be of interest to all animal and evolutionary biologists, regardless of developmental stage or geological age. The Royal Society has assured us that a large audience can be accommodated, but early registration will guarantee admission to the main auditorium.

The list of speakers and session chairs can be found at the end of this email.

Please forward this announcement to anyone who might be interested.

With very kind regards and apologies for cross postings,

Yours sincerely,

Max Telford and Tim Littlewood

Chairs and Speakers:

Andrew Smith Simon Conway Morris Michael Akam Peter Holland Graham Budd, Kevin Peterson Jeff Boore Hervé Philippe Greg Wray Nicole King Jaume Baguñà Ronald Jenner Mark Martindale Gonzalo Giribet Detlev Arendt Max Telford Andrew Peel Billie Swalla Chris Lowe

m.telford@ucl.ac.uk m.telford@ucl.ac.uk

## 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>

## UGuelph AppliedEvolution May15-16 3

Online registration for the 2007 Yodzis Colloquium ($55 CAD for students, $130 for non-students, both including GST) is now available at

http://www.peopleware.net/index.cfm?siteID=323&eventDisp=07YODZIS

In addition, the first general meeting of the Canadian Society for Ecology and Evolution will be in Toronto (appx. 1 hr from Guelph) directly after the Yodzis Colloquium. For information go to http://www.eeb.utoronto.ca/CSEE/ Announcing the 2007 Peter Yodzis Colloquium in Fundamental Ecology

“Applied Evolution: Understanding the Past, Predicting the Future”

May 15th and 16th 2007 University of Guelph, Guelph, Ontario, Canada

The colloquium will focus on the mechanistic basis of adaptation and the potential to predict adaptive evolution in pure and practical applications. There will be a series of keynote lectures and an open poster session, all at a pace conducive to conversation and interaction.

Confirmed keynote lecturers include:

Graham Bell (McGill University) Michael Lynch (Indiana University) David Mindell (University of Michigan) Patricia Schulte (University of British Columbia) Ruth Shaw (University of Minnesota) John Willis (Duke University)

For information, go to

<https://webmail.uoguelph.ca/services/go.php?url=http%3A%2F%2
/www.ecologycolloquia.uoguelph.ca/main.shtml or e-mail the organizers (Brian Husband and Chris Caruso) at <https://webmail.uoguelph.ca/mail//mail/compose.php?to=pycolloq%40uoguelph.ca&thismailbox=INBOX.sent-mail>pycolloq@uoguelph.<https://webmail.uoguelph.ca/mail//mail/compose.php?to=pycolloq%40uoguelph.ca&thismailbox=INBOX.sent-mail>ca Christina (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Axelrod Building 50 Stone Road East Guelph, Ontario N1G 2W1 CANADA 519-824-4120 ext. 52030 carusoc@uoguelph.ca

## 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 de-generated 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 reduced rate registration.

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

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

## 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>

## Uppsala ESEB2007 Aug21-25 ConservationGenetics

ESEB 2007- Symposium 3

As organizers of the following symposium at the ESEB Conference in August 21-25, 2007 in Uppsala, we invite researchers to submit abstracts for contributions to the whole day symposium on:

Conservation Genetics: Genetic deterioration and adaptation to changing environments

The focus of the symposium is on conservation genetics with particular emphasis on the following issues: Loss of genetic variation and inbreeding are threats to population persistence as they may reduce the potential to cope and to adapt to environmental change. In the symposium we are particularly interested to discuss synergistic interactions between inbreeding/loss of genetic variation and environmental stress/changing environments. We welcome contributions that focus on such interactions and that combine approaches from the DNA to the phenotypic level.

Invited speakers are:

Markus Fisher, Institute for Biochemistry and Biology, University of Potsdam, Potsdam, Germany Juan L. Bouzat, Dept. of Biological Sciences, Bowling Green State University, Bowling Green, Ohio, USA Torsten N. Kristensen, Department of Genetics and Biotechnology, Danish Institute of Agricultural Sciences and Aarhus University, Denmark

This symposium is sponsored by the European Science Foundation through the Scientific Programme ConGen. Through this programme we can cover the registration fee for a few of the oral contributors to the symposium. For support of this kind, please apply directly to the symposium organizers (include a copy of abstract and a short motivation) after formal registration and submission of the abstract through the ESEB website.

Organizers are: Kuke Bjilsma, Evolutionary Genetics, University of Groningen, The Netherlands, email: r.bijlsma@rug.nl and Volker Loeschcke, Ecology and Genetics, University of Aarhus, Denmark, email: volker.loeschcke@biology.au.dk

Volker Loeschcke Dept. of Ecology and Genetics Aarhus University Ny Munkegade, Buildg. 540 DK-8000 Aarhus C, Denmark

fax: +45 8942 2722 tlf: +45 8942 3268, cell: +45 2899 2368 email: biovl@biology.au.dk

Volker Loeschcke <volker.loeschcke@biology.au.dk>

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## Uppsala ESEBSymposium Epidemiology

Dear Colleagues

We would like to invite you to submit abstracts for the ESEB XI symposium on "Evolutionary epidemiology and its implications for disease control."

Evolutionary biologists have long focused on the long-term evolution of pathogens, based on game theory, often overlooking the short-term dynamics of infections. Recently, novel approaches, both experimental and theoretical, have started to unravel the short-term evolution of pathogens on the same time scale as transient epidemic dynamics. Integrative methods are needed to understand the dynamics of traits such as virulence or antibiotic resistance, and devise appropriate control measures.

We welcome contributions that rely on experiments or mathematical models for human, animal or plant infectious diseases. The focus will be on novel approaches, especially those associating different disciplines.

Invited speakers: Troy Day (Queen's University, Kingston, Ontario) and Andrew Read (University of Edinburgh).

Deadline for submission of abstracts: April 15th.

ESEB XI website: <http://www-conference.slu.se/eseb2007/index.html> The proceedings of this symposium will be published in the Journal of the Royal Society Interface.

Organisers: Olivier Restif (University of Cambridge) and Sylvain Gandon (IRD Montpellier).

Dr. Olivier Restif CIDC - Disease Dynamics Unit Dept. of Veterinary Medicine University of Cambridge Madingley Road Cambridge CB3 0ES Great-Britain

Tel: +44 (0)1223 337685 Fax: +44 (0)1223 764667

http://www.vet.cam.ac.uk/cidc/ or226@cam.ac.uk
or226@cam.ac.uk

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## Uppsala ESEBSymposium HybridCytonuclearCoevolution

Dear colleagues,

This is a call for abstracts for a symposium at the ESEB XI Congress in Uppsala, Sweden (August 20-25, 2007):

"Cytonuclear coevolution and the evolution of hybrid zones"

The last few years have seen a wealth of data on the coevolution between the mitochondrial and nuclear genomes (cytonuclear coevolution). Specifically, close interaction among mitochondrial and nuclear polypeptides are necessary for optimal function of energy production in mitochondrial membranes. Hence, there is strong selection for coadaptation of linked mitochondrial and nuclear genes. The breaking up of coadapted gene complexes in hybrid zones may lead to dramatic declines in the performance of hybrids, known as hybrid breakdown. This symposium will cover recent developments in the research on cytonuclear coevolution (empirical, theoretical, etc.) and our understanding of hybrid inviability. Given (1) the numerous deep "phylogeographic (mtDNA) breaks" discovered within species, (2) that small cytonuclear incompatibilities may affect fitness, and (3) that cytonuclear interactions can evolve rapidly, cytonuclear coevolution must be incorporated into our understanding of hybrid zone evolution. A main point of discussion will therefore be on the role of cytonuclear coevolution in the development of reproductive isolation and as a possible driving force for speciation.

Two leading researchers on cytonuclear coevolution are invited as speakers:

Professor Ronald Burton - Scripps Institution of Oceanography, Univ. of California, San Diego, USA - http://burtonlab.ucsd.edu/Site/Home.html - Research focus on intraspecific hybrid incompatibility in Tigriopus californicus due to maladaptive combinations of mitochondrial and nuclear genes

Professor David Rand - Department of Ecology & Evolutionary Biology, Brown University, USA - http://www.brown.edu/Departments/EEB/rand/ - Research focus on natural selection of mitochondrial lineages and comparative genomics in Drosophila

If you are interested in participating in the symposium, there are opportunities for talks and posters. The Abstract deadline is April 15) Please send your application through the web portal of the ESEB conference at: http://www-conference.slu.se/eseb2007/ You are most welcome to contact us with any questions. Feel free also to send us info on your recent research on cytonuclear coevolution (e.g. pdfs) for background to a forthcoming review paper. Additional background information is available at: http://www.zoo.utoronto.ca/lindell/-symposium.html See you in Uppsala!

Johan Lindell and Staffan Bensch, Symposium organizers

Johan Lindell Department of Ecology and Evolutionary Biology, University of Toronto E-mail: johan.lindell@utoronto.ca

Staffan Bensch Department of Ecology, Lund University E-mail: staffan.bensch@zooekol.lu.se

johan.lindell@utoronto.ca

## Uppsala ESEBSymposium MHCEvol Aug20-25

Dear Evoldirists,

we invite you to submit your abstracts for the symposium 'Why MHC makes the difference  its role in various fields' at the 11th conference of the European Society for Evolutionary Biology (ESEB) 2007 in Uppsala, Sweden.

Symposium description: The Major Histocompatibility Complex (MHC) plays a key role in the adaptive immune system of vertebrates. Its exceptional polymorphism brings it into the focus of scientists from several fields like evolutionary ecology, immunology, conservation biology and genetics. We would like to discuss the evolutionary processes of maintaining such high polymorphism and its consequences on mate choice, host-parasite co-evolution and speciation as well as its use as a functional marker in population genetics and conservation biology.

We would like talks and posters to present diverse points of view on the evolutionary function of the MHC. To highlight this interdisciplinary approach, we encourage contributions from various fields.

Invited speakers: Simone Sommer, Leibniz-Institute for Zoo- and Wildlife Research, Berlin, Germany. Gabriele Sorci, Biogeosciences, CNRS, University of Bourgogne, Dijon, France

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 reduced rate registration.

Symposium organisers: Tobias Lenz, Max Planck Institute for Limnology, Germany (lenz@mpil-ploen.mpg.de) Christophe Eizaguirre, Max Planck Institute for Limnology, Germany (eizaguirre@mpil-ploen.mpg.de)

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

Tel: +49-(0)4522-763245 Fax: +49-(0)4522-763310 lenz@mpil-ploen.mpg.de http://www.mpil-ploen.mpg.de/english/evoleco/staff/lenz.htm lenz@mpil-ploen.mpg.de lenz@mpil-ploen.mpg.de

## Uppsala EnemiesandDiversification Aug20-25

Call for abstracts for a symposium on 'THE ROLE OF ENEMIES IN DIVERSIFICATION' at the ESEB XI Congress, Uppsala, August 20-25, 2007.

Symposium description: This symposium will gather people working with a mixture of data and theory on the evolutionary consequences of natural enemies on diversification and adaptive radiation of prey lineages.

Confirmed Invited Speaker: Jim Mallet, University College London, United Kingdom

Symposium Organizers: Steven Vamosi, University of Calgary, Canada (smvamosi@ucalgary.ca) Patrik Nosil, Simon Fraser University, Canada (pnosil@zoology.ubc.ca)

Conference details can be found at <http://www-conference.slu.se/eseb2007/> . Thanks! Steve & Patrik

– Dr. Steven M. Vamosi Assistant Professor and Ingenuity New Faculty Department of Biological Sciences, University of Calgary http://-homepages.ucalgary.ca/ ˜ smvamosi/ "Steven M. Vamosi" <smvamosi@ucalgary.ca>

## Uppsala EvolBiol and gender Aug20-25

Call for participation to a symposium at the ESEB XI Congress at Uppsala, Sweden, August 20-25 2007

"Gender perspectives on evolutionary biology"

Gender perspectives on evolutionary biology has uncovered male bias in sexual selection theory and empirical research. It has also enabled researchers to perceive the importance of females for evolutionary processes and explore additional sexual selection mechanisms. However, these perspectives are still unconventional in evolutionary biology and we would like to encourage development in this field by bringing together scholars from different disciplines with practical experience of applying gender perspectives in evolutionary biology. The symposium will cover papers on theory and model development, meta analysis and practical, applied field and laboratory research as well as science criticism. One of the main points of discussion will be future directions for theoretical and empirical research.

Invited speakers will be Professor Patricia A. Gowaty, University of Georgia, Athens, Georgia, USA. & Professor Marlene Zuk, University of California, Riverside, USA.

If you are interested in participating to the symposium, there are opportunities for talks and posters. Please send your application through the web portal of the ESEB conference http://www-conference.slu.se/-eseb2007/ Malin Ah-King, Department of Zoology, Stockholm University, Sweden. E-mail: Malin.Ah-King@zoologi.su.se

Mans Andersson, Department of Gender Studies, Uppsala University, Sweden. E-mail: Mans.Andersson@gender.uu.se

Malin Ah-King <Malin.Ah-King@zoologi.su.se>

## Uppsala EvolGameTheory Aug20-25

Call for participation to a symposium ESEB XI Congress at Uppsala, Sweden, August 20-25 2007

"GAME THEORY IN ECOLOGICAL CONTEXT"

Adding ecological realism to game theoretical models has recently led to exciting new results e.g. on the origin of different strategy types (such as Hawk, Dove and Bourgeois) and revealed that classic results are embedded in a larger framework. Intense research explores the effect of population structure on the evolution of cooperation. These areas are connected to adaptive dynamics, which aims to model evolution starting from population dynamics. The symposium welcomes contributions in any area of game theory and related fields (both theoretical and empirical), but particularly those which contribute to the unfolding synthesis between ecological and evolutionary dynamics.

Invited speakers of the symposium are Olof Leimar (Stockholm University) and John McNamara (University of Bristol). This symposium is organised by Eva Kisdi and Hanna Kokko (University of Helsinki).

Talks and posters contributing to this symposium are welcome! Please submit your abstract through the Congress website, http://www-conference.slu.se/-eseb2007/, before 15 April 2007. For further information, please feel free to contact the symposium organisers.

Eva Kisdi Department of Mathematics FIN-00014 University of Helsinki, Finland eva.kisdi [at] helsinki.fi

kisdi@mappi.helsinki.fi kisdi@mappi.helsinki.fi

## Uppsala EvolutionaryHistories Aug20-25

Call for abstracts for the symposium

"EVOLUTIONARY HISTORIES BEYOND ORGANELLE DNA"

at the European Society for Evolutionary Biology (ESEB XI) conference August 20-25, 2007 in Uppsala, Sweden.

Synopsis: Single locus studies of molecular diversity at mitochondrial or chloroplast loci still prevail although it has been known for long that for example stochastic processes, selection and mode of inheritance may lead to strong discrepancies among evolutionary histories inferred from different loci. The symposium aims to examine the extent of congruence between evolutionary inferences based on organelle DNA and others markers, and the relative value of multi-marker or genomic approaches versus single locus surveys.

Confirmed speakers: Kerry L Shaw, University of Maryland, USA Remy J Petit, INRA Cestas, France

Abstracts can be submitted online until April 15 at http://www-conference.slu.se/eseb2007/. For further information on this symposium, please contact the organisers Gerald Heckel (gerald.heckel@zoo.unibe.ch) or Maarit Jaarola (m_jaarola@bison.zbs.bialowieza.pl).

Dr. Gerald Heckel Computational and Molecular Population Genetics (CMPG) Zoologisches Institut Universitaet Bern Baltzerstr. 6 CH-3012 Bern Switzerland Tel.: +41 (0)31 631 30 29 Fax: +41 (0)31 631 31 88 Email: gerald.heckel@zoo.unibe.ch http://cmpg.unibe.ch/-people/heckel.htm gerald.heckel@zoo.unibe.ch

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## Uppsala GeneMapping Aug20-25

Call for abstracts for a symposium on 'GENE MAPPING IN NATURAL POPULATIONS'. European Society for Evolutionary Biology (ESEB) conference 2007, Uppsala, Sweden.

We are now seeking abstracts for talks and posters for this symposium.

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 are: April 15th: Deadline for submission of abstracts. April 30th: Deadline for reduced rate registration.

Substantial discounts are available for ESEB members.

Background: In recent years quantitative genetics tools have succesfully been applied to wild animal and plant populations, yielding considerable insight into processes of speciation, reproductive isolation, adaptation and microevolution. The logical extension of this work is to identify and/or map the genes reponsible for variation in relevant traits in wild populations, and measure their fitness effects where possible. Gene mapping experiments are now underway in a diverse range of ecologically relevant organisms. This symposium will showcase recent mapping experiments in wild populations of animals and plants. Talks will cover empirical, theoretical and technological breakthroughs.

Confirmed speakers include: Hopi Hoeskstra (Harvard) Loren Rieseberg (University of British Columbia)

If you have any queries please contact Jon Slate (j.slate@shef.ac.uk) or Christian Lexer (c.lexer@rbgkew.org.uk)

Jon Slate & Christian Lexer

Jon Slate <j.slate@sheffield.ac.uk>

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## Uppsala HostParasiteEvolution Aug20-25

Dear Evoldir Members,

We are writing to advertise a symposium at the XI ESEB Congress, Uppsala, 20-25 August. If you are interested in contributing a talk to this symposium, the deadline for abstract submissions is: APRIL 15 (please submit your abstracts to: http://www-conference.slu.se/eseb2007/index.html)

Thanks

Mark Brown & Thierry Rigaud

Host-parasite evolution: consequences of multi-parasite infections and host species assemblages Organizers: Mark Brown (mabrown@tcd.ie) & Thierry Rigaud (thierry.rigaud@u-bourgogne.fr) Description: This symposium will examine the evolutionary consequences of complexity in host-parasite systems, focusing on (i) multiple parasite species sharing the same host and (ii) single parasite species utilising multiple host species. Invited speakers: Sylvain Gandon & Dieter Ebert

Abstract: Classical studies of host-parasite evolution have concentrated on single-species host-parasite systems, due to their empirical and theoretical tractability. However, it has long been known that hosts harbour multiple parasite or symbiont species, and that many parasites with direct life-cycles have multiple concurrent host species. Consequently, to understand the evolution of host-parasite systems evolutionary biologists need to address these more complex interactions. Recent work, both theoretical and empirical, has started to address both sides of the coin. The impact of parasites on their hosts may be modulated, both positively and negatively, by the presence of additional parasite species. From a parasite perspective, this has important implications for the evolutionary trajectory of key features such as virulence or transmission. Similarly, the use of multiple host species has implications for the evolution of host-exploitation strategies. From a host perspective, the evolution of defences against parasites, and consequent life-history trade-offs, may depend on the parasite community as a whole. The time is ripe to bring researchers in this field together within a symposium, providing impetus for the development of this research area as well as important synergies between theoreticians and empiricists.

mabrown@tcd.ie

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## Uppsala PhenotypeDepDispersal Aug20-25

Dear Evoldir Members,

This is a call for the symposium “Process and implications of phenotype-dependent dispersal and settlement”, as part of the 11th European Society for Evolutionary Biology (ESEB) conference (20th-25th August 2007, Uppsala, Sweden). You are still in time to submit abstracts for talks and posters for this symposium.

Confirmed speakers: Dan Bolnick (University of Texas at Austin, USA) Ben Sheldon (University of Oxford, UK)

Background: Evidence and appreciation is mounting for the notion that dispersal and gene flow may not be the random process that most evolutionary theory assumes it to be. When individuals carefully compare available environments with their phenotypes and choose to stay at or move to locations where fitness is expected to be highest, such matching habitat choice may cause individuals with similar phenotypes to end up in the same locations. The resulting spatial structure in ecological traits can have important implications for topics such as the rate and degree of local adaptation, the potential for peak shift, and speciation-with-gene flow. With this symposium we hope to raise the profile for this process by exploring and integrating across neglected and recent studies.

Details of the conference, including an online abstract submission can be found here: http://www-conference.slu.se/eseb2007/ Relevant dates are: April 15th: Deadline for submission of abstracts. April 30th: Deadline for reduced rate registration.

Substantial discounts are available for ESEB members.

If you have any queries please contact Pim Edelaar (pim.edelaar@ebc.uu.se).

PS: note my new email address <pim.edelaar@ebc.uu.se>

Dr. Pim (W.M.C.) Edelaar Marie Curie Post-doctoral Fellow Uppsala University, Department of Animal Ecology http://www.uwyo.edu/benkman/Pim.html http://www.iee.uu.se/zooekol/default.php?type=-personalpage&id=136

Wilhelmus Edelaar <pim.edelaar@ebc.uu.se>

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## Uppsala SexRoleDynamics Aug20-25

Call for poster/presentation abstracts for a symposium on “MATING COMPETITION AND SEX-ROLE DYNAMICS” at the European Society for Evolutionary Biology (ESEB XI) conference August 20-25, 2007 in Uppsala, Sweden.

Symposium Summary:

Parental investment has long been recognized as a key factor underlying the operation of sexual selection. High levels of parental investment reduce the potential reproductive rate (PRR) and may skew the operational sex ratio (OSR), directly influencing the intensity of mating competition. Recent work has highlighted the fact that environmental factors such as ambient temperature and resource availability may disproportionately influence male and female PRR, leading to spatial and temporal variation in sex-roles.

While empirical results fit well with classical theory, recent theoretical approaches have questioned the presumed link between PRR, OSR and sexual selection. At the same time, genomic approaches are allowing the elucidation of the genetic basis of sex-roles and mating preferences. This symposium will consider recent theoretical approaches to the study of mating competition and sex-roles, which together with new genetic data have provoked a reconsideration of classic paradigms of sexual selection.

Confirmed speakers include: Stephen Shuster (Northern Arizona) Lotta Kvarnemo (Göteborg)

Abstracts can be submitted online until April 15 at http://www-conference.slu.se/eseb2007/. For further information on this symposium, please contact Tony Wilson (tony.wilson@zoolmus.unizh.ch) or Ingrid Ahnesjö (ingrid.ahnesjo@ebc.uu.se).

Tony Wilson Assistant Professor, Evolution and Biodiversity Zoological Museum University of Zurich Winterthurerstrasse 190 CH 8057 Zurich Switzerland Tel: 41 44 635 4790 Fax: 41 44 635 4780

tony.wilson@zoolmus.unizh.ch

## ZhejiangU 3rdIntlQuantitativeGenetics Aug19-24

The Third Announcement:

The 3rd International Conference on Quantitative Genetics Zhejiang University, Hangzhou, China, August 19-24, 2007

The 3rd International Conference on Quantitative Genetics (ICQG3) will be held during August 19-24, 2007 hosted by Zhejiang University in Hangzhou, China. As with the 1st ICQG in Ames, Iowa in 1976 and the 2nd ICQG in Raleigh, North Carolina in 1987, the 3rd Conference will be a comprehensive survey of the current status of quantitative genetics. New technologies in areas ranging from genomics and molecular genetics to statistics are providing both opportunities and challenges for our understanding of the genetic basis of quantitative traits in natural populations, the evolution of characters, and use for plant and animal breeding.

The Conference will be held in an international hotel, the Yellow Dragon Hotel, in the downtown of Hangzhou.

The program listing invited speakers is on the website. Registration is now open on-line at http://www.icqg.org/ . The Conference welcomes participants to submit contributed papers. Only an abstract is needed and is to be submitted at registration for the conference. A limited number of contributed papers will be selected for oral presentation in an appropriate session of the conference and all others will be presented in formal poster sessions. Accompanying persons are also welcomed, and a special program for them will be arranged.

Please check out the conference website http://www.icqg.org/ for more information. If you have questions and suggestions, please contact ICQG3@zju.edu.cn.

zeng@statgen.ncsu.edu

# GradStudentPositions

## 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 inbreeding 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

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

dominique.mazzi@ipw.agrl.ethz.ch dominique.mazzi@ipw.agrl.ethz.ch

## ImperialCollegeLondon EvolResponseClimateChange

A funding opportunity is available for excellent candidates (UK degree high 2.1 or 1st class + Masters “Distinction” or equivalent) for a PhD studentship at Imperial College London on evolutionary responses of ecosystems to climate change. The project could involve a combination of theory, laboratory experiments, global database analyses or field-surveys. Please contact Tim Barraclough at t.barraclough@imperial.ac.uk before the 23rd of March if interested in this possibility, including a copy of your CV and one paragraph outline of interests.

—– **MSc course - Ecology, Evolution & Conservation** www.imperial.ac.uk/lifesciences/ecolevolcons —– Dr. Timothy G. Barraclough, Senior Lecturer in Biodiversity and Evolution, Imperial College London and Royal Botanic Gardens, Kew

—– Division of Biology Imperial College London Silwood Park Campus Ascot, Berkshire SL5 7PY, UK Telephone: +44 (0)20 7594 2247 Fax: +44 (0)20 7594 2339 Web-page: www.imperial.ac.uk/-people/t.barraclough t.barraclough@imperial.ac.uk t.barraclough@imperial.ac.uk

## LaurentianU TurtlePopGenet

MSc Position â Laurentian University, Ontario

Trent-Severn Waterway Turtle Population Genetics

I am seeking a highly motivated and independent person with a love of the outdoors to fill an MSc position with field work starting May 2007 to work on turtle species at risk (map turtles and stinkpot turtles) movement patterns and gene flow through the Trent-Severn National Historic Waterway in Ontario, Canada. This is a two-year radio telemetry and population genetics project; previous experience with these field and lab techniques is highly desirable. The graduate student will work as a research technician from May â August 2007, and formally begin in the MSc Program at Laurentian University in September 2007; thus, the student will have a full field season of data collection finished before starting in the MSc Program. The graduate student is encouraged to create and develop an additional project component complementary to the required research. Excellent communication skills are required as the student will be expected to participate in public outreach education programs about reptiles at risk. The graduate student may also be required to participate in surveys for turtle species at risk in other areas of the Trent-Severn Waterway. Laurentian University will provide a GTA during the school year. The project and MSc position are pending funding from Parks Canada.

How to apply: Please send a letter of intent, CV, and unofficial transcript to:

Dr. Jackie Litzgus Department of Biology Laurentian University 935 Ramsey Lake Road Sudbury, Ontario, P3E 2C6, Canada jlitzgus@laurentian.ca http://oldwebsite.laurentian.ca/biology/english/-faculty/litzgus.htm Closing date for applications: 1 April 2007

jlitzgus@laurentian.ca

## LeidenU EvolOfSpeech

The Leiden Institute for Brain and Cognition (LIBC) has a position available for a PhD student for the project:

Towards the template - the early vocal development of songbirds and human infants.

The aim of this interdisciplinary project is to assess the similarities in mechanisms underlying selective vocal learning in human infants and songbirds (zebra finches) by running similar experiments in both models. The project concentrates on the first phase of vocal development, that of storing a representation of the vocal input in memory. It will examine to what extend this process is guided by unlearned initial perceptual biases, what these biases look like and how the input affects the formation of a template that precedes vocal production. The project is a joint project of the research groups Behavioural Biology (Institute of Biology Leiden) (http://biology.leidenuniv.nl/ibl/S8/) and the Department of Linguistics (ULCL) at Leiden University. Requirements: Candidates are expected to have an MSc (drs) degree in Biology, Cognitive Neuroscience or other relevant discipline, and to have a strong interest in experimental and interdisciplinary studies. Experience or qualifications in working with animal models will be of advantage.

Appointment: The appointment is for a period of 4 years and is expected to lead to completion of a dissertation. The gross monthly salary for a PhD candidate is ?1956 in the first year and increases progressively each year to ?2502 in the fourth year. Salary and fringe benefits conform to the Collective Employment Agreement for Dutch Universities. We hope to fill the vacancy as soon as possible.

Applications: Written applications (mentioning reference number 7-092), including a CV with marks obtained and the names, telephone numbers and email addresses of at least two referees (who have agreed to be contacted) should be submitted to: Leiden University, Faculty of Mathematics and Natural Sciences, attn. mw L. den Hollander. P.O. Box 9502, 2300 RA Leiden, the Netherlands, or by email: l.den.hollander@science.leidenuniv.nl. Closing date: 15 April 2007.

Further information: Prof dr Carel ten Cate, Behavioural Biology, c.j.ten.cate@biology.leidenuniv.nl. Dr Claartje C. Levelt, Linguistics, c.c.levelt@let.leidenuniv.nl .

c.j.ten.cate@biology.leidenuniv.nl
c.j.ten.cate@biology.leidenuniv.nl

## LeidenU TheoBiol

1 PhD position (4 years) At the section Theoretical Biology of the Institute of Biology (Leiden University, the Netherlands)

This PhD project is aimed at developing methods and models for studying effects of several factors, such as population structure and genetical mechanisms on introgression probabilities of modified genes. The models are based on stochastic processes, and take inter-individual variation into account. The project is part of a collaboration between mathematicians, ecologists and molecular biologists, funded from the progrqm ERGO of the Dutch government (see http://www.nwo.nl/-nwohome.nsf/pages/NWOA_6JNP94_Eng). Within this project 2 PhD$^1$s and 1 Postdoc will be appointed.

The candidate should have: - A master in Mathematics or Biology, with a specialisation in Mathematical Biology - Experience with stochastic modeling of population dynamical and/or population genetical processes - Sufficient fluency in writing and speaking English

For more information contact: Dr. P. Haccou, email:.p.haccou@ibl.leidenuniv.nl, tel: +31 7171-5274917. A description of the project can be downloaded from our website: http://biology.leidenuniv.nl/-ibl/S11/docs/ERGOproject.pdf Applications quoting vacancy reference number: 7-083 on the letter and envelope can be sent until March 30 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

p.haccou@biology.leidenuniv.nl

## 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 is 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 contract me for details at: 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 daniel.schoen@mcgill.ca

## Muenster Exp mol evol

Open Position (PhD) in Experimental Molecular Evolution

A position for a PhD student is available in the group of Experimental Molecular Evolution group at the newly founded Institute of Evolution and Biodiversity, University of Muenster, starting 1st October 2007 or later. The position is funded by the Volkswagen Foundation, in the context of the “Initiative Evolutionsbiologie” [http://www.volkswagenstiftung.de/foerderung/-impulse/ evolutionsbiologie.html].

