
E v o l D i r

August 1, 2010

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

Foreword

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

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

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Conferences

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Barcelona Biodiversity Oct1-2

Dear colleagues,

You are kindly invited to attend the two-day, international symposium “*Frontiers in Biodiversity: a Phylogenetic Perspective*”, which will be held in Barcelona, Spain, the 1st and 2nd of October 2010.

The symposium is co-organized by the Biodiversity Research Institute of the University of Barcelona (IrBio), the Institute of Evolutionary Biology (IBE, CSIC-UPF) and the Zoological Systematics and Evolution research group on the occasion of *the International year of Biodiversity*.

These are exciting times to conduct research on Biodiversity. The last years have witnessed