Research projects will be in one or more of the following areas (see our research page for details): - Biodiversity and phylogeny of animal oncogenic viruses. - Mechanisms driving evolution in animal viruses. - Evolutionary implications of codon usage differences between virus and host. - Evolution of horizontally transferred genes in bacterial systems. - Implications of codon usage preferences in evolutionary dynamics of Horizontal Gene Transfer events.

Research concept integrates experimental and bioinformatic approaches. Genuine interest in evolution, as well as ability and willingness to work both in silico and in vitro/in vivo are essential. Required qualifications are: - MSc University degree in a biological area such as biochemistry, microbiology or cell biology OR background in bioinformatics and research experience in a biological field (please detail in the application) - Fluency in English (the official language of the group) - Independent and critical thinking abilities to develop individual work - Good social skills; capacity and willingness to develop teamwork - Interest in programming and data mining (basic programming skills will be considered a plus) - Interest in statistics (basic skills in statistics will be considered a plus)

Candidates are encouraged to send informal inquiries to: Dr. Ignacio G. Bravo Experimental Molecular Evolution, Institut for Evolution and Biodiversity, FB Biologie, Westfälische Wilhelms Universität Münster Schlossplatz 4, D-48149 Münster, Germany

http://www.uni-muenster.de/Evolution/-Evolution.ExpMolEvol/ e.mail: i.bravo at dkfz.de.

(Present address, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, 69120, Heidelberg, Germany).

The newly founded Institute for Evolution and Biodiversity in Muenster integrates evolutionary research ranging from bioinformatics and molecular biology to organismic biology and ecology. It includes senior research groups in Animal Evolutionary Ecology, Evolutionary Bioinformatics, Limnology and Plant Evolutionary Ecology, as well as independent research groups on Evolutionary Ecology and Didactics of Biology and in Limnology and Ecology. There is a strong commitment from the University of Muenster itself and from the Faculty of Biology in the development of a strong curriculum in Evolutionary Biology, as expressed also in the funding granted by the Volkswagen Foundation in the context of their “Inititative Evolutionsbiologie” regarding new concepts in evolutionary education.

Muenster hosts many excellent scientific institutions such as a newly founded Max-Planck Institute for biomedical research, a Centre for Nanotechnology and a great number of specialised research areas. Muenster is a dynamic city with a world-famous heritage centre 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 for further details).

Equal opportunity regulations apply.

Dr. Ignacio González Bravo

Deutsches Krebsforschungszentrum / German Cancer Research Centre Infection and Cancer F020 Im Neuenheimer Feld 280 69120 Heidelberg Germany

phone +6221424935 +6221424943 fax +6221424932

i.bravo@dkfz.de

http://www.uni-muenster.de/evolution/expmolevol/ i.bravo@dkfz-heidelberg.de i.bravo@dkfz-heidelberg.de

## Munich EvolFuncGenomics

PhD Student: Evolutionary/Functional Genomics, University of Munich

A PhD student position is available in the laboratory of John Parsch at the University of Munich (LMU). The position is part of a project funded by the German Science Foundation (DFG) to study the molecular evolution of Drosophila genes with sex-biased expression. The work will be primarily experimental, including gene expression analysis and transgenic expriments. The position will be paid as BatIIa/2 (or equivalent) according to the German pay scale. Requirements are a master's degree (or Diploma) in biology and a strong interest in molecular evolution. The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. We have a very international group and the everyday working language is English. The LMU department of biology is housed in the new state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at:

http://www.zi.biologie.uni-muenchen.de/evol Applicants should send a PDF file with a statement of interest, curriculum vitae, and the contact information for at least two referees to:

parsch@zi.biologie.uni-muenchen.de

The University of Munich is an equal opportunity employer with an affirmative action program for the disabled.

## Munich PopulationGenetics

PhD positions: Population genetics, Munich

Two PhD student positions are available in the laboratory of Wolfgang Stephan at the University of Munich. The positions are funded by the German Science Foundation (DFG) to study the genetics of adaptation in Drosophila. The work will be primarily experimental, including gene expression analysis. The position will be paid as BatIIa/2 (or equivalent) according to the German pay scale. Requirements are a master's degree (or Diploma) in biology and a strong interest in molecular evolution and/or population genetics. The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. Our group is very international and the everyday working language is English. The LMU department of biology is housed in the new state-of-the-art BioCenter on the University of Munich High-Tech campus.

More information is available on the web at: http://www.zi.biologie.uni-muenchen.de/evol Applicants should send a PDF file with a statement of interest, curriculum vitae, and the contact information for at least two referees to: stephan@zi.biologie.uni-muenchen.de

The University of Munich is an equal opportunity employer with an affirmative action program for the disabled.

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

## OxfordU MolecularMovements

Evolutionary Analysis of Molecular Movements by Thomas Darden, Jotun Hein and Mark Sansom.

The scholarship is only available to Home and EU students who meet the residency requirements!!! Potential applicants should contact Maureen York (york@stats.ox.ac.uk) for more information.

Background

Comparative Biology is a major contributor to biological understanding and can applied to any biological objects that are homologous. The large application area presently is sequences, but other rising areas include structures, networks, organs and more. The strength of evolutionary comparison is the ability to detect features of functional importance and thus select properties that demands a functional explanation from a sea of noise. The only requirement for evolutionary comparison is that the objects to be compared are homologous. In this sense movements are perfectly homologous as the movements associated an ancestral molecule would be inherited with modification, when the molecule evolved over evolutionary time. Movements of molecules have a series of special properties that singles them out compared to other comparative traits. It we imagined to compare the movements of globins over time, this would involved about 3000 atom positions, that could be observed in 109 time steps of size 10-15 seconds. One could imagine 2-10 globins had been observed and the total data set would be of the order 1010 spatial positions. Due to the increase in use of molecular dynamics, this kind of analysis have great potential and it is clear that analysis of such data would need entirely new approaches.

Proposed Research

Conformational change appears to be essential to the formation of highly specific but relatively low affinity binding complexes that characterize signal transduction in cells. Hubs, or proteins involved in multiple protein-protein complexes are characterized by having either disordered domains or high surface charge. Proteins containing intrinsically disordered regions have been reviewed recently by Dyson and Wright. They emphasize the importance of dynamics, through coupled folding and binding, to forming short term but highly specific interactions. Thus the study of the dynamics of conformationally variable proteins is an increasingly important topic within the structural biology of signalling processes.

Experimental approaches that have been brought to bear on this problem include X-ray crystallography, NMR and other spectroscopic approaches, calorimetry, and finally various single molecule techniques such as AFM. Of these crystallography provides the highest precision but is limited to a specific trapped conformation. Dynamics is inferred from B-factors and more importantly from comparison of different conformations of the same protein involved in different protein-protein or protein-ligand complexes. The spectroscopic and single molecule approaches provide more direct evidence of dynamics, but at a cost of structural precision. Recent advances in NMR techniques offer a particularly promising avenue of approach to both structure and dynamics.

Dynamics of proteins can be efficiently modeled by coarse grained approaches such as Normal Mode Analysis, that describe the low frequency collective modes of activation. This approach has been used to infer dynamics in protein superfamilies, and thus could be used to discuss the question of what characterizes the types of conformations sampled by homologous proteins. However, since these model the protein as a homogeneous elastic body, the efficiency of the approach comes at the cost of a loss of accuracy and of sequence specific information i.e. dynamics is necessarily determined entirely by the shape of proteins regardless of the identity of their amino-acid sequence. A far more precise description is provided by the technique of molecular dynamics simulations, which provides an atomic level description of protein motions. Currently these simulations are limited to the picosecond to the sub-microsecond time scale, and provide high precision but only semi-quantitative accuracy due to limitations in the force-fields. Comparative molecular dynamics of related proteins increases the reliability of the results and provides an avenue to study the evolution of dynamic modes and allowed conformations.

The study of unfolding and refolding of entire domains is currently not feasible within either of the above two theoretical approaches, and experimental results are few. However the EF-hand domain provides a tractable highly interesting example of a domain that is structurally conserved, but conformationally variable and small enough to study with a comparative molecular dynamics approach. These domains provide a “trigger” for signalling events by undergoing

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## Portugal ComputationalBiol

PhD Programmes at Instituo Gulbenkian de Ciencia, Portugal

Call for Applications

INSTITUTO GULBENKIAN DE CIENCIA

* PhD ProgramME in Neuroscience, Brain & behavioural systems

* PhD ProgramME in computational biology

* Gulbenkian PhD ProgramME (Life Sciences)

On-line applications are open to April 20, 2007

Further information on the program is available below and at www.igc.gulbenkian.pt PHD PROGRAMME IN NEUROSCIENCE BRAIN & BEHAVIOURAL SYSTEMS

CALL FOR APPLICATIONS

The Fundação para a Ciência e a Tecnologia (FCT), The Fundação Champalimaud (FC) and the Instituto Gulbenkian de Ciência (IGC), call for applications to a 4-years PhD programme in Neuroscience, Brain & Behavioural Systems. Starting September 17, 2007, a small group of students, supported by FCT fellowships, will receive a full year graduate education by an international Faculty, followed by doctoral thesis work at the Institute, associate laboratories, or elsewhere in the world.

The programme wishes to attract highly motivated and independent thinkers with a strong interest in Biology and Biomedical Sciences, who aim at excellence and cooperativity, and at engaging in innovative, risk-taking research. We seek candidates who are not afraid to work hard and are not easily disillusioned when faced with scientific challenges.

We expect that candidates have successfully completed a minimum of 4 years higher education (for Europeans, 240 ECTS) by September 1st, 2007, in any area of Science, Medicine or Technology, but exceptional cases may be considered. Applicants with a background in physical sciences, mathematics, engineering or computer sciences are encouraged to apply regardless of background in biology. Medically qualified students will be eligible for thesis work in clinical research. Foreign students are eligible for support from FCT, provided they will work in a Portuguese laboratory.

Applications are open to April 20, 2007.

Applicants must submit to <www.igc.gulbenkian.pt> a brief curriculum vitae, names and contacts of references, and a letter of motivation. Applications will be confirmed by email. Address eventual questions to Manuela Cordeiro < mcordeir@igc.gulbenkian.pt> Applicants will be selected for an interview conducted in person or remotely by phone or videoconferencing and will be informed of the final decisions not later than June 1, 2007. Further information on the program is available at <www.igc.gulbenkian.pt> PHD PROGRAMME IN COMPUTATIONAL BIOLOGY

CALL FOR APPLICATIONS

The Fundação para a Ciência e a Tecnologia (FCT), the Siemens SA Portugal and the Instituto Gulbenkian de Ciência (IGC), call for applications to a 4-years PhD programme in Computational Biology. Starting September 17, 2007, 12 students, supported by FCT fellowships, will receive a full year graduate education by an international Faculty at the IGC, Oeiras, Portugal, followed by 3 years of research training at a recognised laboratory anywhere in the world. The program is conducted in close cooperation with the FLAD Collaboratorium in Computational Biology, and with several other institutions in Portugal and abroad.

The program wishes to attract highly motivated and independent thinkers with a strong interest in Biological and Computational Sciences, who aim at excellence and cooperativity, and at engaging in innovative, risk-taking research. We seek candidates who are not afraid to work hard and are not easily disillusioned when faced with scientific challenges.

We expect that candidates have successfully completed a minimum of 4 years higher education (for Europeans, 240 ECTS) by September 1st, 2007, in any area of Life, Exact or Computer Sciences and Technologies, but exceptional cases may be considered. Applicants with unconventional education track records are encouraged. Foreign students are eligible for support from FCT, provided they will work in a Portuguese laboratory.

Applications are open until April 20, 2007.

Applicants must submit to <www.igc.gulbenkian.pt> a brief curriculum vitae, names and contacts of references, and a letter of motivation. Hardcopies of the full application files must also be posted to: PDBC, IGC, Apartado 14, PT-2781-901 OEIRAS, Portugal. Detailed information on the program is available at <www.igc.gulbenkian.pt>. Address eventual questions to < pdbc@igc.gulbenkian.pt>. Applicants will be selected for a decisive interview conducted in person or remotely by phone or videoconferencing, and will be informed of the final decisions not later than June 15, 2007.

GULBENKIAN PHD PROGRAMME

CALL FOR APPLICATIONS

The Fundação para a Ciência e a Tecnologia (FCT) and the Instituto

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## Saskatoon PlantConservationGenetics

A PhD Position in Plant Conservation Genetics

A highly-motivated student is being searched to fill a PhD position in plant conservation genetics available after April 2007 in Dr. Yong-Bi Fu's lab at Plant Gene Resources of Canada, AAFC Saskatoon Research Centre. The research project for the student is open, but preferably on molecular characterization of plant transposon elements. Dr. Fu's lab focuses on the development and application of molecular techniques to address plant conservation issues, particularly in seed genebanks, and to infer crop domestication (http://pgrc3.agr.ca/staff/fu_e.html). A MSc in molecular genetics or biology (not necessarily in plant) is desirable and experiences with gene cloning would be a valuable asset. The successful candidate will be paid the stipend of $24,000 plus health benefits and registered in the Department of Plant Sciences, University of Saskatchewan. Applicants are expected to submit a detailed resume along with a one page research proposal outlining the research they would like to conduct. Proposals should include a brief background statement, objective(s), method and materials and expected outcomes and will be evaluated on originality, impact and feasibility. Informal inquiries concerning the position may be addressed to Dr. Fu at fuy@agr.gc.ca or 306-956-7642.

Yong-Bi Fu, PhD

Plant Gene Resources of Canada / Les Ressources Phytogenetiques du Canada Saskatoon Research Centre / Centre de Recherche de Saskatoon

Agriculture and Agri-Food Canada/Agriculture et Agroalimentaire Canada

107 Science Place

Saskatoon, SK S7N 0X2 Canada Telephone/Téléphone: 306-956-7642 Facsimile/Télécopieur: 306-956-7246

Email: Fuy@agr.gc.ca <mailto:Fuy@agr.gc.ca>

http://pgrc3.agr.ca/staff/fu_e.html

FuY@AGR.GC.CA

## UAkron EvolSynthesis

Ph.D. Position at the University of Akron, working with Dr. Francisco Moore

I am seeking a graduate student that is interested in research that integrates micro evolutionary and macro evolutionary approaches. My lab primarily utilizes long term experimental evolution in bacteria to test macro and micro evolutionary theory. While I am currently most interested in a student willing to work with enteric bacteria, I work in vertebrate and microbial systems and also am interested in computational biology. Ultimately my students must decide on their own system. Critical analysis skills are important and previous experience can be in any field of biology. Optimally, a student in my lab should be inquisitive enough to get into trouble occasionally, and smart enough to always get out of trouble. Training in the Integrated Bioscience Program at U of Akron allows study of paleontology, evolutionary genetics and computational biology as well as a diversity of other interdisciplinary research areas. We are a new program, and we have a large set of faculty that work in Ecology, Evolution, Behavior and Comparative Biology. My fairly minimalist web site is located at http://www3.uakron.edu/biology/moore/PacoMoore.html If you are curious about opportunities for graduate study in my lab or at the University of Akron please contact me!

Paco Moore

Dr. Francisco B.-G. Moore

Integrated Bioscience Program

University of Akron

Akron, OH 44325-3908

moore@uakron.edu http://www3.uakron.edu/biology/moore/PacoMoore.html (330) 972-2572

If all you have is FORTRAN life is just a series of loops.

Faculty In Ecology Evolution, Behavior and Comparative Biology at U of Akron. Dr. Brian Bagatto - Comparative Developmental Physiology of Vertebrates Dr. Todd Blackledge - Evolutionary Ecology of Spiders Dr. Bruce Cushing - Developmental mechanisms regulating social behavior Dr. Joel Duff - Evolution of RNA editing in plants Dr. Peter Lavrentyev - Marine and freshwater microbial food webs Dr. Richard Londraville - Comparative Physiology of Fish Dr. Randy Mitchell -

Evolutionary Ecology Dr. Paco Moore - Evolutionary Synthesis Dr. Peter Niewiarowski - Evolution of Life Histories Dr. Jean Pan - Plant and Microbial Ecology Dr. Lisa Park - Invertebrate Paleontology Dr. Steve Weeks - Evolution of sex-determining mechanisms

moore@uakron.edu

## UAlaskaFairbanks PlantInsectInteractions

MS or PhD Student interested in plant-insect interactions

I am seeking a highly qualified MS or PhD student to work on an NSF-funded project examining plant-insect interactions involving aspen (Populus tremuloides) in Interior Alaska. The research examines the impact of extrafloral nectaries (EFNs) and chemical defense on damage by an herbivore, the aspen leaf miner (Phyllocnistis populiella), that currently impacts 80% of all aspen leaves in the region. Much of our work seeks to understand the mechanisms leading to patterns of mining damage in relationship to the presence of EFNs and focuses on tri-trophic interactions involving both ants and parasitoids.

Competitive candidates will have a sincere interest in and curiosity about plant-insect interactions, a strong background in ecology, a good undergraduate record, superior GRE scores, and strong letters of reference. The successful candidate will be expected to qualify for admittance to the Department of Biology and Wildlife and the University of Alaska Fairbanks Graduate School. More information about our graduate program is available at http://www.bw.uaf.edu/-bw_graduate.php The successful candidate may enter our graduate program in the summer or fall of 2007.

For more information please contact Pat Doak (ffpd@uaf.edu).

Pat Doak Department of Biology and Wildlife Institute of Arctic Biology University of Alaska Fairbanks AK 99775 (907) 474 6449 FAX (907) 474 6716

ffpd@uaf.edu

## 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)

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 j.mallet@ucl.ac.uk

## ULausanne MultigenePhylogenetics

University of Lausanne, Switzerland Department of Ecology and Evolution

PhD position in bioinformatics and molecular phylogenetics

This project aims at better understanding how large multigene data matrices can be efficiently use to build robust and accurate phylogenetic trees. Several aspects will be considered including, (i) the effect of supermatrices with low data density on heuristic search algorithms and the development of specific algorithms to deal with such supermatrices, and (ii) the effect of model parameters on the accuracy and robustness of trees based on multigene data matrices.

I seek a candidate with a strong interest in theoretical aspects of phylogenetic reconstructions and bioinformatics, as well as a good background in evolutionary biology. Candidates must have completed their Master's degree or equivalent in a relevant field. Salary will be based on standards of the Swiss National Science Foundation, which is financing the project.

Our department offers a supportive and stimulating environment, with access to excellent computer facilities (links to the Swiss Institute of Bioinformatics) and molecular labs.

The position can start as early as June 2007, but, later starting dates can be negotiated. To apply, please send, preferably by email: a letter describing your research motivation and experience, a CV, and contact details of two referees. Application deadline is April 30th, 2007.

Further information and address for application: Nicolas Salamin University of Lausanne Department of Ecology and Evolution 1015 Lausanne, Switzerland e-mail: nicolas.salamin@unil.ch tel: +41 21 692 4279 web: www2.unil.ch/phylo

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Nicolas Salamin Department of Ecology and Evolution University of Lausanne 1015 Lausanne Switzerland

ph: +41 21 692 4279 fax: +41 21 692 4165 email: nicolas.salamin@unil.ch web: http://www2.unil.ch/phylo Nicolas.Salamin@unil.ch Nicolas.Salamin@unil.ch

## UNewBrunswick EvolOfMulticellularity

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. 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).

anedelcu@unb.ca

## UNewSouthWales EvolBiol

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 Australias 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 Sydneys 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/bondurianskyrussel 1.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

## UNorthCarolinaGreensboro ApisGenomics

MSc Position at the University of North Carolina, Greensboro

Honey Bee Evolutionary Genomics

I am seeking a highly-motivated Masters student to work on a NSF-funded genomic study of the reproductive ground-plan hypothesis of social evolution. This will involve QTL mapping of ovary size in honey bee workers and follow-up studies. Therefore, an interest in evolution and genetics, as well as experience in basic genetic analyses and quantitative skills is desirable. Additional assets include knowledge of social insects, self-motivation, and some skills in bioinformatics, quantitative genetics, and molecular biology. The research could begin as early as May 2007 but formal start of the MSc Program at UNCG would be in August 2007.

In addition, I seek a student for comparative genomic studies among different species in the genus Apis (honey bees), particularly with respect to genome-wide recombination rates.

Please contact me for more information about the potential projects. Check www.uncg.edu/˜o_ruppel for information about our lab and www.uncg.edu/˜o_ruppel for information on the department.

Please apply as soon as possible with a letter of intent (explain why you are interested and relevant previous research experience), CV (including names of references), and transcripts to:

Dr. Olav Rueppell Department of Biology, 105 Eberhart Bldg. University of North Carolina, Greensboro Greensboro, NC 27403, USA Phone: (1) 336-256 2591 Fax: (1) 336-334 5839 E-mail: olav_rueppell@uncg.edu

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## UOxford ProblemSolvingAdaptation

PhD studentship available on "Individual variation in problem solving ability amongst great tits and new caledonian crows: proximate causes and adaptive significance". http://www.zoo.ox.ac.uk/egi/-studentships.htm Closing date 16 April 2007.

Many thanks

John Quinn

Dr John L. Quinn Departmental Lecturer in Behavioural Mechanisms, EGI, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS. Tel: 0044(0)1865-271203 Mobile: 0044(0)7740-869733 Fax: 0044(0)1865-271168

<http://egizoosrv.zoo.ox.ac.uk/EGI/EGIHome.htm>
http://egizoosrv.zoo.ox.ac.uk/EGI/EGIHome.htm
john quinn <john.quinn@zoo.ox.ac.uk>

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## UTexasArlington XenopusEvolGenomics

A PhD position available in Evolutionary Genomics of Xenopus, the University of Texas - Arlington, beginning Fall 2007.

I am seeking a highly qualified and motivated student with interests in genomics, molecular evolution, bioinformatics and biostatistics. The successful candidate will conduct research on African Clawed Frogs (Xenopus) to address questions about the role of epigenetic variation and gene regulation in the evolution of reproductive isolation and phenotypic differences between species. An essential component of the project involves using RNA protocols, chromatin assays, DNA chips for microarray analysis of gene expression, and embryo injections. Ideally, the candidate should have molecular biology experience together with an understanding of evolutionary mechanisms and a strong quantitative/computational background. Former experience with Xenopus, although not required, will be a great asset.

The University of Texas Arlington, the second largest component of the UT System, is conveniently located in the Dallas/Fort Worth Metroplex, minutes away from the best sports, entertainment and recreational opportunities in Texas. The Department of Biology at UTA provides intellectually stimulating environment with a number of dynamic research groups with strengths in genomics, evolutionary biology, taxonomy, and molecular evolution.

Informal inquiries concerning the project and applications may be addressed to Pawel Michalak, michalak@uta.edu. Applications including a CV, statement of research interest, copies of relevant publications, and contact information of three references should be emailed or mailed to me at the address below.

Pawel Michalak, Department of Biology University of Texas Arlington 501 S. Nedderman 337 Life Science Arlington, TX 76010-0498

Tel.: 817-272-2871 Fax: 817-272-2855 Email: michalak@uta.edu http://www.uta.edu/faculty/michalak
MICHALAK@uta.edu MICHALAK@uta.edu

## 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 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

## 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 ex-tension). 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 museum visits world wide and extensive lab work. Interested ap-plicants 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 cur-riculum 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 Evo-lutionary Biology at the University and the neighbouring Swiss Federal Insti-tute 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 interna-tional 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 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 MolEvol

PhD thesis in molecular evolution/evolutionary bioinformatics

Mobile DNA is DNA that can change its position within a genome. It is an integral component of most bacterial genomes, and also implicated in the spreading of drug resistance genes among pathogenic bacteria. Why does mobile DNA persist in genomes? On one hand, mobile DNA may be a very effective parasite, replicating itself at the expense of its host. On the other hand, mobile DNA can also have beneficial effects, such as occasionally beneficial mutations. An ongoing project in our group aims at resolving the question why mobile DNA is maintained in bacte-rial genomes and in eukaryotic genomes. Despite thirty years of debate, the ques-tion still has no conclusive answer. The availability of many completely sequenced genomes provides a unique opportunity to remedy this situation. We are searching for a Ph.D. student with demonstrable experience and interest in evolutionary biol-ogy and a solid background in bioinformatics.

The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. A sam-ple of our research can be found at http://www.biochem.unizh.ch/wagner/ .Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and /or fundamental organizational principles of life.

The successful candidate will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also necessary is a strong back-ground in biology. We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and independent, and has demonstrated interests in problems of molecular evolution. The working language in the labora-tory is English. German skills are not essential.

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file containing a CV including pub-lication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three refer-ences to jobs_aw@bioc.unizh.ch. Please include the word MOBDNA in the sub-ject line. The application deadline is April 23, 2007.

– Prof. Dr. Andreas Wagner University of Zurich Dept. of Biochemistry, Bldg. Y27 Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Secr. (Christiane Gujan): +41-44-635-6142 Office: +41-44-635-6141 FAX: +41-44-635-6144 Email: aw@bioc.unizh.ch Web: http://www.biochem.unizh.ch/wagner/ aw@bioc.unizh.ch aw@bioc.unizh.ch

## 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 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 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

## WageningenU IntragenomicConflict

PhD position on intragenomic conflict in basidiomycete fungi

A four years PhD position on intragenomic conflicts in basidiomycete fungi ('Nuclear tests in mushrooms', see below for a summary) is available at the Evolutionary Genetics group (Prof. Rolf Hoekstra, Wageningen University, the Netherlands) under supervision of Duur Aanen (http://www.gen.wur.nl/-uk/staff/postdocs/duur+aanen/). The project is in collaboration with the laboratory of microbiology (Prof. Han Wösten, University of Utrecht, the Netherlands, http://www.bio.uu.nl/microbiology/-fung/research/index.html). We are looking for a highly motivated candidate with interests in the fields of evolutionary biology (especially levels of selection and/or social evolution) and microbiology. Knowledge of basidiomycete life cycles and practical experience using microbes is recommended but not necessary. The evolutionary genetics group has a wide interest in fundamental questions in evolutionary biology and uses experimental, phylogenetic and theoretical approaches to study these questions, while the microbiology lab specialises on functional aspects of fungal biology. A description of the PhD project is available upon request, but the final details will be worked out with the candidate, to accommodate interests and strength. The position is supported by the Dutch Science Foundation (NWO-ALW).

Starting date is negotiable, but preferably before July 2007. Knowledge of Dutch is helpful in every day life, but the working language in the group is English. A Diploma or Master degree (or equivalent) in biology or related subject is necessary for admission.

Please send your application by email (all material in one file please) to Duur Aanen. Applications should include a CV, a list of publications (if any) and a statement about research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 30th March 2007 will be given full consideration.

Further information and application: Duur Aanen Laboratory of Genetics Wageningen University and Research Center The Netherlands Tel. +31(0)317 482706 Mobile: +31 (0)6 10327948 Fax: +31 (0)317 483146 http://www.gen.wur.nl/uk/staff/-postdocs/duur+aanen/ Sincerely,

Duur Aanen Abstract Nuclear tests in mushrooms.

The primary aim of the present project is to test the hypothesis that in basidiomycetes, selection on organelles (nuclei and mitochondria) within individuals can have an adverse effect on the fitness of the individual itself. Mushroom-forming basidiomycetes form one of the very few organism groups where somatic fusions between genetically different individuals (haploid mycelia), sometimes more than two, are part of the regular life cycle. Normally, after somatic fusion, haploid nuclei are reciprocally exchanged and migrate throughout the mycelia, while mitochondria do not migrate. This leads to genetic mosaics at various scales (cell, tissue, individual), both with respect to the distribution of nuclei and to the distribution of mitochondria. However, several exceptions have been found to this 'textbook' lifecycle. For example, nuclear migration is not always reciprocal, but sometimes only in one direction (Unidirectional Nuclear Migration). Selective explanations for such aberrations seem problematic, because the ultimate fitness of the resulting dikaryon is reduced. Recently developed theory suggests as a possible selective explanation that selection on organelles within individuals can act in an opposite direction to selection between individuals. This means that selfish nuclear and mitochondrial genes, with an intra-individual advantage but a deleterious effect on the individual, can be selected, which leads to a genomic conflict. The overall aim of the present project is to test this hypothesis, and to explore the balance of selection acting on organelles (nuclei and mitochondria) within and between individuals of the basidiomycete model species Schizophyllum commune.

“Aanen, Duur” <duur.aanen@wur.nl>

# Jobs

## ArlingtonVA BotanicalConservation ResAssoc

http://www.natureserve.org/job/-jobNSBotanicalRA.jsp JOB TITLE: Botanical Research Associate EMPLOYER: NatureServe SUPERVISOR: Director, Botany Department LOCATION: Arlington, VA DATE POSTED: February 2007 CLOSING DATE: Open until filled FLSA STATUS: Exempt

INSTITUTIONAL BACKGROUND : NatureServe, a 501(c)3 conservation science and technology organization, provides the scientific basis for effective conservation action. Together with our international network of over 80 natural heritage programs across the United States, Canada, and Latin America, we are the leading source of information on rare and endangered species and threatened ecosystems. We provide information and tools to conservation groups, government agencies, corporations, academia, and the public to help them make informed decisions about managing our natural resources. With nearly 100 staff and a $10 million annual budget, NatureServe is a recognized leader in the application of scientific information and advanced technology for conservation purposes. NatureServe offers a results-oriented and collaborative workplace where a common mission provides focus and excitement and where staff is empowered to take ownership of projects and mission success. Benefits include a 401K savings and retirement plan; health and dental insurance; short and long-term disability; annual and sick leave; and life insurance.

SUMMARY OF POSITION: The Botanical Research Associate researches, summarizes, revises, and manages information relating to native and exotic plant species of the United States and Canada, with a focus on rare species conservation. This position may work on a variety of projects that involve assessing rangewide conservation status, researching rare plant species attributes (e.g. habitat needs), maintaining database records reflecting differing taxonomic treatments, and evaluating the degree of invasiveness of non- native plant species. The Botanical Research Associate is responsible for reconciling, summarizing, and analyzing botanical data received from NatureServe member programs (Heritage Programs and Conservation Data Centres) and other sources, reviewing scientific journals, and communicating (orally and in writing) about the botanical information holdings and the scientific methodologies of NatureServe and its network of member programs. The Botanical Research Associate is supervised by the Director, Botany Department and supervises no staff.

ESSENTIAL JOB FUNCTIONS: 1. Work collaboratively with other staff in maintaining the accuracy and currency of NatureServe's botanical data for North America, including conservation status, taxonomy, distribution, and U.S. and Canadian federal status. 2. Provide support to North American natural heritage programs by resolving problems related to taxonomic and nomenclatural discrepancies that affect data synchronization with central databases and by providing training, via formal sessions and personal communications, related to NatureServe scientific and technical methodologies. 3. Develop or revise information regarding the conservation status of native plant species, and integrate this information to determine species' overall status according to standard protocols. This work typically involves personal communication with natural heritage field botanists and other experts, as well as literature review. 4. Develop or revise information regarding the degree of impact of non- native plant species on native plants, animals, and ecological communities. This work typically involves personal communication with local and regional experts, as well as literature/ "gray" literature research. 5. Assist in outreach and project development activities related to the needs of federal agencies, universities, and other partners. Assist with grant/proposal writing and/or with project management as needed.

KNOWLEDGE/SKILLS: 1. A master's degree in botany, ecology, or biology with coursework in plant taxonomy, biogeography, and plant ecology. 2. Strong familiarity with major North American geography, landforms, and vegetation types. 3. Demonstrated knowledge of principles and practices of plant classification, synonymy, and nomenclature. 4. Experience with large complex databases, especially with data management, quality control, searching and reporting. Experience with SQL desirable. 5. Familiarity with NatureServe and/or IUCN Red List methods for assessing the conservation status of plant species highly desirable. 6. Knowledge of invasive species issues. 7. Strong writing and editing skills, including experience in summarizing and interpreting scientific data for various audiences. Strong verbal communication skills, including a capacity for explaining complex technical subjects. 8. Demonstrated ability to work independently, set priorities, follow procedures, deal meticulously with details, and work productively with

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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

## Bethesda 2 Genomics Taxonomy

ï»¿Computercraft Corp. - Invertebrate Taxonomist

Invertebrate Taxonomist - Bethesda, MD USA

Computercraft seeks an Invertebrate Taxonomist to join the team of highly skilled and dedicated professional molecular biologists and systematists working onsite at the National Institutes of Health (NIH) in Bethesda, MD. Our scientists work with genomic experts at NIH's National Center for Biotechnology Information (NCBI) in the National Library of Medicine (NLM) to create and enhance a suite of databases and tools available to researchers worldwide. We are currently looking for an invertebrate taxonomist to help maintain the NCBI Taxonomy database for the Taxonomy Project at NCBI.

This technically challenging position requires a PhD with a broad knowledge of invertebrate systematics at the morphological and/or molecular level. Familiarity with the principles of phylogenetic systematics and zoological nomenclature is strongly desired. The successful candidate will be responsible for maintaining the nomenclature and classification of a portion of the taxonomy database. Database curation includes verifying taxon names, ensuring that classification is consistent with current consensus, and interacting with sequence annotators and submitters. Up to 50% of the candidateâs time will be available for independent research. Opportunities for research collaboration exist within NCBI and NIH, as well as within other regional institutions, depending on research interests. Teamwork interaction, excellent verbal communication as well as written and organizational skills are essential for this position.

For consideration please submit cover letter, resume/CV, salary history, salary requirements, and U.S. employment eligibility (you must currently reside in the U.S. and be eligible to work). Please note that incomplete application cannot be considered.

Computercraft Attn: HR 8300 Greensboro Drive Suite 720 McLean VA 22102 703.288.4679 fax hr@computercraft-usa.com

For more information on Computercraft and our other biotechnology positions, please visit us at www.computercraft-usa.com We offer an excellent salary and benefits package, 40-hour week. Computercraft is an Equal Opportunity Employer.

Computercraft Corp. - Metagenome Bioinformatics Scientist

Metagenome Bioinformatics Scientist â Bethesda, MD USA

Computercraft seeks a highly motivated individual to curate environmental sample sequences in GenBank and other related resources at the National Institutes of Health (NIH), National Center for Biotechnology

Information (NCBI). These samples include sequences from more traditional site-directed environmental sample studies (rRNAs, and other loci) as well as more recent âmetagenomicsâ projects involving undirected whole-environment shotgun sequencing strategies.

The NCBI directed project aims to make these data more useful to the relevant research communities. The successful candidate will be in direct contact with all the current research and researchers in this field. Specifically, the individual will work with the external scientific groups that generate and study environmental sequence data, and with the various groups at the NCBI that are involved in the submission, classification and use of these sequences.

The successful candidate will work in the NCBI Taxonomy group and collaborate with experts in GenBank, Genomes, BLAST, and Probe database groups onsite at the NIH campus in Bethesda, Maryland. This is an opportunity for the right person to make a significant contribution to the scientific community.

Responsibilities:

Design a broad strategy to represent and manipulate environmental sequence data (site-specific and metagenomic).

Curate the nomenclature and classification of environmental sequences in the NCBI Taxonomy Database.

Assist in the development of submission tools, annotation guidelines, analysis and statistical software tools for environmental sequences.

Develop resources at the NCBI and contacts with the research community to best support these efforts.

Requirements:

Ph.D. in biology or related field Extensive experience with metagenome/environmental sample studies Excellent oral and written communication skills

For consideration please submit cover letter, curriculum vitae, salary history, salary requirements, and U.S. employment eligibility (you must currently reside in the U.S. and be eligible to work). Please note that incomplete application cannot be considered.

Computercraft Attn: HR 8300 Greensboro Drive Suite 720 McLean VA 22102 703.288.4679 fax hr@computercraft-usa.com

For more information on Computercraft and our other biotechnology positions, please visit us at www.computercraft-usa.com We offer an excellent salary and benefits package with a 40-hour week. An equal opportunity employer.

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## EAWAG Switzerland 3 EvolGenetics

The department of Fish Ecology and Evolution of the Swiss Institute for Aquatic Science and Technology (Eawag) still invites applications for three positions in Ecology, Evolution, Genetics of Aquatic Organisms that were recently announed in separate postings.

1. Tenure Track Group Leader in Ecology/Evolution/Genetics/Conservation of Fish deadline 31 March

2. Fixed term (up to 5 years) research position in molecular genetics deadline 7 April

3. Computational Population Geneticist / Ecologist (2-3 years) shared with the Eawag Department of Aquatic Ecology (Prof. Jukka Jokela) deadline 7 April

Details about the jobs and application procedure are announced here http://www.fishecology.ch/jobs.htm

see also (http://naturejobs.nature.com; http://-naturejobs.nature.com;)

All three jobs are located in the Kastanienbaum Centre of Ecology, Evolution & Biogeochemistry (Lucerne).

The department of Fish Ecology and Evolution is one of three departments in the Eawag Centre of Ecology, Evolution and Biogeochemistry in Kastanienbaum (Lucerne). It is closely affiliated with the Institute of Zoology, University of Bern. The core research of the department involves building and testing general ecological and evolutionary theories using fish model systems, as well as applying such theories to aid the conservation and management of fish populations, communities and biodiversity. The excellent departmental research facilities are located in Kastanienbaum, on the shores of Lake Lucerne, about 20 minutes from Lucerne town and 1.5 hours from Bern University. Facilities include a fully equipped molecular genetics laboratory with two 8 capillary DNA sequencers, newly built outdoor glass troughs with lake water through-flow for experimental work with fishes, modern large cold water and tropical aquarium facilities, a fleet of stationary and portable research vessels and cars for fieldwork.

Applicants should send their applications, including CV, publication list, a two pages statement of research interests, including links to the research program of the department (see www.fishecology.ch), and the names and email addresses of five referees to

Sandra Isenring, Human Resources, Eawag, Ueberlandstrasse 133, CH-8600 Duebendorf or per e-mail to sandra.isenring@eawag.ch, and in one single PDF-file to Ole Seehausen (ole.seehausen@eawag.ch). For questions please contact Ole Seehausen (ole.seehausen@eawag.ch). For information on Eawag please consult http://www.eawag.ch/index_EN, for information on our de-partment please consult www.fishecology.ch

Eawag is the Swiss Federal Institute of Aquatic Science and Technology, a Swiss-based and internationally active research institute within the ETH domain, committed to an ecological, economical and socially responsible management of water.

Ole Seehausen

Institute of Zoology University of Bern Baltzerstr. 6, CH-3012 Bern Phone direct +41 31 631 31 31 Phone secr. +41 31 631 30 09 FAX +41 31 631 30 08 & EAWAG Centre of Ecology, Evolution and Biogeochemistry Seestrasse 79 CH-6047 Kastanienbaum Phone direct +41 41 349 21 21 Phone secr +41 41 349 21 08 FAX +41 41 349 21 68

http://www.fishecology.ch Ole.Seehausen@eawag.ch Ole.Seehausen@eawag.ch

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## EAWAG Switzerland FishEvolution

Research Group Leader in Ecology/Evolution/Genetics/Conservation of Fish (tenure track) at the Eawag Centre of Ecology, Evolution & Biogeochemistry in Kastanienbaum/Lucerne (Switzerland)

We are inviting applications for a tenure track research group leader position in ecology/genetics/conservation of fish at the department of Fish Ecology and Evolution of the Swiss Institute for Aquatic Science and Technology (Eawag), located in Kastanienbaum/Lucerne (Centre of Ecology, Evolution & Biogeochemistry).

We are seeking a dynamic and innovative scientist with an excellent track record in science, and proven ability to attract extramural funding. S/he should be well versed in ecological and evolutionary theories and have strong aspiration for understanding how environmental changes interact with ecological and evolutionary processes to generate and maintain biodiversity at any levels of biological organization from genes to communities. The successful candidate is expected to attract extramural funding from Science Foundation and/or other sources to build a research group in any aspect of ecology, genetics and conservation, seeking to build bridges between theory and conservation/management of fish. We welcome applications both from theoreticians who work closely with empiricists to develop testable theories, and from empirical scientists who conduct theory-driven research. The successful candidate is expected to actively engage in collaborations with other scientists at Eawag . A small contribution to teaching (e.g. one course) at the University of Bern is envisaged, as is the supervision of graduate students. Scientific language of the lab is English, and teaching is in English too. The advertised position is a tenure-track research leader with review for tenure after four years. A formal lectureship affiliation with a university is possible and strongly encouraged.

Requirements: PhD in a relevant field and several years of Postdoc experience

The department of Fish Ecology and Evolution is one of three Eawag science departments in the Centre of Ecology, Evolution and Biogeochemistry in Kastanienbaum (Lucerne) and is closely affiliated with the Division of Aquatic Ecology and Macroevolution of the Institute of Zoology, University of Bern. The core research of our department involves building and testing general ecological and evolutionary theories with fish model systems, and applying such theories to aid the conservation and management of fish populations and communities. The excellent departmental research facilities are located in Kastanienbaum, on the shores of Lake Lucerne, about 20 minutes from Lucerne town and 1.5 hours from Bern University by public transport. Facilities include a fully equipped molecular genetics laboratory with two 8 capillary DNA sequencers, two large newly built outdoor glass troughs with lake water through-flow suitable for population level experimental work with fish, a modern indoor lake water through-flow aquarium system, a large state of the art tropical fish aquarium facility, a fleet of several stationary and portable research vessels and cars for fieldwork. The Center further has fully equipped laboratories for stable isotopes, sedimentology and analytical chemistry. The Center has recently been renamed (previously Limnological Research Centre). Other recently started research groups at the ecology/evolution interface are theoretical ecology (Akiko Satake), evolutionary ecology of algae and experimental evolution (Bas Ibelings), molecular microbial ecology (Helmut Bürgmann), evolutionary ecology (Jukka Jokela), evolution of species diversity (Ole Seehausen).

Applicants should send their applications, including CV, publication list, a short (less than two pages) summary of future research interests, and the names and email addresses of five referees to Sandra Isenring, Human Resources, Eawag, Ueberlandstrasse 133, CH-8600 Duebendorf or per e-mail to sandra.isenring@eawag.ch, and in one single PDF-file to Professor Ole Seehausen (ole.seehausen@eawag.ch). For questions please contact Ole Seehausen (ole.seehausen@eawag.ch). For information on Eawag mission and research please consult http://www.eawag.ch/index_EN, for information on our department please consult www.fishecology.ch Application deadline: March 31, 2007, applications will be considered until the post is filled.

Eawag is the Swiss Federal Institute of Aquatic Science and Technology, a Swiss-based and internationally active research institute within the ETH domain, committed to an ecological, economical and socially re-sponsible management of water. We have an open tenure track position for an outstanding individual as

Ole Seehausen Professor for Aquatic Ecology & Evolution

Institute of Zoology University of Bern Baltzerstr. 6, CH-3012 Bern Phone direct +41 31 631 31 31 Phone secr. +41 31 631 30 09

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## EAWAG Switzerland PopGenet

The department of Fish Ecology and Evolution of the Swiss Institute for Aquatic Science and Technology (Eawag) invites applications for a fixed term (up to 5 years) research position in molecular genetics located in the Kastanienbaum Centre of Ecology, Evolution & Biogeochemistry (Lucerne).

We are seeking a young, dynamic and innovative scientist with a proven track record in molecular population genetics, ecological or evolutionary genetics and a hands-on wet-lab approach. S/he should be well versed in evolutionary and population genetics theory, have strong aspiration for understanding ecological and evolutionary processes that generate and maintain species diversity, and should be keen to work on fish as model organisms. A major focus of the department is genetics of adaptive diversification and speciation using cichlid fish and postglacial fish radiations as model systems. The successful candidate is expected to contribute a strong molecular genetic component to this research program, and to attract extramural funding from Science Foundation or other sources to build a small research group. Some teaching and supervision of undergraduate students is expected from fall 2007. Scientific language of the lab is English, and teaching is in English too. Salary depends on number of Postdoc years.

Requirements: PhD in a relevant field and ideally some years of Postdoc experience

The department of Fish Ecology and Evolution is one of three departments in the Eawag Centre of Ecology, Evolution and Biogeochemistry in Kastanienbaum (Lucerne) and is closely affiliated with the Division of Aquatic Ecology and Macroevolution of the Institute of Zoology, University of Bern. The core research of the department involves building and testing general ecological and evolutionary theories using fish model systems, as well as applying such theories to aid the conservation and management of fish populations, communities and biodiversity. The excellent departmental research facilities are located in Kastanienbaum, on the shores of Lake Lucerne, about 20 minutes from Lucerne town and 1.5 hours from Bern University. Facilities include a fully equipped molecular genetics laboratory with two 8 capillary DNA sequencers, two large newly built outdoor glass troughs with lake water through-flow for population level experimental work with fish, a modern indoor lake water through-flow aquarium system, a large state of the art tropical fish aquarium facility, a fleet of stationary and portable research vessels and cars for fieldwork.

Applicants should send their applications, including CV, publication list, a two pages statement of research interests, including links to the research program of the department (see www.fishecology.ch), and the names and email addresses of five referees to Sandra Isenring, Human Resources, Eawag, Ueberlandstrasse 133, CH-8600 Duebendorf or per e-mail to sandra.isenring@eawag.ch, and in one single PDF-file to Ole Seehausen (ole.seehausen@eawag.ch). For questions please contact Ole Seehausen (ole.seehausen@eawag.ch). For information on Eawag please consult http://www.eawag.ch/index_EN, for information on our de-partment please consult www.fishecology.ch

Application deadline: April 7, 2007, applications will be considered until the post is filled.

Eawag is the Swiss Federal Institute of Aquatic Science and Technology, a Swiss-based and internationally active research institute within the ETH domain, committed to an ecological, economical and socially responsible management of water.

Ole Seehausen University of Berne

ole.seehausen@aqua.unibe.ch

## Europe ArabidopsisEvolGenetics ResAssist

Research Assistant needed for Arabidopsis ecological plant genetics project in Europe.

We are looking for a Research Assistant to participate in a large-scale investigation of the evolution of flowering time in the model plant, Arabidopsis thaliana. Our approach includes analysis of the flowering time response to a wide range of natural and manipulated environments at levels ranging from DNA sequence variation to continental ecotype distributions. This NSF-funded Frontiers of Integrative Biological Research (FIBR) project is a collaborative effort of four US labs (Johanna Schmitt, Brown University; Stephen Welch, Kansas State University; Michael Purugganan, New York University; Richard Amasino, University of Wisconsin) as well as Arabidopsis laboratories at five research institutions in Europe. Part of this study entails establishing a set of five common gardens in Europe at Valencia, Spain; Oulu, Finland; Norwich, UK; Cologne, Germany; and Halle, Germany. At these sites large numbers of A. thaliana accessions will be grown in multiple plantings synchronized with local populations in order to assess geographic and seasonal variation in selection of flowering time and other life history traits.

We are seeking a Research Assistant who would be interested in living at one of the five European field sites and assisting with plant care and measurement. Applicants must have a B.S. degree in biology or a related science. German or Spanish language skills are desirable for this position, but not required.

Prior research experience with plants is necessary because the Research Assistant may operate largely independently for prolonged periods of time. Although the primary duties involve plant care and measurement, the successful applicant will have the opportunity to design and independently conduct plant genetic research projects of joint interest to and in consultation with participating host institution scientists. This Research Assistantship has a strong training component and was conceived as being analogous to a Fulbright fellowship. The successful applicant will be awarded an NSF-fellow position. The fellowship stipend will be $35,000 plus health insurance and other benefits.

To apply, please send a letter of application, resume and contact information for three references (as pdf files) to Stephen Welch (welchsm@ksu.edu <mailto:welchsm@ksu.edu>) or Johanna Schmitt (johanna_schmitt@brown.edu <mailto:johanna_schmitt@brown.edu>). Please reference the position number (W0007455) in the email Subject line. For further information on the project see www.egad.ksu.edu/about.html <http://-www.egad.ksu.edu/about.html> .

APPLICATION DEADLINE: May 15, 2007

– Karlene Varnadore Business Manager K-State Dept. of Agronomy 2004 Throckmorton Hall Manhattan, KS 66506-5501 785/532-7261

Karlene Varnadore <kgv@ksu.edu>

## LouisianaStateU Museum MolGenetTech

Job Description The Austin Laboratory at the LSU Museum of Natural Science is seeking a candidate for a position as a LABORATORY TECHNICIAN. Experience in molecular genetic methods including DNA isolation, PCR, automated sequencing are required. Prior work in genomics and/or phylogenetics and HERPETOLOGY are highly desired.

The position entails laboratory management and research, and the ideal applicant will have had extensive experience in a genetics laboratory (i.e., maintenance of laboratory equipment, facilities and frozen tissue collections, and purchasing of supplies and equipment) and conducting and training students and technicians in various molecular genetic methods (including, for example, PCR, DNA sequencing using capillary sequencers, construction of genomic libraries, development of microsatellite and SNP markers).

Position available Summer/Fall 2007.

Applications will be reviewed starting 15 April.

E-MAIL cover letter, CV, and names, addresses, phone numbers, and e-mail addresses of 3 references to:

Dr. Christopher Austin Assistant Curator/Professor Museum of Natural Science 119 Foster Hall Louisiana

State University Baton Rouge, LA 70803-3216

e-mail: ccaustin@lsu.edu http://www.museum.lsu.edu/Austin/lab.html http://www.lsu.edu/museum ccaustin@lsu.edu

## MRC Bioinformatics curator

EUMODIC Research Curator EUMODIC - EU funded project Bioinformatics Group MRC Mammalian Genetics Unit Oxfordshire

Starting salary £19,238 - £30,589 per annum depending on experience

The Research Curator will work within the Bioinformatics Group, on the EU funded project EUMODIC. They will be responsible for managing and curating the EuroPhenome database, a database of mouse phenotype data. In addition they will be involved in the development and integration of phenotype ontologies with this database, alongside integration with related datasets such as Ensembl.

Applicants should hold a first degree (or higher) in Biological Sciences, Computer Science or Bioinformatics and/or have appropriate experience with mouse phenotype data and/or ontology development. The candidate should be proficient in at least one programming language, preferably Java. A strong background in management of large datasets and data integration, and experience of ontology editors such as Protégé or OBO-Edit, would be an advantage.

In return, we can offer a competitive salary, 30 days holiday and a generous pension scheme.

See the EUMODIC group website www.eumodic.eu for more information on the project and http://www.mgu.har.mrc.ac.uk/ for more information on the Unit's research. Please contact John Hancock (j.hancock@har.mrc.ac.uk) or Ann-Marie Mallon (a.mallon@har.mrc.ac.uk) with any questions.

This post is fixed term for 3 years with possible extension to the project until 31 January 2011.

For an application form please email oxford.recruitment@ssc.mrc.ac.uk, quoting reference number 2007-070/MGU EUMODIC Research Curator.

Closing date for applications: 16 March 2007

Dr John M. Hancock Head of Bioinformatics, MRC Mammalian Genetics Unit, Harwell, Oxfordshire OX11 0RD, U.K.

E-mail: J.Hancock@har.mrc.ac.uk Telephone: +44 (0)1235 84 1014 Fax: +44 (0) 1235 84 1210 WWW: http://informatics.har.mrc.ac.uk/ Personal Page: http://informatics.har.mrc.ac.uk/jmhwww/ j.hancock@har.mrc.ac.uk j.hancock@har.mrc.ac.uk

## McKendreeCollege Temporary EvolBiol teaching

Instructor of Biology

McKendree College invites applications for a temporary one-year, non tenure-track position to start in the Fall 2007 with the option of applying for the full-time tenure track position for Fall, 2008.

Candidate will be teaching Introductory Biology, Principles of Biology II, Genetics, Ecology, and Animal Behavior. A Ph.D. and prior teaching experience are required Interested candidates should submit a cover letter, c.v., three letters of recommendation, and a detailed statement of teaching philosophy to Shirley Jacob, Director of Human Resources, McKendree College, 701 College Road, Lebanon, IL, 62254 or Hr@mckendree.edu. See www.mckendree.edu <http://www.mckendree.edu/> for more information.

"Henshaw, Michael T" <mthenshaw@mckendree.edu>

## MichiganStateU SummerRes LifeHistoryEvol

One NSF-REU (research experience for undergraduates) position is available to work as part of a long-term field experiment designed to test the importance of food abundance to life history evolution in red squirrels. The successful candidate will spend the summer (May to August) working as part of our core data collection crew near Kluane National Park in the Yukon of Canada and will collect additional data as part of an independent research project. Details on the squirrels, the area and the large collaborative project can be found at www.redsquirrel.msu.edu. Transportation to and from the site, food and a monthly stipend will be provided.

Possible undergraduate research projects include:

1. Spruce cone preferences of left- and right-handed squirrels.

2. Behavior and nest attendance of females specializing in the production of many smaller or few high quality offspring.

If you are interested in spending the summer pursuing an undergraduate research project please contact me by email (mcadama@msu.edu) as soon as possible. Include as attachments to your email a cover letter indicating 1) your interest in the project, 2) what specific questions you might be interested in answering (feel free to suggest one that is not listed above), and 3) a statement of why you are suited for the position. Also attach a resume with references. If you are not from Michigan State University then please provide the name of someone at your home university who could potentially provide additional mentorship on your project during the next academic year.

Dr. Andrew McAdam Department of Fisheries & Wildlife 13 Natural Resources Building Michigan State University East Lansing, MI 48824 517-432-0396 mcadama@msu.edu

## 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, Phyton, 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/fcwiki/ francesca ciccarelli

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

## 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 programing (Perl, Python, C++) in UNIX environment (familiarity with Solaris system 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 Institute for Bioinformatics University of Muenster or Dr. Wojciech Makalowski 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 for further details).

wojtek@warta.bio.psu.edu wojtek@warta.bio.psu.edu

## NESCent Phyloinformatics

Phyloinformatics Summer of Code 2007

A collaborative Phyloinformatics Group, sponsored by the National Evolutionary Synthesis Center (NESCent: http://www.nescent.org/), is working to develop user-interfaces, improve software interoperability and support data exchange standards in evolutionary bioinformatics. The specific projects are diverse in nature and range from the development of AJAX components for web-based bioinformatics applications, managing workflows using approaches from functional and logic programming, and developing data exchange standards for phylogenetic substitution models.

The Phyloinformatics group will be sponsoring student collaborators through the Google Summer of Code program (http://code.google.com/ soc), which provides undergraduate, masters and PhD students with a unique opportunity (over three summer months) to obtain hands-on experience writing and extending open-source software under the mentorship of experienced developers from around the world. We are particularly targeting students interested in both evolutionary biology and software development. Students will have one or more dedicated mentors with expertise in phylogenetic methods and open- source software development. Our project proposals are flexible and can be adjusted in scope to match the skills of students with less programming proficiency. If the program sounds interesting to you but you are unsure whether you have the necessary skills, please email the mentors at phylosoc {at} nescent {dot} org. We will work with those who are genuinely interested to find a project that fits your interest and skills. Students will receive a stipend from Google and will be invited to participate in future collaborative events such as the NESCent Phyloinformatics Hackathons (http://www.nescent.org/wg/ phyloinformatics).

TO APPLY: Students must apply on-line at the Google Summer of Code website (http://code.google.com/soc). The application period for students is now open and ends on Saturday, March 24, 2007 (one week from now).

The Phyloinformatics Summer of Code project and ideas page is at the following URL: http://phyloinformatics.net/-Phyloinformatics_Summer_of_Code_2007 The above page also contains links to the GSoC program rules, eligibility requirements, and stipend payment mechanism. We encourage all interested students to email any questions, or self-proposed project ideas, to phylosoc {at} nescent {dot} org. This will reach all prospective mentors.

Eligibility requirements for students: http://-code.google.com/support/bin/answer.py?answer=-60279&topic=10730

Stipend for students: http://code.google.com/-support/bin/answer.py?answer=60322&topic=10731

Please disseminate this announcement to appropriate students at your institution.

Hilmar Lapp Assistant Director for Informatics NESCent

hlapp@duke.edu hlapp@duke.edu

## NESCent Programmer

Research Programmer, Data Modeling and Services

The National Evolutionary Synthesis Center (http://www.nescent.org) seeks a highly motivated Research Programmer responsible for data modeling, database design, middleware implementation, and implementation of web and data services. The incumbent will collaborate with scientists and software developers to develop a novel system for the analysis of developmental and phenotypic diversity data using ontologies. This project is a collaboration with Paula Mabee (U. of South Dakota), Monte Westerfield (U. of Oregon) and the National Center for Biomedical Ontology.

A project home page is being set up. In the meantime, please visit the Informatics Initiative on the NESCent website (http:// www.nescent.org/informatics/initiatives.php) for additional information. Once set up, the project website will be posted along with the job ad on the NESCent employment page: http://www.nescent.org/about/ employment.php#datamodeling.

Job description:

The incumbent will be responsible for creating the data model, schema, server-side middleware, and programming libraries that enable the building of client applications to create, store, browse, search, and manipulate a database of phenotypic knowledge. The incumbent will gather requirements from scientists and collaborating developers; determine functional and technical specifications; analyze, design, develop, maintain, document, and test new and existing database schemas, object models, APIs, and software; use and contribute to standards; advise collaborators and supervisors on emerging technologies in semantic knowledge engineering; create technical documentation, contribute to scientific publications; recommend software fixes and enhancements; present work at scientific meetings; advise supervisor and collaborators of priorities, problems and proposed solutions.

Required qualifications:

* Bachelor's degree in Computer Science, Engineering, Bioinformatics, or related field * Two or more years of significant experience in database design, middleware implementation, API design, and object-relational mapping * Thorough knowledge of relational data modeling, ERDs, and normalizing schemas; experience with translating domain models into relational schemas, experience with data warehousing principles * Proficiency in the DDL and DML elements of SQL, and understanding of advanced elements (e.g., sub-queries, views, triggers, stored procedures) * Demonstrated ability to architect, design, and implement object models and middleware on top of databases * Solid understanding of and experience with modern object-relational mapping and middleware technologies and programming frameworks (e.g., JDBC, J2EE/EJB, CMP, JDO, Hibernate) * Experience with designing, implementing, or using resources in an SOA environment (e.g., SOAP, REST, CORBA, JAX-WS) * Familiarity with basic Semantic Web concepts, terminology, standards, and formats (such as XML, XSD, RDF, RDF/XML, triple stores, reasoning, CL) * Demonstrated ability to communicate effectively with both technical and non-technical scientific audiences

Preferred qualifications:

* Master's or PhD degree in Computer Science, Engineering, Bioinformatics, or related field * Three or more years of relevant and significant experience, and at least two years of experience programming Java * Thorough knowledge of basic and advanced elements of database design and programming, such as views, triggers, stored procedures, query optimization, data warehousing, ideally using a PostgreSQL database * Knowledge of and experience with Semantic Web concepts, terminology, standards, and formats * Prior experience and/or education in biology (in particular genetics and evolution) or using or creating ontologies * Demonstrated ability to work and thrive in a collaborative team environment, and to fluidly interact with local and external open- source developer communities; familiarity with agile development methodologies * Proficient knowledge of software development best practices, such as design patterns, reuse, modularity, unit testing, usability testing * Demonstrated ability to contribute to scholarly publications

To apply, please send cover letter, resume, and the contact information for three references to the Asst. Director of Informatics, Hilmar Lapp (hlapp@nescent.org). Further inquiries about the position may be directed to Mr. Lapp by email, or by phone at +1-919-668-5288.

hlapp@duke.edu hlapp@duke.edu

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## NESCent Programmer Web

Research Programmer, User Interfaces and Web Programming

The National Evolutionary Synthesis Center (www.nescent.org) seeks a highly motivated Research Programmer to be responsible for the design and implementation of web applications and user interfaces. The incumbent will collaborate with scientists and software developers to develop a novel system for the analysis of developmental and phenotypic diversity data using ontologies. This project is a collaboration with Paula Mabee (U. of South Dakota), Monte Westerfield (U. of Oregon) and the National Center for Biomedical Ontologies.

Job description:

The incumbent will be responsible for creating user-friendly, highly interactive web-based or stand-alone client applications that will allow collaborating scientists as well as the scientific community at large to create, store, browse, search, and manipulate a database of phenotypic knowledge using ontologies. The incumbent will gather requirements from scientists and collaborating developers; determine functional models and technical specifications; analyze, design, develop, maintain, document, and test new and existing APIs and software; design, develop, and maintain interactive web applications and dynamic pages; use and contribute to standards; advise collaborators and supervisors on emerging technologies in semantic knowledge engineering; participate in usability testing and translate the results into change recommendations; create technical documentation; contribute to scientific publications; recommend software and user interface fixes and enhancements; present work at scientific meetings; advise supervisor and collaborators of priorities, problems and proposed solutions.

A project home page is being set up. In the meantime, please visit the Informatics Initiatives on the NESCent website (http:// www.nescent.org/-informatics/initiatives.php) for additional information. Once set up, the project website will be posted along with the job ad on the NESCent employment page: http://www.nescent.org/about/ employment.php#userinterfaces.

Required qualifications:

* Bachelor's degree in Computer Science, Evolutionary Biology or related field * Two or more years of significant experience in user interface design and programming, web design, and web application programming * Demonstrated ability to design and implement intelligent and highly interactive user interfaces that meet user requirements * Experience with dynamic and interactive web page programming (e.g., DHTML, JavaScript, AJAX, CSS, services) * Experience with designing, implementing, or using resources in an SOA environment (e.g., SOAP, REST, CORBA, JAX-WS) * Familiarity with web application technology stacks, application servers, and programming frameworks (e.g., J2EE/EJB, JSP, JSTL, JSF, Spring, JBoss, Struts, Apache Cocoon) * Familiarity with basic Semantic Web concepts, standards, and formats (such as RDF, RDF/XML, triple stores, reasoning, CL, metadata) * Demonstrated ability to communicate effectively with both technical and non-technical scientific audiences

Preferred qualifications:

* Master's or PhD degree in Computer Science, Evolutionary Biology, or related field * Three or more years of significant experience in user interface design and programming, web design, and web application programming * Prior experience and/or education in biology (in particular genetics and evolution) * Prior experience in using and creating ontologies * Proficiency in programming data service aggregation (such as XML, XSLT, feeds) * Solid understanding of and experience with web application technology stacks, application servers, and programming frameworks * Knowledge of and experience with Semantic Web concepts, terminology, standards, and formats. * Demonstrated ability to work and thrive in a collaborative team environment, and to fluidly interact with local and external open- source developer communities * Familiarity with agile development methodologies * Proficient knowledge of software development best practices, such as design patterns, reuse, modularity, unit testing, usability testing * Demonstrated ability to contribute to scholarly publications

To apply, please send cover letter, resume, and the contact information for three references to the Asst. Director of Informatics, Hilmar Lapp (hlapp@nescent.org). Further inquiries about the position may be directed to Mr. Lapp by email, or by phone at +1-919-668-5288.

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## NatlInstMalariaRes Delhi AnophelesEvolGenomics

Research Positions on Anopheles minimus Evolutionary Genomics at the National Institute of Malaria Research, Delhi, INDIA

The following positions are to be filled up in an extramural funded project from ICMR, Govt. Of India on Anopheles evolutionary genomics at the National Institute of Malaria Research, Delhi, INDIA

1. Senior Research Fellow (SRF) (two positions) 2. Research Assistant (RA) (one position)

The study aims at looking at the genetic diversity, population structure and demographic history of Anopheles minimus, the principal malaria vector distributed in the north-eastern parts of India. Our approach includes analyses of multilocus neutral DNA markers in the Anopheles minimus genome using genome information of Anopheles gambiae, similar to that have been described earlier in Drosophila (Das, Mohanty and Stephan 2004, Genetics 168: 1975-1985).

For both SRF and RA, masters degree in any branch of modern biology is required. For SRF, a minimum two years of research experience with publications is essential. In addition to PCR and high-throughput DNA sequencing and analyses of DNA sequence data with different population genetic models, the selected candidates also have to travel frequently to north-eastern part of India for field collection of biological samples.

Age, monthly fellowship, and other terms and conditions are as per ICMR and Govt. Of India regulations.

Eligible Candidates may apply with a full CV with two academic reference letters to:

Dr. Aparup Das, Assistant Director Evolutionary Genomics and Bioinformatics Laboratory National Institute of Malaria Research (ICMR) Room No. 100, PVT Block, 2nd Floor 22, Sham Nath Marg, New Delhi - 110 054, INDIA Tel: +91-11-23943342 (direct), 23928804 (Extn. 20) Fax: +91-11-23946150 E-mail: aparup@mrcindia.org; adas@uni-muenchen.de Web: http://www.mrcindia.org/cv/dasa.htm; www.plasmodiversity.org.in

Aparup Das <aparup@mrcindia.org>

## 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 tfulton@naturesourcegenetics.com

## Netherlands EvolEcol

Netherlands Institute of Ecology (NIOO KNAW) is a research institute of the Royal Netherlands Academy of Arts and Sciences (KNAW). It comprises three centers: the Centre for Estuarine and Marine Ecology (CEME) in Yerseke, the Centre for Limnology (CL) in Nieuwersluis, and the Centre for Terrestrial Ecology (CTE) in Heteren. Mission of the NIOO is to carry out fundamental and strategic research in ecology.

NIOO is offering young, talented researchers, tenure-track positions. These staff members are expected to develop their own line of research within a particular field. NIOOs career policy is characterised by flexible personnel management with a focus on the individual. Academic achievements are seen as being central to the academic career and leading for the successful tenure-track procedure. The NIOO offers the candidate excellent research facilities and ample opportunities for professional development and supplementary training and education.

The Department of Animal Population Biology (APB) of the Netherlands Institute of Ecology (NIOO-KNAW) is offering a

Tenure-track position for an Evolutionary Ecologist (m/f) Vacancy number CTE-PVD-07320

Job description The tenure track position is for an evolutionary ecologist, with an affinity for behavioural and physiological work. The research of APB centres around the life-history of animals, and combines long-term population studies on hole-breeding passerines with work in aviaries and molecular techniques. APB has a high reputation within the international scientific community and was recently assessed as excellent in an international peer review. One of the research lines within APB is on avian personalities in the great tit (Parus major). This research is built on field studies (9 years of breeding data on a population where the majority of the birds are of known personality) and aviary experiments (selection lines on personality, 40 aviaries). The senior researcher leading this research line, Dr P.J. Drent, is retiring in the near future, and applicants will be favoured who wish to continue the development of this research.

Requirements We are looking for a scientist with several years of post-doctoral experience and an excellent track record in behavioural ecology in terms of both publications and the acquisition of research grants.

The NIOO has no obligation to teach at University level, but supervision of Masters and PhD students is expected as part of normal research activity. Scientific communication is carried out in English, so knowledge of the Dutch language is not required for this post, but a commitment to learning the language is expected in longer-term staff.

Appointment: The appointment will be on a temporary basis for a maximum of 6 years. The appointed scientist will be evaluated after 3 and on completion of 5 years of employment there will be an assessment of performance based on established criteria. If the outcome of the assessment is positive, the researcher will be promoted to the rank of senior researcher with tenure.

Salary: The salary will dependent on qualifications and work experience from 3060. gross per month up to a maximum of 4190. gross per month (scale 11 CAO-NU) for a full-time job.

Location: Heteren

Information: Additional information about this position is available upon request from Prof. Marcel E. Visser (m.visser@nioo.knaw.nl or +31-26-4791253), head of department Animal Population Biology. More information can be found on the NIOO website (www.nioo.knaw.nl <http://www.nioo.knaw.nl/> ).

Applications: Please send your application including complete curriculum vitae, 3 referees and the reference number to Prof. Marcel E. Visser at NIOO-KNAW, P.O. Box 40, 6666 ZG Heteren, The Netherlands or g.giesen@nioo.knaw.nl .The closing date for application is 15 May 2007, and the interviews will take place in the last week of June.

M.Visser@nioo.knaw.nl M.Visser@nioo.knaw.nl

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## NewYorkU Tech CompFuncGenomics

JOB OPENING: Technician/Lab Manager

We have an opening for a techncian/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. 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

Th 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>

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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)

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 PostgresSQL experience desired Current student in Computer Science or related field Experience with JAVA and/or PHP Domian Knowlege 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

## Paris HostParasite

Oliver Kaltz Laboratoire de Parasitologie Evolutive (CC 237), CNRS-UMR 7103 UniversitÃ© Pierre & Marie Curie 7, quai St. Bernard 75252 Paris France

++33 1 44 27 38 23 (Phone) ++33 1 44 27 35 16 (Fax)

LECTURER (MAITRE DE CONFERENCE) IN EVOLUTIONARY ECOLOGY OF HOST-PARASITE INTERACTIONSThe Laboratory of Ecology & Evolution (CNRS UMR 7103 & 7625, Universit Pierre-et-Marie-Curie, Paris, France) invites applications for a permanent lecturer position (Ma“tre de Confrence) in evolutionary ecology of host-parasite interactions, starting in autumn 2007.The successful candidate should have a strong background in evolutionary ecology (life history theory, population biology, population genetics). Possible areas of research are evolutionary epidemiology, evolutionary immunology or experimental coevolution. Our laboratory has excellent facilities for experimental work on microbial systems and we therefore encourage applications of candidates with experience in microbial ecology and evolution.Teaching (192 hours per year) ranges from introductory lectures in ecology and evolution to advanced courses for Master students. Teaching will be mostly in French and thus a decent command of the French language is required.Applications have to be deposited on the web page of the French Ministry of Education (Ministre de l'Education Nationale, de l'Enseignementet de la Recherche, ”ANTARES“; http://www.education.gouv.fr/personnel/enseignant_superieur/enseignant_chercheur/antares.htm). The deadline for applications is March 30, 2007. Job interviews will be held in spring. IMPORTANT: Only preselected candidates that have already obtained their ”candidacy“ (in French: ”qualification“) as a lecturer can apply for this position. This preselection was held in 2006 (or earlier).For further information, contact Minus van Baalen (minus.van.baalen@ens.fr) or Oliver Kaltz (okaltz@snv.jussieu.fr).Websites: http://parasito-evolutive.snv.jussieu.fr/ and http://ecologie.snv.jussieu.fr/=0DOfficial job profile (n. 1239): http://www.upmc.fr/comspec/session1_2007_mc.html=0D

okaltz@snv.jussieu.fr okaltz@snv.jussieu.fr

## RoslinInst 3 ComputationalGenetics

ROSLIN INSTITUTE (Edinburgh)

Three posts in quantitative and computational genetics and statistical bioinformatics

The Roslin Institute has vacancies for three scientists to work within its numerical genetics group. Roslin Institute is a world renowned centre for research in animal bioscience, with expertise and resources in genetics/genomics, molecular biology and developmental biology. The Institute is located just south of Edinburgh, the beautiful historical and cultural capital of Scotland and there are strong transport links with the surrounding area.

These posts provide the appropriate candidates the opportunity to work within a well established and highly regarded group and interact with scientists at the cutting edge of vertebrate genomics.

Quantitative Geneticist (RI 8/07) A three-year post within the EC funded SABRE project (http://www.sabre-eu.eu/). Working with collaborators across the EU the appointee will work on developing methods for QTL and association mapping, on methods for mapping loci controlling gene expression (eQTL) and on the application of these methods for the analysis of data generated.

Computational Geneticist (RI 9/07) The major objective of this post is to provide input on experimental design, data analysis and interpretation. The main areas of technical expertise required are in quantitative, population and statistical genetics and genomics.

Statistical Bioinformatician (RI 10/07) Working with colleagues in Numerical Genetics at Roslin Institute, the major objective is to assist with use of bioinformatic tools and extraction and analysis of genomic data. The main areas of technical expertise required are in bioinformatics, genomic analysis and statistics.

Starting salaries will depend on qualifications and experience.

The positions are available immediately.

For further information see http://-www.ri.bbsrc.ac.uk/jobsStudentships/index.php

To apply please contact our Human Resource Team (0131 527 4481 or email: Roslin.HR@bbsrc.ac.uk). Please indicate the post(s) of interest to you.

Closing date 29 March 2007. The Roslin Institute is an Equal Opportunities Employer.

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Chris Haley Roslin Institute Roslin Midlothian EH25 9PS, UK Chris.Haley@bbsrc.ac.uk +44 131 5274432 +44 131 4400434

chris.haley@bbsrc.ac.uk

## TexasAMU QuantEvolEcol

Texas A&M University Department of Wildlife and Fisheries Sciences Faculty Position in Quantitative Ecology

The Department of Wildlife and Fisheries Sciences at Texas A&M University seeks an outstanding individual to join the faculty as an Assistant Professor in Quantitative Ecology. This position is a 12-month, tenure-track appointment. This new position is charged with building a successful teaching and research program focused on quantitative approaches to ecology, conservation, and management of wildlife and fishery resources. Appropriate areas of research specialization include investigation of population abundance/dynamics and species interactions, statistical and numerical modeling of ecological processes in space and time, and bioinformatics. Candidates must have a Ph.D. in an appropriate field and a record of research accomplishment as evidenced by authorship of peer-reviewed publications. A record reflecting acquisition of extramural research funding and experience in university-level teaching also is desirable. Additional information on this position, the department, Texas A&M University, and the Interdisciplinary Research Group in Ecology & Evolutionary Biology can be found at http://-www.wfsc.tamu.edu and http://eeb.tamu.edu . To apply: Submit an electronic CV, and statements of teaching and research interests, plus contact information for three references to: Dr. Daniel Roelke, Search Committee Chair, droelke@tamu.edu. Preference will be given to applications received by May 25, 2007. Applications received after this date are not guaranteed a review by the search committee. The position will remain open until a suitable candidate is identified. Texas A&M University is an Equal Opportunity Employer that seeks diversity in its workforce, student body, and program participation. Those requiring assistance in the application process should contact the search committee chair.

– Mariana Mateos, Ph.D. Assistant Professor Section in Ecology and Evolutionary Biology Department of Wildlife and Fisheries Sciences Texas A&M University 320B Heep Laboratory Building 2258 TAMUS College Station, TX 77843-2258 Phone: 979-847-9462 Fax 979-845-4096 Email: mmateos@tamu.edu http://wfsc.tamu.edu/mateoslab/ Mariana Mateos <mmateos@tamu.edu>

## 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 established 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. 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

Mark Achtman <achtman@mpiib-berlin.mpg.de>

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## UCollegeCork MarineMolecularBiodiversity

PROFESSOR OF MARINE MOLECULAR BIODIVERSITY

University College Cork seeks to appoint a Chair in the area of Marine Molecular Biodiversity. The individual appointed should have a proven track record in molecular biodiversity of marine eukaryotes and/or prokaryotes and would be expected to form and lead an active research group and co-ordinate a graduate programme in both areas. The research activity would form a link between the major advances in molecular biology, particularly in the area of genomics and many areas of systems biology, whole organism biology, ecology, biodiversity and systematics. The post will be located in the Environmental Research Institute within the College of Science, Engineering and Food Science.

For informal discussion contact:

Professor Alan Dobson, Tel.: +353 21 4901946 ; email: a.dobson@ucc.ie

Application details and further information at http://www.ucc.ie/en/hr/EmploymentOpportunities/

“Spillane, Charles” <C.Spillane@ucc.ie>

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## UFlorida Genetics SummerInstr

Dear Brian,

Please post the following:

The University of Florida Department of Zoology seeks an Instructor to teach an undergraduate level course in Genetics this summer (2007). The summer semester runs from 14 May to 10 August. Applicants please send a cover letter, CV, statement of teaching interest and the names and contact information for 2 references to Amy Dechow (Coordinator, Administrative Services, Department of Zoology) at adechow@zoo.ufl.edu. Salary is $12,000. Review of applications will begin immediately and continue until the position is filled.

–

Charles F. Baer Department of Zoology 223 Bartram Hall P. O. Box 118525 University of Florida Gainesville, FL 32611-8525 USA

Phone: 352-392-3550 Fax: 352-392-3704 Email: cbaer@zoo.ufl.edu web: http://www.zoo.ufl.edu/faculty/baer.html cbaer@zoo.ufl.edu cbaer@zoo.ufl.edu

## 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 associated 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/pellmyrlabfront.htm "The pure and simple truth is rarely pure and never simple."

gods9193@uidaho.edu gods9193@uidaho.edu

## UMiami VisitingGenomics

Visiting Assistant Professor in Genomics University of Miami at Coral Gables

The Biology Department is seeking a researcher who wishes to pursue genomic research, develop collaborations with young evolutionary and ecological faculty, and establish research and teaching credentials. The successful candidate is expected to have a Ph.D. and a strong research interest in genomics; a record of postdoctoral work is desirable. The position holds PI status for grant applications, and any grants awarded will be transferable when the researcher leaves. Teaching will comprise one undergraduate course each term (e.g., biostatistics in Fall and a specialty upper division course such as genomics in Spring) and one graduate course or seminar. This is a full-time twelve-month research professional position, renewable for three years. Salary is competitive and commensurate with qualifications. Submit application materials electronically. Include a cover letter, CV and descriptions of research interests and teaching philosophy, and have three letters of reference sent to GenomicSearch@bio.miami.edu. Review of applications will begin immediately and will continue until the position is filled.

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Dr Alex Wilson Assistant Professor Department of Biology University of Miami 1301 Memorial Drive Coral Gables, Florida 33146-0421 USA Phone: (305) 284 2003 Office: Cox Science Room 253 http://www.bio.miami.edu/acwilson/home.htm acwilson@bio.miami.edu acwilson@bio.miami.edu

## UNeuchatel Switzerland EvolBotany

The *University of Neuchâtel, Switzerland*, is seeking to hire:

*A Full professor (professeur ordinaire) of Evolutionary Botany*

*Description*: The Institute of Biology at the University of Neuchâtel has an important focus on research in Plant Biology and the successful candidate is expected to make a significant contribution to the field. A comparative approach to research topics such as plant domestication, reproductive biology and invasion is of particular interest. Collaboration with the National Center of Competence in Research "Plant Survival" is expected. In terms of teaching, we seek a highly motivated naturalist giving courses including field work in plant systematics and ecology at the bachelor level and courses reflecting own research focus in the Master in Plant Ecology and Physiology. * Duties*: Full chair (6 hours weekly teaching, management of a research program and conducting various administrative tasks). * Requirements*: The successful candidate holds a PhD in biology and has a strong record of internationally recognized research in evolutionary botany. Teaching in French will be expected at the Bachelor level. * Particularly desired qualities*: . Inclusion of field work in research and teaching . Good knowledge of indigenous plant taxonomy. * Starting date*: January 1st 2008 or to be convened*

Application*: visit _http://www.unine.ch/sciences <http://www.unine.ch/sciences> _under "emploi" for complete information. The University of Neuchâtel, Switzerland encourages female applicants*.

Information*: please contact Prof. Martine Rahier (++41 32 718 3137/2500; _martine.rahier@unine.ch_) * Applications deadline*: June 15, 2007. Send complete application including electronic copy to: Prof. Martine Rahier, Chaire de botanique évolutive, Institut de biologie, Rue Emile-Argand 11, CP158, 2009 Neuchâtel, Switzerland.

Dr. Lena Struwe Dept. of Ecology, Evolution, and Natural Resources/ Dept. of Plant Biology and Pathology Rutgers University 237 Foran Hall, 59 Dudley Road New Brunswick, NJ 08901-8551, USA phone: (732) 932-9711 ext. 235, fax: (732) 932-9441 e-mail: struwe@aesop.rutgers.edu home page: www.rci.rutgers.edu/ ˜ struwe GENTIAN RESEARCH NETWORK: http://gentian.rutgers.edu Director, CHRYSLER HERBARIUM: http://herbarium.rutgers.edu

Lena Struwe <struwe@AESOP.Rutgers.edu>

## 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 continuing 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 or to Associate Professor Rob Brooks (rob.brooks@unsw.edu.au)

An information package is available by clicking <mailto:HERE>HERE, or email senio-rads@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 rob.brooks@unsw.edu.au

## UPompeuFabra Barcelona 3 Bioinformatics

Universitat Pompeu Fabra (Barcelona) (National Bioinformatics Institute / National Genotyping Centre)

Three positions available in the areas of computational and statistical genomics /bioinformatics.

The new Population Genomics Node of the Spanish National Bioinformatics Institute (http://www.inab.org), in collaboration with the National Genotyping Centre (http://www.cegen.org), has vacancies for three people (one programmer, one statistician and one postdoctoral scientist). The Node is located at the Evolutionary Biology Unit of the Pompeu Fabra University (http://www.upf.edu) and is part of the Barcelona Biomedical Research Park (http://www.prbb.org), a renowned centre for Biomedical research that hosts, besides the University, other institutions such as the CRG (Centre for Genomic Regulation) and the CMRB (Barcelona's Centre for Regenerative Medicine). All these research centres share a thrilling and dynamic scientific atmosphere, driven by leading groups in fields such as bioinformatics, molecular biology and evolution. The PRBB is located close to Barcelona's City Centre (right in front of the beach).

These posts provide the appropriate candidates the opportunity to work within a well established group and interact with scientists at the cutting edge of genome bioinformatics.

- Programmer: The person in this post will become part of our team of developpers, mostly in charge of programming applications for the management and analysis of SNP data. Experience in PHP, Java, APACHE and Linux systems are required. Working knowledge of database design and database-oriented programming (MySQL) is also desirable.

- Statistician: The major objectives of this post are to help in the selection of algorithms to be implemented in our applications, to take part in the application design process and to assist with the use of bioinformatic tools for the analysis of genomic data. A degree in Statistics or Mathematics, or comparable experience, is required. The main areas of technical expertise required are bioinformatics, genomic analysis and statistics.

- Postdoctoral Researcher: A two-year post within a funded "PROFIT" collaborative project aiming to the development of tools for analysis of Whole Genome Scan data and to their application in the study of complex traits (particularly diseases). The appointee will work on developing methods for large association studies and on the application of these methods for the analysis of data generated within the collaborative project.

Salaries will depend on qualifications and experience.

The positions are available immediately.

Motivated and potentially competitive applicants should send, preferably via e-mail, a short letter of interest a CV and the contact details of two references to:

Arcadi Navarro i Cuartiellas Unitat de Biologia Evolutiva Universitat Pompeu Fabra Parc de Recerca Biomèdica de Barcelona C/ Dr. Aiguader 88 08003 BARCELONA SPAIN E-mail: arcadi.navarro@upf.edu

– CHANGE OF ADDRESS!!!

Arcadi Navarro i Cuartiellas ICREA Research Professor Unitat de Biologia Evolutiva Departament de Ciències Experimentals i de la Salut Universitat Pompeu Fabra Parc de Recerca Biomèdica de Barcelona Plaça Charles Darwin, 1 08003 Barcelona

Phone 00 34 93 3160844 FAX 00 34 93 3160901

arcadi.navarro@upf.edu

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## URochester UndergradSummer EndosymbiontEvol

Undergraduate Summer Research Fellowships

Summer Research Training Fellowships are available to study molecular ecology of endosymbiotic bacteria in insects at the University of Rochester. The fellowships will include travel expenses, a stipend, and housing for 6-8 weeks. The summer research training program will span June to August (dates are flexible). Interest in one of the following areas; entomology, microbiology, evolution or ecology is required and some experience in PCR is desirable. During the fellowship you will learn the methods involved in identification of insect hosts screening, molecular typing of endosymbiotic bacteria (genus Wolbachia), and analysis of data relating to variation, global distribution and host associations of these endosymbionts.

For more information and to download a copy of the application visit the following website: http://troi.cc.rochester.edu/~wolb/FIBR/education.html mclark11@mail.rochester.edu

## USheffield FieldAssist AvianPopGenet

JOB ADVERT:

Field assistants are required to assist in researching cooperative breeding and migration in the long-tailed tit. The field site is in Estonia, based at an amazing field centre complete with mod-cons and the occasional passing elk! Assistants should have a background or firm interest in zoology, and would suit someone that is looking to progress to doing a PhD or further study of some kind. The field work is tough, challenging, but ultimately rewarding, and if you are into this kind of thing, you will find it fun! Fieldwork will include nest searching, reading colour rings on a very small bird, some mist-netting and navigating yourself through varying terrain! Field conditions vary from sub-zero to very hot during the season, and you should expect to contend with ticks, mosquitoes, the odd brown bear and wet feet! You should be of average fitness and prepared to walk for long distances to find the birds. An enthusiastic approach coupled with keen eyes and ears are essential, as with these, the necessary skills can be taught. Experience in this kind of work is a definite advantage, but all applications will be considered. Fieldwork runs from the 7th April for 6-8weeks, and you should be available at least for the first month. Accommodation is provided and there is some scope for subsidy of food/travel, which we will discuss with the applicant. Applications are invited immediately, and you should send your CV along with a covering letter, and details of 2 referees (if possible, one of whom can comment on your skills during fieldwork) to BETH WOODWARD at b.woodward@sheffield.ac.uk . Review of applications will begin immediately, and continue until the position(s) are filled.

B K Woodward <B.Woodward@sheffield.ac.uk>

## UZurich EvolutionaryEcol

University of Zurich, Institute of Zoology Our Ecology Group invites applications for a

RESEARCH POSITION IN EVOLUTIONARY ECOLOGY

Applicants must possess a Ph.D. plus some postdoctoral experience and should have a good publication record in evolutionary ecology, population or community ecology, conservation biology, population genetics, behavioral ecology or related fields.

Detailed information on the Institute of Zoology is available under www.zool.unizh.ch

The Ecology Group and its research projects are described under www.zool.unizh.ch/Research/-Ecology.html

The successful candidate is expected to participate in ongoing research and teaching programs, establish his/her own programs and attract external funding.

The position is available from September 2007 to January 2011. If you are interested, please send me your application with curriculum vitae, list of publications, summary of research goals and three letters of reference by 15 April 2007. Sorry, we don not accept applications via e-mail.

Prof. Dr. Heinz-Ulrich Reyer, Institute of Zoology, University of Zuerich, Winterthurerstrasse 190, CH-8057 Zuerich, Switzerland Tel.: +41-(0)44-635 49 80, Fax: +41 (0)44 635 68 21 e-mail: ulireyer@zool.unizh.ch

Uli Reyer <ulireyer@zool.unizh.ch>

## WoodsHole ResTech Endosym

Reseach Technician Position Functional and evolutionary genomics of bacterial endosymbionts MBL, Woods Hole, Mass.

Bacterial endosymbionts have played major roles in the diversification of numerous insect lineages. Using both molecular and computational approaches, we are exploring genome evolution and potential functions of these bacterial partners (http://jbpc.mbl.edu/labs-wernegreen.html).

We seek a highly motivated research assistant to contribute to our projects exploring the functional genomics and population dynamics of endosymbionts across different castes and species of ants, and to assist with evolutionary studies of gene content and DNA sequence variation in host-associated bacteria.

Details of the position, including experience required and application instructions, are described on the following website:

http://www.mbl.edu/hr/job_search.php?func=detail&par=job_id=557

Please contact Jennifer Wernegreen (jwernegreen@mbl.edu) with any questions.

Jennifer Wernegreen Josephine Bay Paul Center for Comparative Molecular Biology and Evolution Marine Biological Lab 7 MBL Street Woods Hole, MA 02543 ph: 508/289-7257 (office and voicemail) email: jwernegreen@mbl.edu

Jennifer Wernegreen <jwernegreen@mbl.edu>

# Other

## 18srRNA alignment answers

Dear All, Below are the replies I received on the questions regarding DCSE and 18S rRNA alignments. Firstly, I was stuck by the amount of replies both those containing suggestions and those who simply said that they were in the same situation. Thank you all!

My feeling about it is that all those zoologists/botanists ( i.e. not biochemists or computer programmers) who are working with phylogenetic studies and use rRNA as their target gene need to get together and work out one system to which all those multiple utilities packages and scripts could be adjusted - otherwise they are all lost in translation. Perhaps this will be my next project. Meanwhile I have tried to compile some main answers I had received from you in the order I asked the questions.

Please feel free to contact me if you need any additional information.

1) does anyone know if this software is still in use and if yes where I can get it? DCSE has probably migrated to van der Peer's new location in Belgium, the Antwerp lab having closed and its members dispersed. One person send me a ink to download DCSE from China. http://www.cbi.pku.edu.cn/ftp/ftp-a-d.html Many of you suggested that DCSE should not be used for various reasons such as compatibility of data format, inability to run it ( well I am not surprised - it seems to have been written in the days of Sun Microsystems rule), and general dislike of the package. I have downloaded it and could not install it on BSD or Fedora.

2) if there is an alternative package which can read/edit of assist in alignment of rRNA with secondary structure (i.e. what do YOU use?)

Here the list of packages people suggested to use. Please note that none of the packages can actually align the sequences for you ( apart from ARB see: http://www.arb-home.de/) I have tried ARB (for quite a long time before - it is an excellent and very complex package designed originally for 16S rRNA) but I have some problems making it work with my sequences. See Dave Kysela's excellent tutorial on ARB: http://www.mm.helsinki.fi/users/-GJURGENS/Arb/ARB_tutorial.htm If you want to go ahead with ARB - it may be difficult to install on MAC OS X as the manual on the web site is outdated - contact me, I have done it a few times by now. Also LINUX installation is a bit scary as ARB looks for old libraries which you need to link manually - again contact me if you are stuck.

Other packages( these just let you edit RNA in a nice way): You can access the application at the following address: http://-4sale.bioapps.biozentrum.uni-wuerzburg.de/ jRNA pages http://hymenoptera.tamu.edu/rna Some Perl scripts for conversion http://bioinformatics.org/-paradise/ SARSE (http://sarse.kvl.dk/). PHASE (has some scripts and links) www.bioinf.manchester.ac.uk/-resources/phase/ Max Telford has some scrips: Xstem Ystem to extract data from DCSE RNA database depository online. The scripts are availiabl;e from the author only see his paper: Telford, M. J., M. J. Wise, et al. (2005). "Consideration of RNA secondary structure significantly improves likelihood-based estimates of phylogeny: Examples from the bilateria." Molecular Biology And Evolution 22(4): 1129-1136.

3) if any of you came across any good "practical" guide on how to do the secondary structural alignment for 18S rRNA, whether it is "by hand" or computer software assisted. This is easy to answer there is only one guide, which I found rather useful to start with: http:/-/hymenoptera.tamu.edu/rna/methods.php The above seem to be the amalgamation of all answers I got I am sorry if I forgot anyone.

Consequently, I ended up trying to make ARB work and also doing in parallel a manual alignment based on the published structure. It is very time consuming, but after a few days of staring at 4 colored nucleotides on the screen the world seems so multicoloured I am almost enjoying it. :-)))

Anton Tsyganov mailto:atsyganov@gmail.com mailto:bsatsyganov@swansea.ac.uk

atsyganov@gmail.com

## AFLPOP simulations vs reallocation

Dear All,

I am working on population structure in the red abalone using AFLPs and am using the program AFLPOP (Duschesne and Bernatchez (2002) in Mol Ecol Notes) to reassign individuals to their appropriate source populations.

I have been using the "Simulation: many iterations" option to set the upper bound for the minimum-log likelihood difference that I go on to use in the "Reallocation (source populations)" option. However, I am getting major differences in assignment success between the simulations and reallocations with the same minimum log-likelihood setting (e.g. 80-90% assignment in simulations vs. 50% in reallocations). I even get this difference when I use the example data set in the AFLPOP program package.

Has anyone else had this problem, or is there something that I am missing when setting up the program to run? What type of errors in allele frequency calculations between the two options might account for this?

Any suggestions would be much appreciated!

Best regards, Kristen – Kristen Gruenthal Marine Biology Research Division Scripps Institution of Oceanography University of California, San Diego 9500 Gilman Drive La Jolla, CA 92093-0208

Phone: 858-534-7827 Email: kgruenth@ucsd.edu

## APE web pages

I am pleased to announce the launch of ape's web pages:

http://pbil.univ-lyon1.fr/R/ape/ (if you don't know what is ape, just click on the link above)

You will find general information, screenshots, FAQs, tips for installation, some plans on current developments, some literature pointers, and additional documents. All these will be regularly updated.

There is also a page, in the Literature section, on the book "Analysis of Phylogenetics and Evolution with R" with errata, updates, solutions to exercices, and supplementary materials.

Many thanks to the PBIL at the University of Lyon 1 for hosting these pages.

Emmanuel Paradis – Institut de Recherche pour le Développement UR175 CAVIAR GAMET - BP 5095 361 rue Jean François Breton F-34196 Montpellier cédex 5 France phone: +33 (0)4 67 16 64 47 fax: +33 (0)4 67 16 64 40 mailto: Emmanuel.Paradis@mpl.ird.fr

Emmanuel.Paradis@mpl.ird.fr Emmanuel.Paradis@mpl.ird.fr

## Adansonia digitata samples

Dear EvolDir members. I'm presently doing a Ph.D. study on the African Baobab and amongst other things I'm looking at the phylogeography of the species, but I have an incomplete set of samples.

Does any of you hold samples - preferably with exact geographical data - that you are willing to share. I've got samples to "trade". Seeds are preferred.

Regards

Andersansl@life.ku.dk

anderslarsen333@hotmail.com

## Adansonia digitata samples error

Dear members

There was an error in my e-mail address in the request for samples of Adansonia digitata material. The correct address is ansl@life.ku.dk

Anders

Anders S. Larsen Mimersgade 118, 5.tv. 2200 Copenhagen N Phone no. +4535854345 Mobile no. +4561334345

anderslarsen333@hotmail.com

## Ailanthus samples

Dear all,

I am currently studying Ailanthus altissima (Mill.)SWINGLE as invasive and I would like to compare genetic characteristics of invasive populations with native ones. I have many populations from Europe, I would be very interested in getting samples from Hawaii, USA, Canada, Southern Africa, Australia, New Zeeland, and of course from the native area, China.

I am using microsatellite allele frequencies, so I need at last 10 specimens for each population. Freshly collected materiel would be great and only small amounts of sample are needed (few leaves should be perfect). I can also cover all postage costs. If you can help me or know of someone who might be able to, please contact me via email at eric.motard@univ-paris-diderot.fr.

By advance, thank you very much, Eric MOTARD PhD student Laboratoire de Physiologie de lArbre Université Paris7 Denis Diderot Case courrier 7079 2, Place Jussieu 75005 PARIS FRANCE

"eric.motard" <eric.motard@paris7.jussieu.fr>

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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 – 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 Debapriyo Chakraborty <debapriyo@ncbs.res.in>

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## AmerGenetAssoc FundingSpecialEvents

SPECIAL EVENT AWARDS FROM THE AMERICAN GENETIC ASSOCIATION

The Council of the American Genetic Association invites applications from members of the Association for support of special events that further the purposes of the Association. The Association expects to make one or two awards of approximately $10,000-15,000. Eligible events include specialized workshops open to Association members in areas of great current interest and short courses in organismal genetics, but any event that would advance the purpose of the Association is eligible for support. We encourage members to think creatively about the types of events they could offer with support from the Association and to propose topic areas that have not been previously covered.

An application for a Special Event Award should include the following items of information: 1. The name(s) and title(s) of the individual(s) who will be responsible for organizing the event and overseeing the expenditure of any funds awarded. 2. The institution to which an award should be made, including the complete address of the relevant institutional department and the signature of an authorized institutional representative indicating the institution's willingness to administer the award if granted. 3. The title of the event for which an award is requested. 4. A rationale for the event explaining (a) why the event is timely or needed, (b) how the planned event will address the perceived need, and (c) how support from the American Genetic Association will improve the event, e.g., by making it possible or by making it more affordable for graduate students and post-doctoral research associates. The rationale need not be longer than 1 page. 5. A description of the event including: a list of primary participants (e.g., workshop leaders, course instructors, keynote speakers), dates and location of the event, a preliminary schedule for the event, and a plan for how participants will be selected (if participation is limited). The description need not be longer than 2 pages. 6. A budget for the event showing how funds provided by an award from the Society would be used to support event activities. If funds are also being sought from other sources, the budget should show both how funds from the Association will be used and how funds from other sources will be used. (The sources of other funds need not be identified, but the application should indicate whether the funds are in hand.)

Applications for a Special Event Award should be sent electronically as Word or pdf attachments to the Association office (agajoh@ncifcrf.gov). The Council will review all applications received before May 15, 2007 and will decide on an award at its annual meeting in July 2007.

Questions about the award can be sent to me, ashley@uic.edu .

– Mary V. Ashley Professor Department of Biological Sciences University of Illinois at Chicago 845 W. Taylor St., M/C 066 Chicago, IL 60607

Phone: (312) 413-9700 FAX: (312) 996-9462 E-mail: ashley@uic.edu

http://www.leap.uic.edu http://www.uic.edu/depts/-malab/ ashley@uic.edu ashley@uic.edu

## Ant olfactory learning

Electrifiable grids

Hello, I'm interested in olfactory learning in ants and I want to do an experiment in which I use electric shocks as a form of conditioning. I have tried for several weeks to obtain the electrical circuit material that is often used in learning experiments in Drosophila (a.k.a. print plates). Unfortunately, the only company I've found that can produce the electrical plates charges $900 US, which is over my budget. Does anyone have electrifiable grids that I can borrow? I am willing to pay for any shipment costs. Also, any help or advice would be greatly appreciated.

Thanks for your time.

Ellen

– Dr. Ellen van Wilgenburg Ecology & Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 USA

Tel.: +1 949 824 2615 email: evanwilg@uci.edu

Ellen van Wilgenburg <evanwilg@uci.edu>

## 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@bgnet.bgsu.edu

rwoodru@bgsu.edu

## BAC cloning kit

Dear all,

Has anyone used a BAC cloning kit? Can anyone indicate a good one and preferably cheap?

Thank you!

Sara Carvalho Instituto Gulbenkian de Ciência Portugal saracarvalho@igc.gulbenkian.pt

Sara Carvalho <saranlcarvalho@gmail.com>

## Bird parasite DNA

Hi,

I am looking for Haemoproteus, Leucocytozoon and avian malaria parasite DNA to use as positive control for PCR.

Thank you,

Ghislaine

Ghislaine Mayer, Ph.D. Assistant Professor Department of Biology Virginia Commonwealth University

1000 W. Cary St. Office: room 345 Room 126 Richmond, VA 23284-2012 Ph: 804-828-0828 Fax: 804-828-0503

gmayer@vcu.edu

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## CT SNPs

SNPs

It is known that two thirds of SNPs are C>>T, that is Cytosine substituted by Thymine.

Assuming that this is an average number (that is, taken from the entire genotyped population), Would any body know to what degree variation exists between individuals?

For example, how frequent is an individual half (rather than two thirds) of whose SNPs are C>>T?

In addition, does anybody know of variability in the nature of SNPs (such as C>>T), between loci on chromosomes or between loci in genes?

Thanks in advance,

Yair Itay

moranuri@gmail.com

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## ChristchurchNZ SSESSB UndergraduateDiversity

For the fifth consecutive year, the Undergraduate Diversity at SSE/SSB program, funded by a the Undergraduate Mentoring in Environmental Biology (UMEB) program at NSF, will take place again at the 2007 meeting of the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB) this June in Christchurch, NZ. However, because this is a bridge year for funding of this program, it will be scaled down considerably. This year the program will defray the costs of travel and lodging for 3 minority undergraduates from the US and Puerto Rico to attend the SSE/SSB meetings up to $1300. Arrangements will be made for registration costs of the meeting to be covered as well. Students are expected to give a poster on their research at the meetings. The mentoring component of the program will be less formal than in previous years. The students are expected to meet and share a meal with Scott Edwards, who will be attending the program. It is also hoped that the students can on an informal basis be put in touch with specific graduate student, postdoc and faculty attendees who will be attending the meeting, as well as a special session to interact with undergraduates from New Zealand. Pending renewal of funding, we expect the program to resume its normal quota of 15-20 students in 2008.

The application deadline is April 10, 2007. Applications will consist of a title, author line and abstract of the poster to be presented by the undergraduate; a one page statement of academic interests and career goals and of how attending the Evolution meetings will help meet these goals; and one letter of recommendation from the undergraduate's research advisor. The letter should indicate how inclusion of the student will increase diversity of the group participants and whether or not the student plans to attend graduate school or medical school. All materials should be submitted as pdf files and emailed to Scott Edwards, edwardsadmin@oeb.harvard.edu. Applications will be accepted only from students registered or very recently graduated from U.S. institutions, including Puerto Rico (i.e., no later than having finished classes during the winter or spring semesters before the meeting) and traveling to the meeting from within the US. Students demonstrating a need for funds to attend SSE/SSB will be given preference, and will be selected so that as a group, they will maximize cultural diversity among undergraduates at the meetings. See the following URL for further details on this program:

http://www.oeb.harvard.edu/faculty/edwards/-community/application.html

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## Concentrated DNA Extractions

Dear All,

I have a question about the best way to get more concentrated DNA extractions by evaporation (or any other way). How do most of you people normally do it knowing that I can only use standard lab material?

Best regards,

Philippe Helsen.

Philippe Helsen University of Antwerp - Campus Groenenborger Dept. of Biology - Evolutionary Biology

Group Groenenborgerlaan 171 B-2020 Antwerp Belgium

philippe.helsen@ua.ac.be phone: xx-32-3-265.34.70 fax: xx-32-3-265.34.74

philippe.helsen@ua.ac.be

## Data for MarginalPop Metaanalysis

Steve Lougheed and I are reviewing studies on plants and animals that have investigated geographic variation in population genetic diversity and structure, particularly studies comparing the genetic structure of geographically central versus peripheral populations.

If you have done such a study, we are very interested in including your data in our meta-analysis. So, we'd love to receive, at the email address below, PDFs of your published papers or unpublished manuscripts or data.

The data set we compile will be made available to all when we publish our review.

Thank you

Chris Eckert Department of Biology Queen's University Kingston, Ontario K7L 3N6 Canada eckertc@biology.queensu.ca

eckertc@biology.queensu.ca eckertc@biology.queensu.ca

## Drosophila virilis samples

Dear Colleaques,

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. lacicola, 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 JyvÃ¤skylÃ Finland

tel +358 14 260 4247 mobile +358 40 7717398 e-mail mkankare@bytl.jyu.fi

mkankare@bytl.jyu.fi

## Excursions around the Evolution meeting

Dear EvolDir members,

Two years ago, when the Evolution meeting was in Alaska, I posted here a proposal for post-conference travel, looking for buddies, which resulted in a really good boat trip on Nenana River and a great hike in Denali with some truly fine people. This year the Evolution meeting is in New Zealand and I am going to do this again. Moreover, since I am, as are some other Evolution 07 participants, staying in New Zealand for another meeting a week later (namely, ISEPEP2, http://www.otago.ac.nz/isepep2), I have both pre- and post-conference plans, for which I would like to find co-travelers.

Pre-conference Cook Islands stopover. Air New Zealand allows inexpensive stopovers en route to and from NZ if you book on-line (http://www.airnewzealand.com/airfares_offers/web_specials_flights/flights/default.htm). Cook Islands (http://www.southpacific.org/text/finding_cooks.html ; http://cookislands.bishopmuseum.org <http://cookislands.bishopmuseum.org) are among the best (and the least visited) coral reef diving/snorkeling places in the South Pacific (or world). I have a preliminary agreement with a colleague who can introduce us to an excellent local naturalist/diver/wild life enthusiast, who can guide us to the most interesting places and show us the best of land and sea biodiversity. There is an AirNewZealand flight to Rarotonga (RAR) from LA on June 10th, allowing a 5-day stop-over. I have just booked my ticket and the cost (from LAX to CHC roundtrip) is US$ 1,155 + 241 tax = 1,396, which is better than many non-stopover fares currently available. Most passport holders do not need a visa to enter Cook Islands (even Russians), if they have an outbound ticket. Please e-mail me if you'd like to join me for this trip. We can discuss accommodation and natural history options.

Post-conference hiking. These plans are a lot less defined, but I need to spend 8 days between Evolution and ISEPEP meetings somewhere on South Island and something is telling me that one can do it in many very exciting ways. Please e-mail me with your hiking/skiing/boating suggestions.

– 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

“Yampolsky, Lev” <YAMPOLSK@mail.etsu.edu>

## 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>

## Gel sticking problem

Dear collegue

I am a researcher tha work the AFLP technique, But I have a problem now , and it is related top the gel, the gel sticks to both plate, I tried several times with other materials for example, I changed the bind and repel silane, The 6% Acrylamide solution , TBE buffer and treated both glasses with 10%NaOH, but I didnt success. Would you please recommend, how can I solve its difficulty. Thank you so much.

Best regards Mahtab Yarmohammadi

mahtab yarmohammadi <mahtab_yarmohammadi@yahoo.com>

## GeneticDistance with indels

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.

Maria Cristina Mosco Postdoctoral Researcher University of Rome ”La Sapienza” Department of Genetics and Molecular Biology Via dei Sardi, 70 00185 Rome, Italy Phone +39 06 4991 7807 - FAX +39 06 44 41 591 e-mail: cristina.mosco@uniroma1.it

cristina.mosco@uniroma1.it
cristina.mosco@uniroma1.it

## 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. Qeusto muovo 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 risulati diversi. Ciao Federica Costantini

Federica Costantini,PhD

Laboratorio di Ecologia sperimentale

Centro Interdipartimentale di Ricerca per le Scienze Ambientali in Ravenna

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skype username: fedealpha

Pagina WWW:

<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

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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> 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.

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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 missing 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

## Gotland FieldAssistVolunteer

Volunteer field assistant position for a project on dispersal in a fragmented population of birds (Gotland, Sweden, May-June 2007)

Dispersal between breeding sites is a major life-history trait that affects multiple evolutionary processes in natural populations, but its determinism is still poorly known in many cases. We have been conducting for several years a series of experiments aimed at understanding the factors influencing dispersal behaviour in a fragmented population of hole-nesting passerine birds (collared flycatchers Ficedula albicollis, great tits Parus major). Our experiments investigate (i) the role of maternal effects and in particular egg components, (ii) the relative influence of early and late factors during the development of young, and (iii) the role of external information on habitat quality, on natal and breeding dispersal behaviour. These experiments are conducted in collaboration with researchers from Universities of Lyon I (France), Uppsala (Sweden), Oulu (Finland), and New South Wales (Australia). We are currently looking for volunteer field assistants to take part in field work during spring 2007 on the Swedish island of Gotland. The duties of these field assistants will include (i) participating in catching, ringing and measuring breeding adults of these two species before laying, during incubation, and during the nestling feeding period, and (ii) participating to the training of the students of the team in ringing and measuring nestlings, and to the management of the everyday team work (minimum 8 h of work per day, and up to 12-13 h during the peak period of catching). Therefore, we are looking for volunteers strongly experienced in adult passerine bird catching, handling, ringing and (if possible) measuring.

Conditions: Availability: the assistant has to be available from the beginning of May until the beginning of July (i.e. for a minimum of 8-9 weeks). Driving license: the study sites are located up to 15 km of distance from each other, thus travel between sites are by car and by bike. Local transport means will be provided. Expenses coverage: accommodation on the island of Gotland will be paid. An indemnity of about 1 000 per month will be provided, plus around 400 for the travel to Gotland.

If interested by this announcement, or for more information, please contact me so that we can discuss it; please also send me a CV detailing your experience in ringing and handling passerine birds:

Blandine Doligez Department of Biometry and Evolutionary Biology (CNRS UMR 5558) University Claude Bernard (Lyon I) - Bâtiment Gregor Mendel 43, boulevard du 11 novembre 1918 F - 69622 Villeurbanne Cedex

Tel.: +33 4 76 37 38 01 or +33 4 72 43 14 04 - Fax: +33 4 72 43 13 88 E-mail: doligez@biomserv.univ-lyon1.fr

doligez@biomserv.univ-lyon1.fr
doligez@biomserv.univ-lyon1.fr

## Humingbird blood samples

I have small quantities of blood from 23 species of hummingbirds from the eastern slope of the equatorial Andes (1300-3500 m), stored unrefrigerated in 95% Ethanol. Before I freeze-dry them for isotopic analysis, I can take out a bit if someone needs it. I study altitudinal migration, so I toyed with the idea of trying to look at population structure in sedentary vs migratory birds. If someone needs this for an existing study or wants to chat about collaborating on that or other ideas, write

jessica.hardesty@duke.edu

Cheers!

Jessica Hardesty PhD Candidate University Program in Ecology Duke University

arielle cooley <acooley@gmail.com>

## Inconsistant micros answers

Several people expressed an interest in hearing the responses I got to my microsatellite question. My original question asked for help with the following two problems with microsatellites I had developed for frogs:

(1) the microsats don't amplify consistently (i.e. one sample may give nothing for one PCR but work beautifully the next time under the same conditions), and (2) my results are largely not reproducible among PCRs (i.e. I get different peak sizes in successive PCRs of the same individual a large percentage of the time). These problems happen for all 8 of the microsats I developed.

Here are the answers I got:

- You sometimes have drop out of alleles (especially the longer ones) and also some loci that differed by one allele between runs due to A-overhangs. You can prevent by adding a 30 min step at around 60 degrees to the PCR, but I'm not sure about the allele drop out.

- Amphibian microstatellies are just difficult. Some have had luck chelexing their already extracted DNAs.

- Check your primer sequences again and try to redesign primers. As well try to standardize your PCR with lower annealing temperatures. - inconsistant amplification is mostly a handling and/or contamination problem. Are you sure your conditions are always REALLY the same? Do you vortex/centrifuge all eppis after thawing? Could it be that you use different batches of water/buffer/plasticware? Try to use fresh batches, re-dilute your primers from stock.

- different peak sizes: may occur due to in vitro slippage events (in fact, during your PCR the same effect happens that leads to polymorphism in nature: loops form during strand synthesis). This can be circumvented by optimization of PCR chemistry (try different Mg and dNTPs concentrations), choice of enzyme (try at least 2-3 different brands to see which one works best with your template), not too many cycles (maximum 32, less are better; not more than needed for a clear signal on the capillary), and a long final extension at 68 (15 min).

- With degraded DNA the low template number causes some alleles to be amplified over others, almost randomly.

- I know of others who have had problems similar to yours on the ABI 3130 capillary machine. Many of the problems went away once formamide was used in the prep of the samples for loading into the sequencer.

- Have you tried running the diagnostic tests on your PCR machine? If it's not heating to the same temperature consistently that could explain your problem. Likewise, if you use different PCR machines you could see a similar effect.

Corinne L. Richards email: clrichar@umich.edu Ph.D. Student University of Michigan Museum of Zoology Division of Reptiles and Amphibians & Department of Ecology and Evolutionary Biology

clrichar@umich.edu clrichar@umich.edu

## Inconsistent microsats

Dear EvolDir members,

I have a question for any of you who have used or developed microsatellites. I recently developed a set of microsatellite primers and upon genotyping, found two disturbing problems: (1) the microsats don't amplify consistently (i.e. one sample may give nothing for one PCR but work beautifully the next time under the same conditions), and (2) my results are largely not reproducible among PCRs (i.e. I get different peak sizes in successive PCRs of the same individual a large percentage of the time). These problems happen for all 8 of the microsats I developed.

I have tried re-extracting DNAs (which appear fine on a gel) so that they are fresh as well as varying the amount of DNA used in the reactions.

Do you have any suggestions as to what might be going wrong?

Thanks, Corinne Richards

Corinne L. Richards email: clrichar@umich.edu Ph.D. Student University of Michigan Museum of Zoology Division of Reptiles and Amphibians & Department of Ecology and Evolutionary Biology

clrichar@umich.edu clrichar@umich.edu

## Journal EvolBioinformatics

Dear colleagues

The publishers of Evolutionary Bioinformatics* have recently replaced their website management platform and as a result, they now offer automated subscription and unsubscription to the journal's emailing list. This requires you to set up an account on their website.

You can set up an account by going to their home page (http://www.la-press.com) where you will find a link to the main pages of Evolutionary Bioinformatics.

Allen Rodrigo Associate Editor Evolutionary Bioinformatics

*Evolutionary Bioinformatics is the official journal of the Bioinformatics Institute (New Zealand), and is committed to the open-access delivery of publications on computational evolutionary biology and evolutionary bioinformatics.

a.rodrigo@auckland.ac.nz a.rodrigo@auckland.ac.nz

## K12 proposals

Dear Evolution Colleagues,

The National Math and Science Initiative (NMSI) and the UTeach Institute at the University of Texas at Austin are soliciting proposals from qualified universities throughout the United States to participate in a dramatic initiative to increase the quality and quantity of K-12 mathematics, science, and computer science teachers. NMSI, in conjunction with the UTeach Institute, seeks proposals through a competitive Request for Proposal process from non-profit institutions of higher education located throughout the country to implement teacher preparation programs based on the very successful UTeach program. In its ten years, UTeach has graduated more than 1000 undergraduates with a B.A. degree in a natural science and teaching credentials, 86% of whom have gone on to teach K-12 science. NMSI and the UTeach Institute encourage institutions of higher education interested in participating in this initiative to submit a preliminary proposal describing the setting at the institution of higher education and the environment in which the UTeach program will be implemented. NMSI and the UTeach Institute will identify candidates who have the necessary resources to successfully implement the program and invite them to both attend a proposal preparation conference and to submit a full proposal. Full proposals will be submitted through and endorsed by the Governor's office of the institution's home state. Finalists will be interviewed before grant awards are made. Each stage of this process is described in detail in the Request for Proposal found at http://www.uteach-institute.org/go/institute/publications/request-for-proposal, including information theUTeach program.

While proposals must ultimately be submitted by a University president (with approval of the home state governor), we strongly encourage science faculty to take the lead in organizing these proposals. Given current challenges to evolution education around the United States, it would be particularly valuable to see strong involvement by evolutionary biologists in organizing and implementing these science-teacher training programs. Such programs are a substantial undertaking, but are also vital to improving early science and math education nationwide. I strongly encourage you to look at the Request for Proposals URL listed above and consider taking this opportunity to contribute to science teacher training.

Information on submitting proposals is available at http://www.uteach-institute.org/go/institute/publications/request-for-proposal . Sincerely,

Dan Bolnick

Dr. Daniel Bolnick Assistant Professor Section of Integrative Biology/UTeach Program University of Texas at Austin Austin TX 78712

office: (512) 471-2824 lab: (512) 471-1964 fax: (512) 471-3878

danbolnick@mail.utexas.edu

## Laminar Flow Hood

We are looking for a laminar flux hood for cell culture and wanted to get some advice.

Specifically, has anyone had experience with the NUAIRE PSM2? We can get it through BMS at a pretty good price, but we know very little about it (other than the technical specs). Any advice would be much appreciated.

Thanks,

Alexis

Station d'Ecologie Expérimentale du CNRS (USR 2936) Laboratoire Evolution et Diversité Biologique

09200 Moulis

France

Alexis Chaine <alexis.chaine@lsm.cnrs.fr>

## MHC CloningArtefacts

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 K1221from 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 misincorporated 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.

Many thanks in advance/

Erik Hagström email: hageri@kth.se

hageri@kth.se

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## MHC CloningArtefacts 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

My questions was:

Hello,

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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 proofreading 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 noiose"), 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 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 it 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

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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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## Meditest Incubator

We are currently looking for a constant temperature incubator (0C-40C) for cell culture (actually, protist culture - so constant temperature is quite important) and could use a bit of advice.

Has anyone heard of a Meditest incubator? We have found a good price on a Meditest 600, but know very little about its quality. As a point of comparison, we are also considering a Sanyo, which is a bit more expensive, but we know it provides excellent temperature stability.

Thanks!

Alexis

Alexis Chaine <alexis.chaine@lsm.cnrs.fr>

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## Megabace Fragment Analysis

Dear Evoldir members,

We perform fragment analysis (AFLP) on a 96 capillary Megabace and afterwards analyze the data with the software program Fragment profiler. We do find it difficult to transport information about the selected peaks to other programs due to the awkward export format of Fragment profiler.

1) Does anybody know how to export peak areas with Fragment profiler to an excel file in such a way that a columns represent the size of the fragments and rows the different samples in such away that sizes of the different samples are aligned ?

2) Are there software extensions written to Fragment profiler (prefereably freeware) that overcome these problems?

3) Are there alternative software programs (preferably freeware) to analyze fragment runs from Megabace platforms?

Thanks in advance,

Klaas Vrieling

k.vrieling@biology.leidenuniv.nl

## Micro identification answers

Dear Evoldir members,

I listed the answers addressed to my query about clonality and definition of Multilocus Genotypes (MLG). To give some precision about the context of my study, I work on the assessment of the structuration of genetic diversity in several populations of Potamogeton pectinatus, an aquatic macrophyte reproducing by both clonal and sexual reproduction. I analysed genetic diversity and clonality with the help of 9 nuclear microsatellites. Some MLGs are very distinct from each other (i.e. differing by two or more alleles) but some are not so distinct (only one difference). My question was to have your opinion about the best way to treat those MLG.

I am very grateful to each of you who spent time to answer to my question and I hope that the answer listed below could be useful for others!

stef

___________ Original message :

Dear EvolDir members,

I have a methodological question that deals with the assessment of clonal diversity with microsatellite loci. Could we consider that each observed multilocus genotype (MLG) mirrors reality? Or is it more realistic to consider two or more MLG differing by only one allele at a locus (out of several) as a unique MLG? For example, could one consider the two following MLG to be different or identical? :

(1) 0102 0202 0405 0405 0103 0203 0405 0405 (2) 0102 0202 0405 0405 0103 0202 0405 0405

Does someone know papers, methods or softwares that could help to take a decision by taking into account allelic frequencies or genotyping error rates?

thank you very much for any help and advices!

Stef

sfenart@vub.ac.be

———- ANSWERS:

Hi Stef,

I would consider those two examples of MLG different i.e. not identical. I do not know about software that would decide for you what is identical - I would say that such individuals must be the same on all loci, then they are likely to be a product of asexual (clonal) reproduction. For that you can just use excel file and function of finding identical individuals. However, identical can be also product of sexual reproduction (recombination) and to distinguish between those two - Software MLGsim (Stenberg et al. 2003, Molecular ecology notes, 3: 329-331) calculates probability that two and more identical (same on all loci) multilocus genotypes are the result of sexual reproduction and not asexual (clonal) reproduction. It works on microsatellite data, using allele frequencies and sample size. I'm uncertain, but I don't think it takes into account genotyping errors.

Hope this helps a bit. It's very interesting question, and I would be interested in the responses you get. Can you please summarize them and forward to me?

Good luck,

Monika

email: mzavodna@purdue.edu

_________ Hi Stef,

An addition to my previous email: I've heard from my colleage that Genalex software (Peakall and Smouse, 2006, Molecular Ecology notes, 6: 288-295) is also able to identify identical MLG (function 'matches' or so). You can probably check it out, I am uncertain about details.

Monika

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Calculating the probability of identity will help you determine whether you can answer this question. We did this for a wild rice species from texas in the attached article, using an Excel spreadsheet. You can always modify the PID formulas to add genotyping error, but testing whether the probability passes some kind of threshold is where it would get a bit complicated.

Best,

M. Antolin

Richards, C. M., M. F. Antolin, A. Reilley, J. Poole, and C. Walter. 2006. Capturing genetic diversity of wild populations for ex situ conservation: Texas wild rice (Zizania texana) as a model. Genet Resour Crop Evol Published online: 7 December 2006

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Dear Stef, interesting question about the genotypes & clones... sorry that I cannot help a lot, but would be interested in reading the answers that you get, please post them!

Just a thought: my hunch is that the inferences you make from your genotype data will largely depend on the method you use for genotyping, i.e. types of markers. Because, for instance microsatellites are well known for high mutation rates... so especially if your example of the two genotypes was based on microsats, these two would, in my view, clearly point towards not only common ancestry but actual possibility of grouping them together as a single "clonal lineage". Very often it is useful to group genotypes in such a way, simply because it provides more clarity in your dataset. e.g. if your two genotypes (1) 0102 0202 0405 0405 0103 0203 0405 0405 (2) 0102 0202 0405 0405 0103 0202 0405 0405

are compared with a third one:

(3) 0101 0303 0405 0505 0101 0101 0202 0303

the number 3 is clearly very distant from the first two...

hope this helps. good luck!

Ruza

– ~~~~~~~~ Ruza Bruvo Department of Animal and Plant Sciences The University of Sheffield Western Bank Sheffield S10 2TN

— / —

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

## Mismatch Distribution answers

Hi to everybody, In this opportunity, I let to know the answers that I received about the problem of interpretation mismatch distribution and raggedness index. The problem was:Results that the curve is unimodal but the signicance of raggedness index is not significant under the null hipothesis of neutral evolution. The analysis was performed in DNAsp with coalescent simulations considered no-recombination and observed theta values. The question is: The populations suffer or not an expansion? Almost responses coincide in that the first step is realizing a neutrality test (e.g., Fu 1997), if is this statistic is significant negative the next step is perform a mismatch distribution, to characterize the expansion. In addition, the program Arlequin 3.00 (Excoffier et al 2005) permits test the demographic and spatial models of expansion with bootstrap approach.

This message is also for Allegra Briggs and Arnaud Bataille (I hope that this responses are useful for you).

Thanks very much to everyone who replied, your answer were very useful.

Ahh!! I forgoted, excuse me for my poor english.

Best regards, Juan Jose Martinez Cat. Genetica de Poblaciones y Evolucion FCEF y N - UNC Cordoba, Argentina juan_jmart@yahoo.com.ar

> Si el test no es significativo no puedes rechazar la Ho (pob. estacionaria). Sin embargo los analisis basados en la mismatch distribution son poco potentes, (ver Ramos-Onsins y Rozas 2002) y sobre todo para regiones nucleares (con recombinacion), aunque creo que trabajas con regiones mitocondriales. Te aconsejaria que miraras el comportamiento de los estadisticos R2 (Ramos-Onsins y Rozas 2002) y el Fs de Fu (Fu 1997). Saludos, Julio Rozas

> Yes, mismatch distributions are difficult to interpret. I have never done the analysis in DnaSP but it is probably similar to Arlequin, which I use. It is ok to have significant fit to a unimodal curve but non- significant raggedness index because they are measuring slightly different things. Mismatch is describing pairwise differences between haplotypes but raggedness is the variation around the curve. An empirical mismatch distribution that does not deviate from a unimodal distribution of pairwise differences among haplotypes and has a smooth distribution (Harpending, 1994) suggests recent population expansion (Slatkin and Hudson, 1991; Rogers and Harpending, 1992). In other words, a mis-

match distribution, P > 0.05 means you cant reject the null hypothesis of population expansion. A non-significant raggedness index means you have a relatively good fit of your data to a model of population expansion. At any rate, this is how I understand it. You might find some helpful information at http://www.rannala.org/ gsf/, especially under Arlequin re. mismatch distributions. Also see Harpending, H. C. (1994). Signature of ancient population growth in a low-resolution mitochondrial DNA mismatch distribution. Human Biology, 66, 591-600. for discussion of raggedness index. Rogers, A. R., & Harpending, H. (1992). Population growth makes waves in the distribution of pairwise genetic differences. Molecular Biology and Evolution, 9(3), 552-69. Slatkin, M., & Hudson, R. R. (1991). Pairwise comparisons of mitochondrial DNA sequences in stable and exponentially growing populations. Genetics, 129, 555-62. for some discussion. Good luck, Kathryn

> Supongo que la razón or la que tus resultados no son significativos bajo la hipótesis de evolución neutral, es precisamente porque la población está se está expandiendo. En DNAsp puedes realizar diferentes tests de neutralidad. Si tu población se está expandiendo, tus resultados deben ser negativos y no significativos en el test D de Tajima (lo cual indica desviación de neutralidad debido a expansión, selección o "hitchhiking"), resulados negativos y no significativos de los tests D* y F* de Fu & Li (lo cual indicaría que no hay selección o hitchhiking) y resultados negativos y significativos del test Fs de Fu (lo que indicaría crecimiento poblacional). Has tratado de usar el programa ARLEQUIN? En el puedes hacer análisis de mismatch distribution y probar si tus datos se desvían de dos modelos diferentes: uno de expansión puramente demográfica y el segundo de expansión geográfica. Espero que esto sea de ayuda. Y perdón por mi español, estoy un poco fuera de práctica. Saludos... Rodrigo

> The test is evaluating a null hypothesis of a population expansion. The failure to reject the null hypothesis (the non-significant raggedness index) indicates that you don't have any support for a stable (non-expanding) population - which is thought to result in a highly multi-modal, and therefore ragged, signal. Failure to reject

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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

## NESCent Phyloinformatics

Phyloinformatics Summer of Code 2007

A collaborative Phyloinformatics Group, sponsored by the National Evolutionary Synthesis Center (NESCent: http://www.nescent.org/), is working to develop user-interfaces, improve software interoperability and support data exchange standards in evolutionary bioinformatics. The specific projects are diverse in nature and range from the development of AJAX components for web-based bioinformatics applications, managing workflows using approaches from functional and logic programming, and developing data exchange standards for phylogenetic substitution models.

The Phyloinformatics group will be sponsoring student collaborators through the Google Summer of Code program (http://code.google.com/ soc), which provides undergraduate, masters and PhD students with a unique opportunity (over three summer months) to obtain hands-on experience writing and extending open-source software under the mentorship of experienced developers from around the world. We are particularly targeting students interested in both evolutionary biology and software development. Students will have one or more dedicated mentors with expertise in phylogenetic methods and open- source software development. Our project proposals are flexible and can be adjusted in scope to match the skills of students with less programming proficiency. If the program sounds interesting to you but you are unsure whether you have the necessary skills, please email the mentors at phylosoc {at} nescent {dot} org. We will work with those who are genuinely interested to find a project that fits your interest and skills. Students will receive a stipend from Google and will be invited to participate in future collaborative events such as the NESCent Phyloinformatics Hackathons (http://www.nescent.org/wg/ phyloinformatics).

TO APPLY: Students must apply on-line at the Google Summer of Code website (http://code.google.com/soc). The application period for students is now open and ends on Saturday, March 24, 2007 (one week from now).

The Phyloinformatics Summer of Code project and ideas page is at the following URL: http://phyloinformatics.net/Phyloinformatics_Summer_of_Code_2007 The above page also contains links to the GSoC program rules, eligibility requirements, and stipend payment mechanism. We encourage all interested students to email any questions, or self-proposed project ideas, to phylosoc {at} nescent {dot} org. This will reach all prospective mentors.

Eligibility requirements for students: http://code.google.com/support/bin/answer.py?answer=60279&topic=10730

Stipend for students: http://code.google.com/support/bin/answer.py?answer=60322&topic=10731

Please disseminate this announcement to appropriate students at your institution.

Hilmar Lapp Assistant Director for Informatics NESCent

hlapp@duke.edu hlapp@duke.edu

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## Nulls and pop structure

Dear EvolDir,

Is there anything approaching a consensus on what can be done if we have data on a set of microsatellites and many loci have null alleles? Say you have spent lots of time & money developing and scoring a set of loci in your favourite species but most show deviations from HW consistent with nulls. You might be interested in patterns of differentiation (Fst, AMOVA) and detecting potential cryptic population structure (Structure/BAPs-style analyses).

I have looked at the literature and so far as I can tell the most common strategy is to use the standard techniques, acknowledge that nulls are a potential problem, and hope the reviewers are kind and understanding.

What's the alternative? Is there a review out there on which are the most robust analyses to use under these circumstances (I'd guess AMOVA and ?). Are there any that explicitly do not assume HW? Can you calculate conventional Fst and use bootstrapping to analyse patterns despite null alleles? There is clear inconsistency in the literature on this point.

I suspect this is a common problem and some idea of 'the best' approach to use would be very useful to many researchers?

Cheers, 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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## 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

## Old JEB issues

I am missing the hard copy of JEB for 2004. Blackwell's does not have those back issues. I would like to acquire those issues from anyone willing to part with them and am willing to pay a reasonable price plus shipping.

Best wishes,

Steve Stearns Department of Ecology and Evolutionary Biology Yale University

stephen.stearns@yale.edu

## PCRmultiplex software

Hi,

I am trying to develop primers for PCR multiplex in 8 species of Gadidae, do you know some software for this purpose? I am also interested in software to perform RFLP analysis on these same species. Do you know free software to do that ?

Thank you in advance for all your answers,

Regards,

– Véronique Verrez-Bagnis Ifremer Département Sciences & Techniques Alimentaires Marines Rue de l'Ile d'Yeu, B.P. 22105 44311 Nantes Cedex 3 - France

Tél. : +33 (0)2 40 37 40 81 Fax : +33 (0)2 40 37 40 71 E-mail : vverrez@ifremer.fr

Site Web Ifremer : htpp://www.ifremer.fr Site web FishTrace : htpp://www.fishtrace.org Veronique.Verrez@ifremer.fr Veronique.Verrez@ifremer.fr

## Plant genomic DNA extraction Kits

Dear colleagues,

I have always used Qiagen's Dneasy Kit to extract clean plant DNA for sequencing and genotyping. However, it has come recently to my attention that VWR is selling an EZNA kit that seems very similar for 1/4 of the price! Has anyone used the EZNA kit and could give me some feedback? Or has anyone tried other kits (besides qiagen) and had success with high throughput sequencing and genotyping applications? Thanks in advance for any help!

Dr. Paula X. Kover University of Manchester Faculty of Life Sciences Manchester, UK

"Paula X. Kover" <kover@manchester.ac.uk>

## Polyploid SSR answers

Thanks for the helpful suggestions on different programs that I have been playing around the last week. Here is a summary:

(1) STRUCTURE accepts polyploid SSR data with null allele treated as "-9" in my case. It gives you no. of estimated clusters and membership coefficient at both individual and population levels, which is useful to look at population structure (esp. in graphic presentation).

(2) SPADEGI accepts polyploid SSR data with null alleles treated as "0" only. It computes some basic statistics such as allele no. per locus, gene diversity (He), Fis, Fst at population level. At individual level, I use Rousset's distance to look at relatedness.

(3) TETRASTAT accepts tetraploid data with null alleles treated as "0". It computes He, H' (diversity) locus by locus, and Gst at population level, which is comparable with SPAGEDI.

(4) If you are interest in clustering at individual level, you may also consider converting genotypic data into binary. With this binary matrix, you can do NJ, PCA, and other diversity measures in many programs, which give you a lot more flexibility.

Up till now I still can't find one program that run exact test in polyploids. However, one suggestion is that if your tetraploid is of disomic inheritance (or under this assumption), you may try spliting each locus into two diallelic loci and run exact test in GENEPOP (I prefer the web-base version).Therotically, these two loci should be linked from your results and you can group them as one pair and compare their linkage with another pair. If you find contradiction within or between pairs, this approach might not work for your data or your allelic designation is not correct.

I will keep an eye on programs for exact tests particularly and pls let me know if you find one. Thanks!

Eugenia PhD candidate Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, Canada

eugenia.lo@utoronto.ca

## Polyploid SSR question

Hi, I have some microsatellite data from polyploids and I am interested to test recombination by doing Fisher's exact test and measure gene diversity & Fis within polyploid populations. Could anyone suggest me softwares feasible for this purpose in polyploids?

Thanks!

Eugenia PhD candidate Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, Canada

eugenia.lo@utoronto.ca eugenia.lo@utoronto.ca

## Silk DNA

Subject: DNA from silk

Hello,

We would be interested to hear from anyone who has successfully extracted DNA from spider silk (or any other kind of silk). Being able to do this would enable us to non-destructively study trapdoor spiders, which otherwise have to be dug out with a crowbar! Many thanks!

Oliver

Oliver Berry

Population Genetics Laboratory, School of Animal Biology (M092) The University of Western Australia Crawley, 6009 Western Australia

ofb@cyllene.uwa.edu.au

## SocSystBiol ErnstMayrAward

Ernst Mayr Award

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

Who is Eligible. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. To be considered, students should 1) submit their titles for the SSB Meeting in Christchurch, New Zealand (http://-www.evolution2007.com/), and indicate at the time of submission that their talk is a potential competitor for the SSB Ernst Mayr Award; 2) submit a 400-word abstract of their talk to the awards chair.

The paper may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenting the paper and the intention is that person will be senior author on the published version of the paper. Previous Mayr award winners are not eligible.

Judging. Based on the submitted abstracts, the Mayr Awards committee (appointed by the Awards Chair) will select a maximum of 15 applicants for inclusion in the Ernst Mayr session at the Christchurch meetings, which will be held at a single venue in a separate session.

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

Notification of Winner. The winner of the award will be announced at the SSB business meeting at Christchurch, during the banquet or awards ceremony at the annual meeting, and an announcement will be published in Systematic Biology.

Abstract submission. Abstracts should be submitted in the text of an e-mail; please include name and complete contact information. Applications should be sent to Dr. Kelly R. Zamudio, SSB Award Committee Chair, at krz2@cornell.edu E-mail submissions are required. Application deadline is 15 April 2007 (same deadline for title submissions for the conference).

Additional information can be found at: http://-systbio.org/?q=node/10 –

krz2@cornell.edu krz2@cornell.edu

## SocSystBiol MiniPEET

Mini-PEET awards to enhance transfer of taxonomic knowledge

SSB is pleased to announce the availability of awards to enhance the transfer of taxonomic expertise, modeled after the highly successful PEET program at NSF. Unlike the NSF PEET program, awards will not be limited to taxonomically understudied taxa; the primary purpose of this program is to pass on taxonomic expertise in general. The awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group. This would support the PEET goal of passing on taxonomic expertise before it is lost. Activities can include a trip to the taxonomists' laboratory, or pay for the taxonomist to visit the applicants' laboratory for a period of time. Requests for support may be in any amount up to $3,000.

A complete application includes: 1) a brief description of the project 2) justification of the importance of the taxon 3) an itemized budget 4) the applicant's CV 5) a letter of support from the taxonomic expert 6) a letter of recommendation (if the applicant is a student or post-doc)

The total application should be no more than two pages long, not including the curriculum vitae and letters of support.

Requests and inquiries should be sent to Dr. Kelly R. Zamudio, SSB Award Committee Chair, at krz2@cornell.edu

E-mail submissions are required, and applicants are encouraged to use pdf format for all documents.

Application deadline is March 31, 2007.

Additional information can be found at http://-systbio.org/?q=node/26 –

krz2@cornell.edu krz2@cornell.edu

## SocSystBiol TravelAwards

Scholarships and travel awards for scientists from developing countries to obtain modern systematics training in the United States

SSB announces the availability of scholarships for scholars from developing countries to attend workshops and courses in systematics, or to visit a lab engaged in systematic research for training. The emphasis of this program is the transfer of knowledge to the scholar's home country. Therefore, applicants should currently be in their home country or have definite plans to return in the near future. Courses such as the Molecular Evolution Workshop at Woods Hole or the applied Systematics Course at Bodega Bay are examples of courses that are appropriate for this funding, in addition to other equivalent opportunities. Support for attending a course will be contingent on admission to the course through the normal admissions process.

Applicants should submit:

1) a CV 2) a letter detailing the purpose of the visit (what class will you take or what lab will you visit) and how the knowledge acquired will be transferred to your country of origin 3) a justification of the course or lab visit as providing appropriate training 4) a letter of recommendation from a researcher familiar with the scholar's work 5) if funds will be spent on visiting a lab in the US for systematic training, please also submit a letter from your host expressing interest in your visit.

E-mail submissions are required, and applicants are encouraged to use pdf format for all documents. Applications should be sent to Dr. Kelly R. Zamudio, SSB Award Committee Chair, at krz2@cornell.edu

Application deadline is March 31, 2007

More information can be found at http://systbio.org/-?q=node/25 –

krz2@cornell.edu krz2@cornell.edu

## 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, especially 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 strucutre 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 strucutre". 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>

## Software TESS Spatial genetics

TESS New release version 1.1

The new version includes admixture analysis and many other optional features which are described in the updated reference manual. The reference manual also includes guidelines for using TESS and some answers to FAQs.

TESS is a computer program that implements a Bayesian clustering algorithm for spatial population genetics. The method is based on a hierarchical mixture model where the prior distribution on cluster labels is defined as a Hidden Markov Random Field. Given individual geographical locations, the program seeks population structure from multilocus genotypes without assuming predefined populations. Instead the program builds a network structure indicating which individuals should be considered a priori genetically close to each other.

TESS takes input data files in a format compatible to STRUCTURE. It returns graphical displays of cluster membership probabilities and geographical cluster assignments from its Graphical User Interface. Is it particularly useful for seeking genetic barriers or genetic discontinuities in continuous populations.

The program is available at the following url

http://www-timc.imag.fr/Olivier.Francois/tess.html
The reference for the method is

O. François, S. Ancelet, G. Guillot (2006) Bayesian clustering using hidden Markov random fields in spatial population genetics. Genetics, 174: 805-816.

Do not hesitate to contact me, send comments or ask questions at <Olivier.Francois@imag.fr>

best wishes, olivier

Olivier Francois <olivier.francois@imag.fr>

## Software indel-Seq-Gen

I am happy to introduce a new protein sequence simulator, indel-Seq-Gen:

Strope, CL, Scott, SD, and Moriyama, EN. 2007. indel-Seq-Gen: A New Protein Family Simulator Incorporating Domains, Motifs, and Indels. Mol. Biol. Evol. 24(3):640-649.

indel-Seq-Gen has the capabilities to simulate heterogeneous evolution, allowing the user to set subsequence parameters, such as amino acid frequencies, differing substitution matrices as well as insertion/deletion parameters such as the length distribution, frequency, and indel model. indel-Seq-Gen also introduces a novel quaternary invariable array that allows unique control of motif conservation.

Source code and executable files (Macintosh OSX10.2.8, OSX10.4.7, and Linux) for

indel-Seq-Gen is available from: http://bioinfolab.unl.edu/~cstrope/iSG

Cory Strope http://bioinfolab.unl.edu/~cstrope Bioinformatics Lab, N169, Beadle Center

Cory Strope <corystrope@gmail.com>

## Structure problems

Hi,

I have been running a number of data sets in Structure (Pritchard et al. 2000, Falush et al. 2003) with no glitches. However, recently when I run Structure it hangs up. I get a windows error reporting window and structure moves to the next run. This happens only for certain values of K and only for one of my data sets. For example it will run fine for K=2 to K=9 and hang at K then I start at K and it hangs at K. I restart at K then it hangs at K and K. then I start at K and then well...so far so good. Any insight on why this might be happening would be greatly appreciated.

Thanks in advance,

David

–

David Rosenthal, PhD Biology Department PO BOX 751 Portland State University Portland OR 97207 503 869 8855

http://web.pdx.edu/~drosen/Index.html drosen@pdx.edu drosen@pdx.edu

## TRF-length analysis service

Subject: TRF-length analysis service wanted!

Dear all, I am looking for a lab or a technician with experience in the analysis of telomere restriction fragment (TRF) length who for payment would analyse about

300 Reed bunting (Emberiza schoeniclus) samples for me. I would therefore be grateful for any information on people or labs to contact. The samples are frozen whole blood, that have to be extracted first. Preliminary tests on TRF-length analysis were fine.

Contact: Christian Mayer Institute of Zoology Winterthurerstrasse 190 CH-8057 Zurich Switzerland + 41 446354968 christian.mayer@zool.unizh.ch

Christian Mayer <christian.mayer@zool.unizh.ch>

## Teaching biostatistics

Dear colleagues,

About five years ago, I posted an inquiry on ecolog and evoldir asking what those of you who teach biostatistics used in the way of 1) textbooks and 2) software. I got about 40 replies, suggesting that there was significant interest in the community. A conversation with a colleague has suggested that it would be a good idea to update things. If you wish, you may reply directly to me rather than the list. In a week or so, I will compile the answers and post them on the two groups.

The question is about a one semester course in biostatistics for biology majors and perhaps graduate students. As an undergraduate, I took an intense semester course with lab under the able tutelage of Jim Collins (now Associate Director for Biosciences at NSF). It was one of the most memorable and useful courses I have ever taken. My vision in teaching biostatistics has been to offer something similar, however some of us may teach much larger courses without labs and I expect folks would like to hear about those as well. So, please take a moment and answer the following questions

1) What is the general layout of your biostats course? Large or small? Does it have a lab? Homework exercises? Workshop or lecture format? 2) What textbook(s) (if any) do you assign and why? 3) What software (if any) do your students use for homework and/or labs? Why? 4) Any additional comments?

Thank you for your interest!

George W. Gilchrist Email: gwgilc@wm.edu Director of Graduate Studies Phone: (757) 221-7751 Department of Biology, Box 8795 Fax: (757) 221-6483 College of William & Mary Williamsburg, VA 23187-8795 http://gwgilc.people.wm.edu/ "George W. Gilchrist" <gwgilc@wm.edu>

## Tortoise CRamplification

Hi

I am having trouble amplifying the control region in gopher tortoises, Gopherus polyphemus. I am trying to amplify the entire region, which should be around between 1-1.5kb. I have designed several sets of primers in conserved domains flanking this region (e.g. cytb, 12S, and tRNAs). I continue to get multiple bands and when I get a band of the appropriate size it is difficult to sequence, perhaps because it is very AT-rich. There is no reason to believe that there is a gene rearrangement in this tortoise species. Sequencing of Testudo, Indotestudo, and Geochelone showed no gene rearrangements. However, the pancake tortoise, Malacochersus tornieri, has a duplicated control region and tRNA-phe. I have heard of other people having trouble amplifying the control region in turtles. Does anyone have suggestions?

Thanks You,

Rachel Wallace Graduate Student, PhD. Department of Biological Sciences University of New Orleans 2000 Lakeshore Dr. New Orleans, LA 70148

Rachel Agnes Wallace <rwallace@uno.edu>

## UMinnesota SSB proposals

Proposals for 2008 Symposia due June 1, 2007 The Society for Systematic Biologists invites proposals for symposia at the 2008 SSB meeting to be held at the University of Minnesota in Minneapolis, Minnesota 20-24 June 2008. The meeting will be held jointly with the American Society of Naturalists and the Society for the Study of Evolution. Proposals should include (1) a descriptive title, (2) one or two paragraphs explaining the purpose of the symposium and its relevance to systematics, (3) a list of presentations including proposed speakers, their institutions or affiliations, and their presentation titles, (4) an indication of whether the speakers have been invited and whether they have agreed to participate, and (5) the proposed length of each talk. Symposia are restricted to half-day sessions. The society is particularly interested in symposia whose topics do not overlap with those from previous meetings, that introduce new ideas or synthesize important concepts, or those that are particularly good examples of the analysis of empirical data. Proposals that unite systematics with other fields are also desirable. We encourage participation from young investigators and others typically under-represented in symposia. Limited funding is available. Proposals will be discussed and two will be selected at the SSB Council meeting during the 2007 annual meeting in Christchurch, New Zealand. Soon after, organizers will be notified of the status of their proposals. Proposals should be sent by email to the Program Chairperson, George D. Weiblen, gweiblen@umn.edu (Department of Plant Biology, University of Minnesota, 1445 Gortner Avenue, Saint Paul, Minnesota 55108 USA).

George Weiblen

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

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

## 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

## 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 New office: 375 Foster Hall New lab: 301 Foster Hall http://biology-web.nmsu.edu/twright "Timothy F. Wright" <wright@nmsu.edu>

## 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 re-send you message to me at 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 New office: 375 Foster Hall New lab: 301 Foster Hall http://biology-web.nmsu.edu/twright "Timothy F. Wright" <wright@nmsu.edu>

## Working with multiple copy genes

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 homgygosis 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 legitimally 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

– Xavier Turon Dept. of Animal Biology (Invertebrates) Fac. of Biology Univ. of Barcelona 645, Diagonal Ave 08028 Barcelona

e-mail: xturon@ub.edu phone: 34-93-4021441 fax: 34-93-4035740

Xavier Turon <xturon@ub.edu>

## modified Genographer software

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/ 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) 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

Heidi M. Meudt, Ph.D. Research Scientist, Botany Museum of New Zealand Te Papa Tongarewa P.O. Box 467 Wellington New Zealand heidim@tepapa.govt.nz phone: +64 4 381 7127 fax: +64 4 381 7070 website: http://www.tepapa.govt.nz/TePapa/English/CollectionsAndResearch/ResearchAtTepapa/Projects/Plants/ -and-

Adjunct Research Associate School of Biological Sciences Victoria University 1-85 Kelburn Parade Room 507, New Kirk Building Wellington New Zealand phone: +64 4 463 5026 fax: +64 4 463 5331 website: http://www.vuw.ac.nz/sbs/staff/-

staff_research_fellows/meudt-heidi/meudt-heidi.aspx HeidiM@tepapa.govt.nz HeidiM@tepapa.govt.nz

## r8s dates

Dear All: I wonder if anyone has encountered the following situation using the program r8s? I rooted a cluster of species of interest with 4 outgroup taxa and pruned the most distant one in order to run r8s. For calibration, I assigned a date to the root of the ingroup. The estimated times of divergence for nodes within the ingroup do make sense, but I can't figure out why the dates for divergence nodes for the remaining ougroup taxa do not. Values are roughly double what they are when I make these outgroup taxa the subjects of a separate study in which they constitute the ingroup. Many thanks in advance for your thoughtful opinions. Bill Chapco.

William.Chapco@uregina.ca

# PostDocs

## BrownU VertebrateMorphology

POSTDOCTORAL TEACHING AND RESEARCH ASSOCIATE IN VERTEBRATE MORPHOLOGY

The Department of Ecology and Evolutionary Biology at Brown University is seeking a Postdoctoral Associate to assist in teaching human anatomy to medical students and to conduct research in vertebrate morphology. The primary teaching responsibility is in the Human Morphology course for first year medical students, with additional duties teaching advanced medical students and preparing anatomical teaching materials. Brown offers many opportunities for research collaborations with faculty in evolutionary morphology and excellent facilities for morphological research (see http://www.brown.edu/Departments/EEB/research/morphology.htm).

This position is available for the 2007-2008 academic year with a possibility for a two-year renewal. Applicants must have experience with a cadaver-based gross anatomy course, a doctorate, and potential for excellence in teaching and research in evolutionary morphology.

Applicants should submit a CV, statement of teaching philosophy and research interests, up to three representative reprints, and names of three references. Send materials to Dr. E.L. Brainerd, Box G-B210, Department of Ecology and Evolutionary Biology, Brown University, Providence RI 02912, or send by email to anatomysearch@brown.edu.

Application review will begin March 20, 2007

Brown University is an Equal Opportunity/Affirmative Action Employer.

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Elizabeth L. Brainerd Department of Ecology and Evolutionary Biology Box G-B210 Brown University Providence, RI 02912 Office: 401-863-9261 Lab: 401-863-1032 Fax: 401-863-7544 e-mail: brainerd@brown.edu Lab Web Page: http://www.brown.edu/Departments/EEB/brainerd_lab
Beth Brainerd <brainerd@brown.edu>

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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 formation 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

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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) or John Swaddle (jpswad@wm.edu) in the Biology department, and Sebastian Schreiber (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>

## 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 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-Angele.Grandbastien@versailles.inra.fr

## IndianaU EvolutionaryGenomics

POSTDOC IN EVOLUTIONARY GENOMICS

An NSF-funded postdoctoral position is available in the lab of Matthew Hahn in the Department of Biology at Indiana University. The work will examine the evolution of gene gain and loss through the study of gene families. Our lab has developed the statistical and computational tools necessary to study these phenomena, and we are looking for a motivated individual to apply the methods to interesting biological questions. The postdoctoral candidate will also be encouraged to carry out independent work in the lab.

There is a wide variety of research going on in the lab in addition to the current project, including studies of nucleotide, protein, and gene expression variation within and between species. For a summary of work in the lab, please see: http://www.bio.indiana.edu/ facultyresearch/faculty/Hahn.html

The candidate must have a Ph.D., preferably in population genetics, statistical genetics, computational biology, or phylogenetics. Programming skills aren?t required, but the candidate must be willing to learn. Salary is $40-$45K (plus benefits) commensurate with experience. The anticipated start date for this position is August 1, 2007.

Indiana University has a large and active group in evolutionary genetics, and considerable resources are offered by IU's Center for Genomics and Bioinformatics. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

To apply, please send a CV and two references to Dee Verostko at dverostk@indiana.edu with ?Hahn application? in the subject line. Review of applications will start immediately and will continue until the position is filled.

Indiana University is an Equal Opportunity / Affirmative Action Employer.

Matthew Hahn Assistant Professor Department of Biology & School of Informatics 1001 E. 3rd St. Indiana University Bloomington, IN 47405 Phone: (812)856-7001 http://www.bio.indiana.edu/facultyresearch/-faculty/Hahn.html http://www.bio.indiana.edu/-~hahnlab Matthew Hahn <mwh@indiana.edu>

## LeidenU PlantIntrogression

1 POSTDOC (F/M) (0.75 position, 4 years), vacancy reference number: 7-085 In the section Plant Ecology of the Institute of Biology Leiden University (IBL), Faculty of Sciences.

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 on 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 en 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.

Postdoc position In collaboration with a PhD student the postdoc will estimate population dynamic parameters such as gene flow and degree of introgression from field and lab work. The focus of the postdoc is on the estimation of these parameters with the aid of molecular markers. In addition the postdoc will develop molecular markers to estimate the introgression of crop genes and transgenes into wild relatives.

The candidate should have: - a PhD on an ecological or molecular biological subject - knowledge of modern molecular techniques - knowledge of existing models that estimate gene flow, effective population sizes, hybridisation and selection on markers with molecular markers - knowledge of software to analyse molecular data - Sufficient fluency in writing and speaking English

The salary in the first year is ??? 2740,00 gross per month increasing to ???3597,00 gross per month in the fourth year (on the basis of an full time appointment). The appointment is temporal with a length of 4 years for a 0.75 position.

For more information contact: Dr. K. Vrieling, email: k.vrieling@Biology.leidenuniv.nl, tel: +31 71-5275136 Dr. P. Haccou, email:.p.haccou@ibl.leidenuniv.nl, tel: +31 7171-5274917. For the ERGO program see: 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 March 30 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

"K. Vrieling" <k.vrieling@biology.leidenuniv.nl> "K. Vrieling" <k.vrieling@biology.leidenuniv.nl>

## 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

## LouisianaStateU Museum AvianSystematics

POSTDOC POSITION

SYSTEMATICS OF A NEOTROPICAL DIVERSIFICATION: THE OVENBIRDS AND WOODCREEPERS (FURNARIIDAE)

ATTENTION: Molecular systematists and ornithologists

We are looking for a person to fill a 2-year NSF-funded postdoctoral position to reconstruct a molecular-based phylogeny of all species within the Neotropical avian family Furnariidae (ovenbirds and woodcreepers). This project investigates a spectacular adaptive radiation of birds, with the vast majority of the species occurring in South America.

The successful applicant must have skills in molecular systematics (primer design, PCR amplification, DNA sequencing, and knowledge of phylogenetic analyses). Additional desirable skills are experience organizing and leading collecting expeditions to Central and South America, and experience with GIS analysis (ArcView, GARP analysis, etc.), population genetics, and comparative phylogeography.

The position is available after April, 2007 and renewal for the second year will be contingent on progress and productivity. Review of applications is ongoing and will continue until the position is filled.

Applicants must have a Ph.D. in biology or a related field. Please send your CV, a statement of research interests, and the names, phone numbers, and email addresses of three references to: Dr. Robb T. Brumfield, Museum of Natural Science, 119 Foster Hall, Louisiana State University, Baton Rouge, LA 70803 (voice: 225-578-3081; fax: 225-578-3075; e-mail: brumfld@lsu.edu). For additional information and links go to http://www.museum.lsu.edu/brumfield/research/ projectfurn.htm

brumfld@lsu.edu brumfld@lsu.edu

## Lucerne ModellingPopGenetics

Computational Population Geneticist / Ecologist Location: Eawag Centre of Ecology, Evolution & Biogeochemistry in Kastanienbaum (Lucerne)

The Fish Ecology and Evolution department (Ole Seehausen) and the Aquatic Ecology Department (Jukka Jokela) at the Eawag Centre of Ecology, Evolution & Biogeochemistry in Kastanienbaum, are seeking to fill a 2-3 year Postdoc position for theoretical work at the in-terface between population genetics, biodiversity theory and conservation biology. We wish to investigate the relationships between environmental heterogeneity, neutral genetic, and adaptive diversity using the evolutionary melting pot aquatic biota of perialpine drainages.

We are looking for an advanced Postdoc to develop theoretical models for investigating the relationships between environmental heterogeneity, genetic variation and adaptive diversity, including the emergence of functional polymorphisms and speciation. The ideal candidate will have a PhD in theoretical biology, computational population genetics or a related field, and will have extensive modeling experience in evolutionary genetics and/or metapopulation ecology.

The Postdoc is expected to interact closely with an existing research team, including PhD students and another Postdoc who does molecular genetic and ecological analyses (stable isotopes, morphometrics) on aquatic organisms at three trophic levels, and to guide PhD students.

For information on our departments please consult www.fishecology.ch and www.eawag.ch/research_e/lim/e_index.html. For specific information please contact Ole Seehausen (ole.seehausen@eawag.ch) and Jukka Jokela (jukka.jokela@eawag.ch). Send application letter, CV and publication list, and contact details of three referees by email to Sandra Isenring, Human Resources, Eawag, Ueberlandstrasse 133, CH-8600 Duebendorf or per e-mail to sandra.isenring@eawag.ch

Deadline is 7 April 2007, but applications will be considered until the post is filled.

Eawag: Swiss Federal Institute of Aquatic Science and Technology

– Ole Seehausen University of Berne ole.seehausen@aqua.unibe.ch

ole.seehausen@aqua.unibe.ch

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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 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 ir preferred, together with knowledge of techniques of DNA double strand breakage (tunel assay, comet assay, markers, etc).

If you are interested, please contact prof. Claudia Ricci, Department of Biology, Universita' di Milano, claudia.ricci@unimi.it http://users.unimi.it/ricci diego.fontaneto@unimi.it

## 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, Phyton, 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/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

## Montpellier HumanEvolBiol

POST-DOCTORAL POSITION in Human Evolutionary Biology Section Genetics and Environment, Institute of Evolutionary Sciences, University of Montpellier, France.

Project: Evolution of handedness in human populations Part 1. Social status and handedness Social status is a fitness component in humans, as in other social species with dominance relationships. Associations between socio-economic status and handedness have been found in a western society in a population of children and in several large cohorts of adults. We propose to investigate this relation in other cultures, especially in traditional or sub-traditional societies that have not experienced the demographic transition. Part 2. Sex and handedness There are more left-handed men than women, in most societies so far investigated. Why left-handed women still exist is not well understood, in light of the advantage found, in fighting interactions, which does not concern women. One possible explanation is an indirect advantage for women, through their sons, because there is a maternal component in the inheritance of left-handedness. This aspect has only been explored theoretically, and requires empirical evidence. These two parts are to be completed with other aspects, according to competence and expertise, e.g. the temporal variation of handedness (through bilateral asymmetries in past remains), and the investigation of the evolutionary causes of historical and geographical variations.

Research team: Human evolutionary biology http://-www.evolutionhumaine.fr/index_ang.php Duration: 24 months (including at least 6 months of field work)

Salary: 1,430-1,741  monthly, net (according to experience)

Candidate: The candidate should have: - a phD in Evolutionary Biology or Evolutionary Anthropology, - some experience with field work, preferably in non-western countries, - a strong motivation to improve the understanding of human evolution!

Application: CV, list of publications, names and email addresses of at least two research scientists able to fully evaluate the candidate, and cover letter should be sent to Michel Raymond (raymond@isem.univ-montp2.fr) and Charlotte Faurie (faurie@isem.univ-montp2.fr).

Charlotte Faurie

Institut des Sciences de l'Evolution (CNRS UMR 5554) Université Montpellier II - CC 065 Place Eugène Bataillon F-34095 Montpellier cedex 05 TEL: +33 (0)467 144 632 FAX: +33 (0)467 143 622 www.evolutionhumaine.fr faurie@isem.univ-montp2.fr faurie@isem.univ-montp2.fr

## Potsdam Theor Pop Genetics

A 2 year position for a postdoc with a strong background in modelling in either population genetics or evolutionary ecology is available at the University of Potsdam (close to Berlin/Germany). The position will start on 1 June 2007 or later and forms part of the Marie Curie Transfer of Knowledge Project FEMMES (FEedback Mechanisms in Models for Ecological forecastS, http://www.bio.uni-potsdam.de/professuren/oekosystemmodellierung/-aktivitaten/femmes_cobo/femmes).

FEMMES aims to develop innovative models that describe how dynamic feedbacks between different hierarchical levels (from genotypes to communities) affect the response of ecological systems to environmental change. The project will run over a period of 4 years, comprises a total of five positions for visiting scientists, and is jointly hosted by the Department of Plant Ecology and Nature Conservation, and the Department of Ecology and Ecosystem Modelling.

The fellow will be based at the Department of Plant Ecology and Nature Conservation, a research group with broad experience in the development of individual-based and spatially-explicit ecological models (e.g. Grimm et al. 2005 Science 310: 987-991). In collaboration with host scientists and a senior FEMMES fellow (Calvin Dytham, University of York, UK), the fellow will work on the incorporation of population-genotype feedbacks into such process-based models. The work will be linked to ongoing research projects on the dynamics of fragmented populations, the response of species to climate change, the dynamics of biological invasions, or the spread of transgenes (for details on some of these projects see http://www.bio.uni-potsdam.de/-professors/plant-ecology-and-nature-conservation/-research/main-research/view?set_language=en).

The Department of Plant Ecology and Nature Conservation resides in the picturesque Park of Sanssouci, a UNESCO World Heritage Site. Potsdam is a pleasant town a mere 20 minutes from Berlin with its rich cultural life.

Applicants should hold a PhD and should be fluent in English, but knowledge of German is not required. The Marie Curie Programme is primarily aimed at non-German citizens of the EU or associated countries, but applicants of any nationality may be eligible under certain conditions. Salary is in accordance with the EU payscale for experienced researchers, and includes social security contributions. Additionally, fellows receive travel and mobility allowances. For details on eligibility, salaries and allowances see http://ec.europa.eu/research/fp6/-mariecurie-actions/action/knowledge_en.html To apply, please submit a CV and contact details of references by e-mail to Frank Schurr (schurr@uni-potsdam.de) or Florian Jeltsch (jeltsch@uni-potsdam.de). The deadline for applications is 13 April 2007.

– Dr. Frank Schurr Plant Ecology and Nature Conservation University of Potsdam Maulbeerallee 3 14469 Potsdam Germany Tel: +49 331 977-1944 Fax: +49 331 977-1948

schurr@rz.uni-potsdam.de schurr@rz.uni-potsdam.de

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## PrincetonU MolEvoDevo

Post-Doctoral Positions in Molecular Developmental Evolution Princeton University, Princeton, NJ, USA

Several Postdoctoral Research Associate/Associate Research Scholar positions are available in the laboratory of Professor David Stern to study the molecular mechanisms that have caused functional evolution of the shavenbaby-ovo (svb) gene.

At least one position will focus on the molecular changes at svb that have evolved in the Drosophila sechellia lineage leading to their novel larval trichome pattern. (For more information see: Sucena & Stern. 2000. Divergence of larval morphology between Drosophila sechellia and its sibling species due to cis-regulatory evolution of ovo/shavenbay. PNAS.97:4530-4534).

Another position is available to study the molecular changes at the svb gene in the D. virilis group of species that have led to parallel evolution of trichome patterns (For more information see: Sucena et al. 2003. Regulatory evolution of shaven-baby/ovo underlies multiple cases of morphological parallelism. Nature. 424:935-038).

We have recently made considerable progress identifying the evolved regions of svb and future work focuses on a molecular functional characterization of the consequences of individual mutations in the svb regulatory region. Experience with Drosophila genetics, developmental biology, molecular biology and/or protein/DNA interactions is therefore highly desirable. Candidates should be available to start the position in 2007.

Further information about the lab and research environment can be found at www.princeton.edu/~dstern Please send applications, including a letter of interest, CV, publications list and contact information for three letters of reference to piaellen@princeton.edu

Princeton University is an Equal Opportunity/Affirmative Action Employer. For information about applying to Princeton, please link to http://web.princeton.edu/sites/dof/ApplicantsInfo.htm . dstern@Princeton.EDU dstern@Princeton.EDU

## QueensU 2 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.eeb.princeton.edu/ ~ dushoff/, http://www.eeb.princeton.edu/ ~ dushoff/, www.math.mcmaster.ca/earn/, and 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

## QueensU MathEvolInfluenza

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.eeb.princeton.edu/ ~ dushoff/, http://www.eeb.princeton.edu/ ~ dushoff/, www.math.mcmaster.ca/earn/, and 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

## Seattle ModellingFishPop

Population modeling post-doctoral opportunity at the Northwest Fisheries Science Center, Seattle, WA

The Northwest Fisheries Science Center, Conservation Biology Division, is seeking a quantitative population biologist to develop improved methods of quantifying the effects of harvest on the viability of Pacific salmon stocks. Successful applicants will have excellent modeling, programming, data analysis and statistical skills and an interest in conservation and natural resource management. The NWFSC (http://www.nwfsc.noaa.gov/) is one of the premier fisheries research centers in the Pacific Northwest with programs in conservation biology, population genetics, toxicology, stock assessment, population biology, fish ecology, fisheries technology and risk assessment. The postdoctoral positions are part of the National Research Council Research Associateship Program (http://www7.nationalacademies.org/rap/); salary is $45,000 U.S. per year, plus travel for meetings and other support. The fellowship is funded for 2 years. You must have received your PhD degree WITHIN the last five years. U.S. citizenship is not required. Application deadline is May 1, and tenure should begin in the summer or fall of 2007. Contact Michael Ford (mike.ford@noaa.gov) for more information.

Mike.Ford@noaa.gov Mike.Ford@noaa.gov

## Smithsonian HawaiianSongbirdPhylogenetics

Postdoctoral Position: Phylogenetics of Hawaiian Songbird Lineages

A postdoctoral research position to conduct molecular and morphological phylogenetic analyses of Hawaiian songbird lineages is available for up to two years beginning as early as June 2007 (the second year of funding is contingent upon satisfactory performance in the first year). Most of the species under study are extinct or endangered, so museum specimen and subfossil bone material will be analyzed using ancient DNA methods. Applicants should have a background in molecular methods (PCR, DNA sequencing) and phylogenetic analysis. Experience with ancient DNA methods and morphological character analysis are a plus. Some paleontological fieldwork in Hawaii is expected, as well as museum sampling visits. Please send a letter of application detailing your experience in the relevant areas, a full curriculum vitae, examples of your work (pdfs), and the names, addresses, phone numbers and email addresses of at least two references who know your research experience and abilities. Research will be conducted in the Genetics Program located in the National Zoological Park and the National Museum of Natural History, both located in Washington, DC. Email application materials to Dr. Rob Fleischer (fleischerr@si.edu) and Dr. Helen James (jamesh@si.edu). Review of applications will begin on 15 March 2007.

Robert C. Fleischer, Ph.D. Head, Center for Conservation and Evolutionary Genetics National Zoological Park National Museum of Natural History Smithsonian Institution 3001 Connecticut Ave., NW Washington, DC 20008 USA phone:1-202-633-4190 fax: 1-202-673-0040 email: fleischerr@si.edu

“Fleischer, Robert” <FleischerR@si.edu>

## 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/%7Ewiuf/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/> 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/fakult... 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

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 H-Guldbergs Gade 10, Building 1090 DK- 8000 Aarhus C, Denmark Phone +45 8942 3123 E-mail: enette@birc.au.dk

enette@birc.au.dk

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## UAdelaide AncientBovines

Evolutionary genetics of bovid genomes over 60,000 years

ARC Senior Research Associate

3 year position available immediately

Level B (salary range of AUD$63,487 - AUD$75,392)

A 3-year postdoctoral position is available at the Australian Centre for Ancient DNA (http://www.adelaide.edu.au/acad), The University of Adelaide, to study the genetics of ancient bovid populations. The ARC-funded project will analyze nuclear QTL in bison and aurochs specimens, in collaboration with Prof J. Taylor and R. Schnabel at the Animal Genomics Centre at the University of Missouri (http://animalgenomics.missouri.edu). The postdoctoral fellow will be responsible for collecting and analyzing samples, project logistics and liaising with the University of Missouri collaborators. The aim is to apply cutting-edge genomics, SNP-screening and chip-based approaches to ancient DNA extracts and libraries using new molecular biology methods. The project may involve fieldwork, collecting samples in European, Russian and North American museums, and complex and technically challenging ancient DNA techniques.

The ACAD is a leading international ancient DNA research centre with on-going projects on human evolution, Late Pleistocene animal and plant population genetics and systematics, genetic impacts of climate change, molecular dating methods, and geological and sedimentary DNA studies. Research teams feature both international and Australian researchers and collaborators, ranging from archaeologists to genomics researchers. Adelaide is a scenic, vibrant cosmopolitan city with notably inexpensive living conditions, and direct access to the coast and extensive wine areas.

Enquiries can be directed to Prof. Alan Cooper (alan.cooper@adelaide.edu.au), and applications quoting the reference number (12593) should be forwarded to Ms Maria Lekis at maria.lekis@adelaide.edu.au by Monday 19 March 2007.

Jeremy Taylor Professor and Wurdack Chair in Animal Genomics S135 ASRC University of Missouri 920 East Campus Drive Columbia, MO 65211-5300 Voice: (573) 884-4946 Fax: (573) 882-6827 E-mail: taylorjerr@missouri.edu http://animalgenomics.missouri.edu

<http://animalgenomics.missouri.edu taylorjerr@missouri.edu

## UAdelaide BovineAncientDNA

Evolutionary genetics of bovid genomes over 60,000 years

ARC Senior Research Associate 3 year position available immediately Level B (salary range of $63,487 - $75,392)

A 3-year postdoctoral position is available at the Australian Centre for Ancient DNA (http://www.adelaide.edu.au/acad), The University of Adelaide, to study the genetics of ancient bovid populations. The ARC-funded project will analyze nuclear QTL in bison and aurochs specimens, in collaboration with Prof J Taylor and R Schnabel at the Animal Genomics Centre at the University of Missouri (http://animalgenomics.missouri.edu). The postdoctoral fellow will be responsible for collecting and analyzing samples, project logistics and liaising with the University of Missouri collaborators. The aim is to apply cutting-edge genomics, SNP-screening and chip-based approaches to ancient DNA extracts and libraries using new molecular biology methods. The project may involve fieldwork, collecting samples in European, Russian and North American museums, and complex and technically challenging ancient DNA techniques. The ACAD is a leading international ancient DNA research centre with on-going projects on human evolution, Late Pleistocene animal and plant population genetics and systematics, genetic impacts of climate change, molecular dating methods, and geological and sedimentary DNA studies. Research teams feature both international and Australian researchers and collaborators, ranging from archaeologists to genomics researchers. Adelaide is a scenic, vibrant cosmopolitan city with notably inexpensive living conditions, and direct access to the coast and premier Australian wine areas.

Enquiries can be directed to Prof. Alan Cooper (alan.cooper@adelaide.edu.au), and applications quoting the reference number (12593) should be forwarded to Ms Maria Lekis at maria.lekis@adelaide.edu.au by Monday 19 March 2007.

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Prof. Alan Cooper, Federation Fellow

Darling Blg (DP 418), Rm 209b University of Adelaide North Terrace Campus South Australia 5005 Australia

Email: alan.cooper@adelaide.edu.au Ph: 61-8 -8303-5950/3952 Fax: 61-8-8303 4364

http://www.ees.adelaide.edu.au/acad/ alan.cooper@adelaide.edu.au

## UBern PlantInvasionBiol

Postdoctoral position in plant invasion biology at the University of Bern, Switzerland

We are seeking a postdoc highly motivated to work on determinants of plant invasiveness in field, garden, and molecular lab. The work will mainly involve comparative research on congeneric pairs of invasive and non-invasive plants species native to Switzerland.

The position will be in the new group of Markus Fischer at the Institute of Plant Sciences of the University of Bern (http://www.botany.unibe.ch/), Switzerland, and is funded within the framework of the NCCR (National Competence Center in Research) “Plant Survival” (http://www2.unine.ch/nccr). . We offer a stimulating research environment in a lively and social institute in a beautiful city close to the Alps. The position will be for a period of two years, and should start as soon as possible (1 May 2007 or soon thereafter). The salary will be about 70’000 CHF per year.

Requirements for the position include a PhD in population biology, evolutionary ecology, or related fields, a proven record of research, experience with field work, garden or greenhouse experiments, and lab work, statistical and writing skills, as well as a driver’s licence.

For more information on this position and research in our lab contact Markus Fischer at Markus.Fischer@ips.unibe.ch or Mark van Kleunen at vankleunen@ukzn.ac.za . Applicants should e-mail a short statement of research interests, curriculum vitae, and contact details of three references to both Markus Fischer at Markus.Fischer@ips.unibe.ch and Mark van Kleunen at vankleunen@ukzn.ac.za. The application deadline is 10 April 2007.

Markus Fischer

Professor of Plant Ecology

Institute of Plant Sciences University of Bern Altenbergrain 21 3013 Bern Switzerland

Phone Tel. +41 31 631 49 43 Fax +41 31 631 49 42 e-mail markus.fischer@ips.unibe.ch

for biodiversity exploratories see http://www.bio.uni-potsdam.de/biodiversity-exploratories/ for group in Potsdam see http://www.bio.uni-potsdam.de/-professuren/biozoenose-botanik/ Markus Fischer <Markus.Fischer@ips.unibe.ch>

## 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 postdoctoral 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 candidate, 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.

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

Mark Achtman <achtman@mpiib-berlin.mpg.de>

## UCDavisGenomeCenter GenomeEvol

Comparative Genomics Postdoc A postdoctoral position is available in the research group of Dr. Katherine Pollard at the UC Davis Genome Center. We recently developed a computational approach to detect rapidly evolving genomic regions and applied it to identify the elements of the human genome that have diverged most since our common ancestor with chimps. The successful candidate will take a lead role in extending these comparative genomic methods to study lineage-specific evolution in vertebrates, flies, and possibly other phylogenies.

Qualifications The applicant must have a PhD in (bio)statistics, applied math, computer science, bioinformatics, molecular biology or a related field, with experience analyzing genomic data. Ability to program (e.g. in R/Splus, C, or Perl) is essential. Candidates interested in doing some experimental work are invited to apply - opportunities may be available in the labs of collaborators.

Term Two years, with possible extension. Start date in 2007. Applications will be accepted until the position is filled.

To apply Please apply by email to postdoc at wald dot ucdavis dot edu and include: - CV (including record of peer-reviewed publication), - cover letter describing current research activity, - names and email addresses of three references.

Details at http://docpollard.com/jobs.html kspollard@ucdavis.edu kspollard@ucdavis.edu

## UCaliforniaSanDiego ViralEvolution

Postdoctoral position VIRAL EVOLUTION AND DYNAMICS Department of Pathology University of California San Diego

DESCRIPTION: A fully funded postdoctoral position (up to two years) will be available starting July 1st, 2007 to work on the evolution, dynamics and epidemiology of the human immunodeficiency virus (HIV), Influenza A and Hepatitis C. Because of the requirements of the funding mechanism, this position is open to US citizens and Permanent Residents only. Salary is set using standard NIH scales, and is commensurate with experience.

RESEARCH GROUP: The position is based in the laboratory of Dr. Simon Frost (http://www.simonfrost.com). The successful candidate will interact with Drs. Sergei Kosakovsky Pond (http://www.hyphy.org/sergei/) and Art Poon in developing, implementing and applying cutting edge statistical methods, for the analysis of viral sequences and immunological data. There is the potential to develop and co-supervise undergraduate and graduate research projects.

LOCATION: University of California, San Diego. The position is based at the Antiviral Research Center (http://www.avrctrials.org), situated in the Hillcrest area (http://www.hillquest.com) near downtown San Diego.

REQUIREMENTS: A Ph.D. in statistics, population genetics, mathematical or computational biology, or similar. Evidence of research productivity as indicated by scholarly publications is required. Sound skills in C/C++ programming, algorithms and methods and the analysis of sequence and/or population dynamic data are a prerequisite. Experience in advanced statistics (random effects models, Markov Chain Monte Carlo, machine learning) a plus. Evidence of strong communication and teamwork skills is highly desired.

APPLICATION: Please send letter of interest, C.V., and the names and contact details of three referees by April 9th, 2007 to: Postdoctoral Position in Viral Evolution and Dynamics, Dr. Simon Frost, UCSD Antiviral Research Center, 150 W. Washington St., San Diego CA 92103, USA. Electronic application materials (PDF, Word) are preferred - please email to sdfrost at ucsd.edu. Review of applications will begin immediately, and continue until the positions are filled.

spond@ucsd.edu spond@ucsd.edu

## UCopenhagen EvolChemCommunication

POST-DOC position evolution of chemical communication, Copenhagen

The position is funded by the European Community via the Marie Curie Excellence grant CODICES (Chemical Communication Code of Insect Societies). This interdisciplinary project aims at understanding the evolution of communication in social insects. The methodology is a combination of behavioural experiments, genetic, chemical and neuro-physiological studies. The work is inspired by general principles of kin-selection and economic optimality, allowing predictions both on proximate and ultimate aspects of communication systems. Social insects are important model systems for studying social evolution and complex interactions. There is evidence that social insects use the mixture of long-chain hydrocarbons on their cuticle for nest-mate recognition.

We are looking for a talented synthetic organic chemist to implement the synthesis of biologically active cuticular hydrocarbons of ants. The position is initially for three months and immediately available. The candidate should hold a Ph.D in organic chemistry and be highly interested in chemical ecology. He/She will join and international team working on an interdisciplinary project (www.bi.ku.dk/codices).

Applications should include CV, list of publications, research interests, letter of motivation, name and email address of one referee, and be sent by email to Dr. Patrizia D'Ettorre at pdettorre@bi.ku.dk as soon as possible.

Patrizia D'Ettorre Institute of Biology Department of Population Biology University of Copenhagen DK-2100 Copenhagen, Denmark Phone +45 3532 1257 Fax +45 3532 1250

"D'Ettorre, Patrizia" <PDEttorre@bi.ku.dk>

## UEdinburgh CompBiol

University of Edinburgh School of Biological Sciences Postdoctoral Research Fellow

A computational biologist is required to join the group of Professor Andrew Leigh Brown (http://homepages.ed.ac.uk/eang09/LeighBrownGroup.html), on a BBSRC-funded position to analyse the genetic determinants of virulence in avian influenza using computer modelling approaches. The project will form part of a major new initiative in influenza research centred at the University of Edinburgh, and will link with the Edinburgh Parallel Computing Centre to analyse statistical models in the massively parallel BlueGene environment. A PhD and experience in scientific computing and either statistical analysis or biomathematics is required; familiarity with analysis of molecular sequence data would be helpful.

Informal enquiries: A.Leigh-Brown@ed.ac.uk Tel: +44-131-650-5523 Web: http://homepages.ed.ac.uk/eang09/LeighBrownGroup.html Fixed Term: 3 years

Salary: £32,795 - £39,160

Closing date: 13 April 2007

Website for application: www.jobs.ed.ac.uk Ref: 3007126

A.Leigh-Brown@ed.ac.uk A.Leigh-Brown@ed.ac.uk

## 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>. – 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>

## UGlasgow PlantGenomics

UNIVERSITY of GLASGOW Faculty of Biomedical & Life Sciences Division of Environmental and Evolutionary Biology

POST-DOCTORAL RESEARCH ASSISTANT IN PLANT GENOMICS AND ADAPTATION

SALARY £23,002 - £25,889 / £25,889 - 31,840 per annum

Ref: 13138/DPO/A3

This post is available at either a grade 6 or grade 7 depending on qualifications and experience.

We are seeking a Post-Doctoral Research Assistant 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 molecular basis of adaptation and species formation are fundamental questions in evolutionary biology, with relevance also to crop biology. Specifically, tools and approaches developed for natural populations are valuable for studying crop domestication. The impending completion of the genome sequences of the two Brassicaceae Arabidopsis lyrata and Capsella rubella, together with the available sequence of A. thaliana, offers opportunities to study adaptation using molecular evolutionary approaches complemented by functional analyses. Our consortium will exploit this resource to study variation in underlying differences, including two ecologically important traits, flowering time and self-incompatibility (SI).

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

Further particulars about the post and the research environment can be found at: http://www.gla.ac.uk/ibls/news/posts.html and http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PQdGnd Letters of application, including two CVs, the names, postal and e-mail addresses and fax numbers of two academic referees, should be sent to: Caren Cunningham, IBLS, West Medical Building, University of Glasgow, Glasgow, G12 8QQ, UK quoting the reference number 13138/DPO/A3.. Closing Date: 13 April, 2007. This post is available for up to 3 years. Please send notes of interest or informal enquiries by email to Barbara Mable (b.mable@bio.gla.ac.uk) as soon as possible.

– Dr. Barbara Mable Senior Research Fellow Division of Environmental and Evolutionary Biology Rm 404 Graham Kerr Building University of Glasgow Glasgow, Scotland G12 8QQ email: b.mable@bio.gla.ac.uk Phone: +44 (0)141 330 3532 Mobile: +44 (0)791 083 3819 Fax: +44 (0)141 330 5971

b.mable@bio.gla.ac.uk b.mable@bio.gla.ac.uk

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## UIdaho PlasmidGenomics

POSTDOCTORAL POSITION IN COMPARATIVE PLASMID GENOMICS

UNIVERSITY OF IDAHO

The position is immediately available in the lab of Eva Top for a period of 2 years.

A large-scale comparative genomics project is underway at the University of Idaho to assess the genetic and functional diversity of broad-host-range (BHR) plasmids that horizontally transfer genes within and between bacterial species. The postdoctoral scientist will be involved in annotating the complete sequences of up to 100 BHR plasmids, analyzing the diversity and likely function of accessory’ genes, and assessing the phylogenetic relatedness of genes found in plasmid backbones’ to determine the evolutionary history of these plasmids. This will require applying existing methods and devising novel methods used for comparative genomics of prokaryotes. By interpreting this wealth of new plasmid genome information the postdocoral fellow will have the opportunity to improve our insight in the biology, ecology and evolution of plasmids and their hosts. The plasmids are being sequenced by JGI and the project is funded by the NSF Microbial genome Sequencing Program.

This interdisciplinary project is in collaboration with Biology faculty, Drs. Celeste Brown, Jack Sullivan, and Larry Forney, and professors of Art and Design Frank Cronk and Jill Dacey. The position offers the opportunity to carry out research in a dynamic and interdisciplinary research environment with excellent resources (http://www.ibest.uidaho.edu/ibest/index.html and http://www.ibest.uidaho.edu/ibest/index.html www.sci.uidaho.edu/biosci/CRePE/index.html and http:// www.bcb.uidaho.edu/default.aspx?pid=85454 ). The candidate should have a Ph.D. degree in bioinformatics/ computational biology, microbiology or related discipline. He/she should also be able to demonstrate experience in comparative analyses of prokaryotic genomes, and ability to publish scientific papers as first author in peer-reviewed journals, and presenting data at scientific meetings. Some knowledge of prokaryotic molecular biology or genetics and biology and ecology of plasmids is also required. Moreover, the postdoctoral fellow should be able to work well in an interdisciplinary team. Preference will be given to individuals who have had training in computational biology, one or more years of experience in the field of microbial genome analysis, some experience in empirical microbiology and/or molecular biology research, programming skills in C++, PERL or similar languages, and a strong interest in bacterial plasmids, microbial evolution, and phylogenetics.

The University of Idaho is an equal opportunity/affirmative action employer. Moscow, the home of the University of Idaho is a city of 22,000 people, nestled between Moscow Mountain and the beautiful rolling hills of the Palouse. With a small town friendliness and safety, and many cultural activities, Moscow is referred to as the “Heart of the Arts”. It is also a great place for those who love the outdoors, with beautiful rivers, lakes, and diverse mountains within short driving distance (http://www.moscow.com). The University of Idaho and Washington State University, just eight miles apart, share many collaborative programs and research activities.

Please apply via the following website: https://www.sites.uidaho.edu/ AppTrack/Agency/Applicant/ViewAnnouncement.asp? announcement_no508078967 Make sure you include a letter, your CV, and the names and contact information of three references. For more information, please contact Eva M. Top, University of Idaho (evatop@uidaho.edu). Evaluation of candidates will begin after March 30.

Dr. Eva Top Associate Professor Department of Biological Sciences University of Idaho 347 Life Sciences South Moscow ID 83844-3051 Phone: 1-208-885-5015 Fax: 1-208-885-7905 http://www.sci.uidaho.edu/biosci/labs/-top/ evatop@uidaho.edu evatop@uidaho.edu

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## ULausanne ModelingDispersal

POSTDOCTORAL POSITION Modelling long-distance gene flow in plant species

European Project ECOCHANGE (Challenges in assessing and forecasting biodiversity and ecosystem changes in Europe)

A postdoctoral position is available to work with Jerome Goudet (University of Lausanne, Switzerland) and Oscar Gaggiotti (Laboratoire dEcologie Alpine, Grenoble, France) in the context of a project funded by the European Union. Its overall aim is to assess and forecast changes in terrestrial biodiversity and ecosystems and changes in the ability of biodiversity and ecosystems to supply goods and services and to buffer against climate and land use change.

The postdoctoral researcher will participate in a subproject aimed at estimating dispersal abilities of plant species. In models predicting the evolution of ecosystems according to climate and land use changes, the dispersal abilities of the organisms are of crucial importance. Short distance dispersal is relatively well known for plants. However, rare long distance events are extremely difficult to estimate, despite the fact that they have a crucial impact on the ecosystem evolution in changing environments. According to pilot studies from some of the consortium partners, it seems that the geographic distributions of the different alleles are linked to the dispersal potential and might therefore be useful to estimate long-distance dispersal.

The postdoc will carry out a theoretical study to: (i) asses the potential use of genetic markers to evaluate the tail of dispersal curves for plants and (ii) propose an experimental protocol for estimating the dispersal abilities of 100 dominant plant species in European ecosystems.

Requirements for the position include (1) a proven record of research; (2) a PhD in biology, mathematics, statistics, or related area; (3) excellent quantitative and computational skills. The ideal candidate should be well acquainted with scientific programming in C/C++.

Applications are welcome from candidates in any country. Screening of applicants will begin March 26, 2007. Starting date: as soon as possible.

Highly motivated applicants are encouraged to email a statement of research interests, CV, and contact details for three references to both Jerome Goudet (Jerome.Goudet@unil.ch) and Oscar Gaggiotti (Oscar.Gaggiotti@ujf-grenoble.fr).

– Oscar Gaggiotti Professor Equipe Genomique de Populations et Biodiversité LECA UMR CNRS 5553 Université Joseph Fourier BP 53 38041 GRENOBLE France Tel.: 33(0)4 76 51 41 15 Fax: 33(0)4 76 51 42 79 http://www-leca.ujf-grenoble.fr/-membres/gaggiotti.htm http://www-leca.ujf-grenoble.fr/projets/gaggiottiprojets/IMPBioFr.htm oscar.gaggiotti@ujf-grenoble.fr oscar.gaggiotti@ujf-grenoble.fr

## 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 postdoctoral 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

pascal.poulin@rsvs.ulaval.ca

## UMissouriColumbia 2 BovineSNPs

Division of Animal Sciences

University of Missouri, Columbia

Two postdoctoral positions in Quantitative and Population Genomics are available within the Animal Genomics group to work on high-resolution SNP data generated in cattle and closely related species. The Animal Genomics group is collaborating in the development of an Illumina iSelect Infinium SNP assay for cattle which is expected to generate at least 48K bovine SNP genotypes per assay. The “SNP Chip” is expected to be available by June 2007 and more than 9,000 samples representing at least 10 breeds of cattle, bison, buffalo, gaur, banteng, anoa, sheep and ancient auroch and bison will be genotyped at the University of Missouri in Spring 2007. These samples are expected to produce over 400M genotypes which will be used in projects to: 1) Characterize linkage disequilibrium and population characteristics (admixture, inbreeding, effective population size, phylogeny) within cattle and closely related species, 2) develop novel approaches to the fine-mapping of QTL based upon historical selection, and 3) map/fine-map QTL associated with fertility, production and feed efficiency traits in beef and dairy cattle using association and joint linkage/linkage disequilibrium approaches. The successful candidates will be responsible for the analysis of data modules using existing analytical tools as well as developing novel methods for analyzing high density SNP data in livestock populations. Candidates should have completed a Ph.D. in genetics, statistics, computational or evolutionary biology or related discipline. Previous experience in computer programming, population or quantitative genetics and with the analysis of genomic data is desirable.

The successful candidates will have the opportunity to participate in the largest population and QTL mapping projects conducted to date within a livestock species. The candidates are expected to provide intellectual leadership to the projects in both analysis and the authorship of publications. Both positions are available for up to two years with reappointment in the second year conditional upon satisfactory performance during the first year. These positions are not eligible for tenure. Salary will be within the range $32,000-$45,000 commensurate with qualifications and experience. Benefits include medical insurance, paid leave and paid holidays. An overview of the Animal Genomics group can be found at (http://animalgenomics.missouri.edu <http://animalgenomics.missouri.edu/> ). Information about the University of Missouri and the Division of Animal Sciences can be found at http://www.missouri.edu/ and http://www.missouri.edu/

For further information contact Dr. Jerry Taylor at taylorjerr@missouri.edu or (573) 884-4946. Interested candidates should e-mail their CV and contact information for 3 references to taylorjerr@missouri.edu. Applications will be accepted until suitable candidates have been identified.

The University of Missouri System is an Equal Opportunity/Affirmative Action institution and is nondiscriminatory relative to race, religion, color, national origin, sex, sexual orientation, age, disability or status as a Vietnam-era veteran. The University of Missouri is in compliance with Title VI of the Civil Rights Act of 1964, Title IX of the Education Amendments of 1972, Section 504 of the Rehabilitation Act of 1973, and of the Americans with Disabilities Act of 1990.

Jeremy Taylor Professor and Wurdack Chair in Animal Genomics S135 ASRC University of Missouri 920 East Campus Drive Columbia, MO 65211-5300 Voice: (573) 884-4946 Fax: (573) 882-6827 E-mail: taylorjerr@missouri.edu http://animalgenomics.missouri.edu

taylorjerr@missouri.edu

## UPompeuFabra Barcelona GenographicProject

Post-doc position, Genographic Project,

Evolutionary Biology, Universitat Pompeu Fabra (UPF), Barcelona

A five-year post-doc position is available at the Evolutionary Biology Unit (http://www.upf.edu/cexs/recerca/bioevo/index.html), Universitat Pompeu Fabra (Barcelona). The position is linked to the Genographic Project ( <https://www3.nationalgeographic.com/genographic> https://www3.nationalgeographic.com/genographic). Applicants must have a wide knowledge in human genetic diversity, and knowledge of a second European language, besides English. The duties of the position include sampling European human populations, typing and analysis of several genetic markers.

Phlebotomist skills will be encouraged. The successful applicant will be an organized autonomous person, with social skills, free to travel.

The position is aimed at a postdoctoral level; a non-tenure-track full-time position for a maximum of five years.

Applicants should send:

* CV

* A letter describing their research interests

* Two names (with e-mail addresses and phone numbers) of researchers for reference before April 1st, 2007, to merche.corral@upf.edu

david.comas@upf.edu

## 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> 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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## USheffield ZebraFinchGenomeMapping

Postdoctoral position - University of Sheffield, UK.

Mapping the zebra finch genome.

Dr Jon Slate, Professor Terry Burke and Professor Tim Birkhead FRS are seeking a postdoc to work on a BBSRC-funded project to map the zebra finch genome, and to address evolutionary questions relating to recombination rates and levels of linkage disequilbrium. The successful applicant will be responsible for the accumulation and (more importantly) analysis of molecular marker data. The linkage map forms an important part of an ongoing project to sequence and assemble the zebra finch genome. SNP genotyping has been outsourced and data will be available early on during the project. This is an ideal opportunity to join a large, high profile grade 5* research department, working on a project of international significance. The post is tenable immediately for a period of three years.

Applicants should have a PhD and an existing publication record in one or more of the following disciplines: gene mapping, bioinformatics, statistical genetics, comparative genomics, population genetics, molecular ecology, molecular evolution. They should be a motivated scientist with the ability to analyse large datasets, work independently and produce work to fairly tight deadlines.

The Department of Animal & Plant Sciences is an internationally leading (RAE 5*) department with strengths in several areas of biology including Evolutionary Biology, Global Change Biology, Conservation Biology & Biodiversity and Population and Community Ecology. Furthermore, Sheffield is very affordable, within easy reach (walking distance) of the Peak District National Park and claims to be England's greenest city. The city centre has undergone substantial redevelopment and contains a diverse range of cultural activities, museums, cinemas, restaurants etc.

Applications should be made through the University of Sheffield website: http://www.sheffield.ac.uk/jobs/research.html, quoting job reference no PR2791. Closing date is 13th April 2007.

For further details please contact Jon Slate. j.slate@shef.ac.uk http://www.jon-slate.staff.shef.ac.uk/ Jon Slate <j.slate@sheffield.ac.uk>

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## UToronto 2 EvolEcol

Postdoctoral Positions in Quantitative and Evolutionary Ecology Department of Ecology and Evolutionary Biology, University of Toronto

Two postdoctoral positions are available in Spring 2007.

1. A position to work with a multi-disciplinary team of academic and government scientists (Peter Abrams, Marie-Josee Fortin, Don Jackson, Brian Shuter) on the spatial ecology of aquatic ecosystems. Areas of interest include (i) statistical approaches to identifying and quantifying how biomass at several trophic levels varies spatially and the associations between that variation and physical habitat features; (ii) associations between the success of an invasive species and spatial variation in the distribution and dynamics of its prey; (iii) mechanistic modelling of the role of spatial variation in determining interaction strength between ecosystem components and consequent implications for ecosystem dynamics; The candidate would have access to a rich, multi year data base documenting the impacts of an invasive predator (the double crested cormorant) on the fish communities resident in large coastal areas of Lake Huron.

2. A position in theoretical evolutionary ecology. The person hired would have wide latitude to work on their own choice of projects, but some should be in collaboration with Peter Abrams on one or more of the following topics: (1) developing models of the dynamics of ecologically important behaviours; (2) examining the impact of adaptive behaviour on evolutionary change in traits with related ecological functions within sets of interacting species; (3) modeling coevolution in variable

environments.

Positions are for 2 years; initial salary is $40,000 Canadian per year.

Send a curriculum vitae, copies of 2 publications, and names of two people who could provide letters of references to:

Peter Abrams Department of Ecology and Evolutionary Biology Zoology Bldg. University of Toronto 25 Harbord St. Toronto, ON M5S 3G5 Canada

email: abrams@zoo.utoronto.ca (application by email is fine, as are electronic copies of publications; applications should arrive by April 15, 2007; starting date is flexible within 2007)

Peter Abrams Dept. of Ecology & Evolutionary Biology University of Toronto, Zoology Bldg. 25 Harbord St. Toronto, Ontario M5S 3G5 Canada 416-978-1014 fax 416-978-8532 abrams@zoo.utoronto.ca

Peter Abrams <abrams@zoo.utoronto.ca>

## UToronto EvolBiology

University of Toronto EEB Post-Doctoral Fellowships

The Department of Ecology and Evolutionary Biology < www.eeb.utoronto.ca> at the University of Toronto invites applications for Departmental Postdoctoral Fellowships in the areas of Ecology and Evolutionary Biology, broadly defined. One position is available this year, and we expect that another will become available next year through an ongoing EEB Post-Doctoral Fellowship Program. Positions are for two years, subject to review after one year, and can begin as early as July 1, 2007. The salary is $40,000 Canadian per year, with research expenses covered by the Post-Doctoral Advisor.

The Fellow will be a fully participating member in the Department. Candidates must identify and communicate with a potential advisor (or advisors) in advance of the application process. All full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors (see <www.eeb.utoronto.ca/postdoc/> for a list of potential supervisors). Opportunities for teaching in an upper level course may be available.

To apply, applicants should submit a cover letter, a curriculum vitae, a short (1-2 page) description of research accomplishments, and a short (1-2 page) description of proposed research plans indicating potential faculty mentor(s), and copies of two publications. Applicants should include names and e-mail addresses for two potential referees. Applicants should also indicate the date they will be available to begin the position. All application materials must be submitted as PDF's in a single email to: Kitty Lam (klam@eeb.utoronto.ca). Queries about the EEB Post Doc fellowship program can be directed to Prof. John Stinchcombe <stinchcombe@eeb.utoronto.ca>. Evaluation of Applications will begin on April 30, 2007.

Toronto is a vibrant, multicultural city on the shore of Lake Ontario, with rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life. The EEB department is home to an interactive, collegial group of ecologists, geneticists, and evolutionary biologists, and currently supports a strong group of Post-Doctoral Fellows with diverse research interests.

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John Stinchcombe Department of Ecology and Evolutionary Biology University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

http://www.botany.utoronto.ca/ResearchLabs/-StinchcombeLab/ stinchcombe@eeb.utoronto.ca

## UWindsor CoralReefFishConnectivity

Post-Doctoral Researcher Great Lakes Institute for Environmental Research (GLIER).

We invite applicants for a Post-Doctoral Researcher Position in the field of reef fish population connectivity in the Meso-American barrier reef system (MBRS). The project involves microsatellite genetics and otolith microchemistry in the bicolour damselfish off Mexico, Belize and Honduras. The successful candidate will be responsible to organize intensive sampling trips to the MBRS. The position will thus include both field and lab expertise. Existing samples will allow the analysis of other species to test hypotheses concerning the evolution and ecology of connectivity in coral reef fishes.

The candidate should have proven skills in molecular genetics and/or otolith microchemistry as well as experience in SCUBA diving and field techniques. The individual should also have a good track record in analysis and publishing, and have the ability to work well in collaborative research.

The GLIER offers a collaborative environment, with state-of-the-art faculties in genetics, genomics, and elemental and stable isotope analyses. GLIER faculty have expertise in the fields of aquatic invasions, evolutionary and conservation genetics, environmental science, genomics, and ecotoxicology.

The position is for one year, but can be renewed, with a flexible start date as early as May 2007. Stipend is competitive, and research travel and other costs will be paid. Review of applications will begin April 1st, 2007. Interested applications should send their CV, a brief statement of research interest, and the e-mail addresses for at least two referees to:

Daniel Heath Great Lakes Institute for Environmental Research University of Windsor E-mail: dheath@uwindsor.ca Phone: (519) 253-3000, Ext 3762 Fax: 971-3616

dheath@uwindsor.ca

## YaleU SexualSelection

Postdoctoral Position Available To Study Sexual Selection and Mating Systems

A postdoctoral position is currently available in the lab of Suzanne Alonzo (PI) at the Department of Ecology and Evolutionary Biology at Yale University to develop theory and/or conduct empirical work on sexual selection and the evolution and ecology of mating systems. A Ph.D. in evolution, ecology or related field is required. A background in sexual selection and evolutionary ecology is absolutely necessary. The postdoctoral researcher will work independently and in collaboration with the PI to determine the precise questions to be addressed.

For this position you MUST have one (or both) of the following areas of expertise:

1) Evolutionary theory of sexual selection: Applicants should have a background in sexual selection theory and have previous experience developing mathematical models on reproductive behavior or sexual selection. Individuals with experience using quantitative genetics are especially encouraged to apply.

AND/OR

2) Paternity analysis: Individuals with experience collecting and analyzing DNA paternity data (especially using microsatellites and in fish) are also strongly encouraged to apply. Empirical work will be conducted on Mediterranean wrasses or North American tessellated darters.

Review of applications begins immediately and will continue until the position is filled. Start date is flexible but the position is available immediately and must begin by December 1, 2007. The position is for one year and is renewable contingent on the availability of funding. Please submit a curriculum vitae, brief statement of research interests, up to 3 relevant manuscripts and 3 professional references to Suzanne H. Alonzo by email (Suzanne.Alonzo@Yale.edu) or mail (Department of Ecology and Evolution, Yale University, P.O. Box 208106, New Haven, CT 06520-8106).

Yale University is an Equal Opportunity/Affirmative Action Employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

Suzanne.Alonzo@Yale.edu

# WorkshopsCourses

## Durham NESCent CompPhyloinformatics Jul9-19

Computational Phyloinformatics: A Course at NESCent. 9 - 19 July 2007

The National Evolutionary Synthesis Center (Durham, NC, USA)

http://www.nescent.org/summer_course Computational Phyloinformatics is a new course that aims to give students practical knowledge and hands-on skills in phyloinformatics.

SYNOPSIS Biologists are faced with ever larger datasets, more complex evolutionary models, and more elaborate analytical methods. Seldom is it sufficient to run a dataset through an off-the-shelf program on a desktop PC; increasingly, biologists need to write scripts to interface with internet services and databases, build analytical pipelines, customize analyses, and distribute computation over multiple processors.

This course is designed to give graduate students, postdocs, and researchers in phylogenetics who have an interest in writing programs and scripting analyses the skills needed to tackle the grand challenges posed by the Assembling the Tree of Life program, Evo- Devo, Metagenomics, Phylogenomics, and other emerging research areas. Students will learn how to build and compute with phylogenetic databases; they will learn "power-user" skills for scripting analyses in Mesquite and HyPhy. Students choose between either a Java- or a Perl-based environment for learning how to write basic phylogeny programs: parsing NEXUS files; traversing and computing over trees; and making practical use of phylogenetic libraries (e.g. PAL, JEBL, BioJava; BioPerl, Bio::Phylo, CIPRES interface). These skills will be learned in a biological context, touching on a diverse array of topics such as automated base calling, ancestral state and continuous character reconstruction, model selection, parametric bootstrapping, etc.

INSTRUCTORS Organizer: William Piel (william.piel@yale.edu) Hilmar Lapp David Maddison Wayne Maddison Jeff Oliver Sergei L. Kosakovsky Pond Stephen Smith Arlin Stoltzfus Rutger Vos

PREREQUISITES Biology: A solid understanding of phylogenetics – for example, having already taken the Workshop on Molecular Evolution (http://www.molecularevolution.org/) or equivalent coursework or experience.

Computing: Prior experience with either Perl or Java; or, having read and studied the recommended books on either language (see web site). Students will be using Mac OSX computers in the course, so should have experience with basic Unix shell commands.

FEES Tuition is $500.00. Housing is $440 for single occupancy, $220 for double occupancy in housing provided at Duke University. Travel awards of up to $620 each are available to subsidize travel expenses for applicants from underrepresented groups.

HOW TO APPLY Students may apply through the website (www.nescent.org/ summer_course). You will be asked to provide a resume, two references, a brief description of your computational and phylogenetic background, and your reasons for taking the course. Applications are due by April 15, 2007. International students may wish to apply for Travel awards from the Society of Systematic Biologists (due date: March 31, 2007, see website for details).

William Piel <william.piel@yale.edu>

## KansasStateU ArthropodGenomics Apr20

KSU Arthropod Genomics <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, 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: Srini 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

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## KristinebergMarineResStation Sweden SummerCourseBiodiversity

MGE Summer Course

Analysing Biodiversity & Life History Strategies

9th - 20th of July, 2007

Kristineberg Marine Research Station (KMRS), Sweden

Info doc and application at www.marine-genomics-europe.org <http://www.marine-genomics-europe.org/> Training & Education.

Deadline for application April 30, 2007

Aims

to present the diversity of animal life in the ocean and introduce the latest methods in analyzing this variation. To foster cross-over between ecological/whole-organism and molecular approaches.

Topics

Diversity of meiofauna, large data sets and genomic approaches in metazoan systematics, phylogeography of marine species, DNA barcoding and modern taxonomy, marine life cycles and larval diversity, reproductive systems in marine invertebrates, biodiversity indices and marine communities

Target group

PhD students (at least in their second year) and post docs with basic knowledge in phylo- and population genetics. This course is open to MGE members as well as non-members.

Costs; course, accommodation and meals

The course fee is paid by the MGE Network for all academics (pre and post doc). The accommodation for PhD students is also paid for by the MGE. Lunches and coffees are included in the course fee as well as the get-together (Sunday the 8th), the excursion (Sunday the 15th) and the farewell dinner (Friday the 20th). All participants pay their own travel.

General outline

We intend to introduce the participants to current topics in biodiversity research and developmental biology. The course has a rather broad focus and will concentrate on methods and applications in these fields, while less emphasis will be placed on theoretical backgrounds. Principally we will use the mornings for lectures given by experts in the field and the afternoons for practical work such as software exercises, wet labs and mini research projects in smaller groups. The goal of the projects is to get the participants in direct contact with the diverse marine fauna on the Swedish west coast and confront them with typical problems related to the analysis of patterns of diversity. The course focuses almost exclusively on marine invertebrate animals.

Application

To apply, please fill in the application form and e-mail to Ulrika Hjelm (ulrika.hjelm@kmf.gu.se), together with a 2-page CV before April 30, 2007. This information + application form can also be found on the MGE website: www.marine-genomics-europe.org <http://www.marine-genomics-europe.org/> under Training & Education.

Matthias Obst, PhD Kristineberg Marine Research Station Kristineberg 566 450 34 Fiskebäckskil Sweden Tel: +46 (0) 523 18553 Fax: +46 (0) 523 18502 Email: Matthias.Obst@biology.au.dk or matthias.obst@kmf.gu.se

homepage

http://www.kmf.kva.se/users/matthiasobst/-index.htm http://www.galathea3.dk/dk/Menu/-Forskning/Dolkhaler <http://www.galathea3.dk>

Matthias Obst <matthias.obst@kmf.gu.se>

## Lisbon Extending the Darwinian Framework Sept10

Extending the Darwinian Framework: New levels of selection and inheritance

Workshop, September 10th 2007, Lisbon.

http://www.uea.ac.uk/ ˜ e197/darwinWorkshop.html This workshop will explore the formation of new levels of selection and inheritance, the origin of the first evolutionary units and novel modes of natural selection. Recent work in a variety of fields has presented a challenge to standard gene-centric evolutionary theory. Higher-level and non-genetic sources of heredity have been discovered. Artificial selection experiments have demonstrated a response to selection of whole microbial ecosystems, with concomitant implications for the formation of new evolutionary units. These results bear important relation to long-standing questions regarding the formation of new levels of biological organisation. The debate over levels of selection has an extended history. However, given recent empirical results and outstanding unresolved issues, it again seems pertinent to ask: What can selection act on? What sources of heritable variation exist? How can selection bring about new units of selection? And how can artificial life models help to answer such questions?

Hywel Williams University of East Anglia, UK

Hywel Williams <h.williams@uea.ac.uk>

## MLBS EvolBiol

SUMMER FIELD COURSE OPENINGS STILL AVAILABLE Mountain Lake Biological Station - <http://mlbs.org/>MLBS.org Dear Biologist,

There are still openings in our summer field courses at Mountain Lake Biological Station (University of Virginia).

Summer 2007 course offerings: Ecological Applications of GIS Stream Ecology Herpetology Behavioral Ecology Plant Biodiversity and Conservation Dates, fees, descriptions, and on-line application here: <http://-mlbs.org/courses.html>http://mlbs.org/courses.html Please forward this information to students you think might be interested. Thanks for your help!

Best wishes,

Eric Nagy

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake Biological Station Research Assistant Professor, Department of Biology University of Virginia / P.O. Box 400327 Charlottesville, VA 22904-4327 USA street address: 485 McCormick Road / 238 Gilmer Hall tel: +1-434-982-5486 (+1-540-626-5227 summer) fax: +1-434-982-5626 (+1-540-626-5229 summer) cel: +1-434-906-3122 eml: enagy@virginia.edu<mailto:enagy@virginia.edu> skype: flightofthesandor web: <http://-faculty.virginia.edu/nagy>faculty.virginia.edu/nagy MLBS web page: <http://www.mlbs.org/>mlbs.org

enagy@virginia.edu

## Montana ConservationGeneticDataAnalysis Sep11-16

2nd Conservation Genetics Data Analysis Course Recent Approaches for Estimation of Population Size, Structure, Gene flow, Landscape Genetics, Selection Detection & Bioinformatics

11 - 16 September, 2007, Flathead Lake Biological Station, Montana

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 28 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program). Deadline for application is 15 June, 2007

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

Instructors:

Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, Center for Investigation of Biodiversity and Genetic Resources at the University of Porto (CIBIO), Portugal & University of Montana Albano Beja-Pereira, Center for Investigation of Biodiversity and Genetic Resources at the University of Porto (CIBIO), Portugal David Lynn, Simon Fraser University, Burnaby (Vancouver), Canada Mark Miller, Utah State University, Salt Lake, USA Jonathan Pritchard, University of Chicago, Logan, USA Mike Schwartz, US Forest Service, Missoula, USA David Tallmon, University of Alaska, Juneau, USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, Seattle, USA

Location: The course will be held at the beautiful Flathead Lake Biological Station near Glacier National Park (see ?Location? at http://popgen.eu/-congen2007/, click ?Site Map? then ?Location Map?). The International airport is 40 miles drive north of the Biological Station (see http://www.iflyglacier.com/).

Application and cost: For detailed information see http://popgen.eu/congen2007/. Accommodations and meals are included in the registration fee. Cost: $US 1,100 per person (plus $200 if payment arrives after June 15) will cover all meals, lodging, transportation to and from the airport, and a visit to Glacier National Park. Up to two reduced-cost scholarships could be available for candidates with no funding.

congen@popgen.eu

conservation genetics course <congen@mail.icav.up.pt>

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## Trento Italy AnimalPopGenet Sep6-8

It gives us great pleasure to announce that the INTERNATIONAL WORKSHOP PGAC II - Population Genetics for Animal Conservation II' will be held at the Centre for Alpine Ecology (CEA) on Monte Bondone, near Trento, Italy, September 6-8, 2007. This workshop will be hosted by CEA, in collaboration with the University of Ferrara (Department of Biology)

ALL RELEVANT INFORMATION IS AVAILABLE AT the web site http:// www.cealp.it (or send an e-mail to pgac2@cealp.it).

We would especially encourage applications for THREE FULL BURSARIES that are offered for attendance at the workshop to young doctoral or post-doctoral researchers from countries where animal conservation is particularly urgent, but severely underfunded.

Invited speakers include: Karina Acevedo-Whitehouse (Institute of Zoology, UK) Eric Anderson (NOAA Fisheries Service, Santa Cruz, USA) Jon Ballou (Smithsonian's National Zoological Park, USA) Peter Beerli (Florida State University, USA) Giorgio Bertorelle (University of Ferrara, Italy) Luigi Boitani (University of Rome "La Sapienza", Italy) Mike Bruford (University of Cardiff, UK) Armando Caballero (University of Vigo, Spain) Rob DeSalle (American Museum of Natural History, NY, USA) Oscar Gaggiotti (Université J Fourier, Grenoble, France) Ilkka Hanski (University of Helsinki, Finland) Rus Hoelzel (University of Durham, UK) Michael Hofreiter (Max Planck Institute, Leipzig, Germany) Craig Moritz (University of California, Berkeley, USA) Rasmus Nielsen (University of Copenaghen, Denmark) Stephen Palumbi (Stanford University, USA) Josephine Pemberton (University of Edinburgh, UK) Craig Primmer (University of Turku, Finland) Pierre Taberlet (Université J Fourier, Grenoble, France)

The aims of the workshop are to identify recent theoretical and methodological developments in population genetics suitable for understanding (and possibly solving) problems of animal conservation, to discuss recent solutions to past and present controversies in conservation genetics, and to allow theoretical and applied biologists to meet and discuss advanced methods of data analysis and software tools.

The scientific committee: Giorgio Bertorelle, University of Ferrara, Italy Mike Bruford, University of Cardiff, UK Claudio Chemini, CEA, Viote del Monte Bondone, Trento, Italy Heidi Hauffe, CEA, Viote del Monte Bondone, Trento, Italy Elena Pecchioli, CEA, Viote del Monte Bondone, Trento, Italy Cristiano Vernesi, CEA, Viote del Monte Bondone, Trento, Italy

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## UBath MicrobialMathModels Jun5-7

EPSRC Workshop:

Mathematical Models and Experimental Microbial Systems: Tools for Studying Evolution, 5-7 June 2007, University of Bath, UK

This EPSRC funded workshop is intended to provide an arena for much-needed interaction between microbial experimentalists, theoretical biologists and mathematicians focused around the following evolutionary questions:

1. What determines species diversity?

2. How did cooperative behaviour evolve?

Based around the above questions the workshop days will be divided into the following three themes:

1. Consumer-resource experimental systems and diversification in constant environments.

2. Host-pathogen experimental systems and diversification in non-constant environments.

3. Cooperative experimental systems and evolution of cooperation.

For more details and to register please go to:

http://www.bath.ac.uk/math-sci/bics/mmems/

For all scientific enquiries contact Ivana Gudelj (i.gudelj@maths.bath.ac.uk). For administrative enquiries e-mail:

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## UManchester QuantEvolGenetics

We are starting a new, one-year, MSc course in Quantitative Evolutionary Genetics at the University of Manchester in September 2007. We expect to be able to fund some studentships on this course: full studentships (tuition fees and stipend) for UK-based students or partial studentship (tuition fees only) for EU students.

The course is aimed at graduates in biology who would like to specialise in evolutionary genetics and at graduates in the physical sciences (maths, computer science, etc) who would like to apply their numeracy skills to some exciting and challenging topics in evolutionary genetics. The course contains taught components: on population and evolutionary genetics, programming, statistics, etc, but a substantial portion of the degree is research-based involving a long and a short research project. Projects will be offered by staff in the Faculty of Life Sciences working on a wide range of evolutionary topics (see http://www.ls.manchester.ac.uk/research/themes/evolution/ and http://www.ls.manchester.ac.uk/research/themes/bioinformatics/) for some indication of the range of topics covered). There is also the opportunity to work on projects with staff from Computer Science and Mathematics.

Anyone wishing to apply for this MSc course should send their CV by email to Cathy Walton (Catherine.walton@manchester.ac.uk) as soon as possible. Please also feel free to ask me further questions about the course on the same email address.

I would very much appreciate it if you could bring this course to the attention of suitable prospective students.

Many thanks.

Cathy Walton University of Manchester

Catherine.Walton@manchester.ac.uk

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# Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX 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 formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

# Afterward

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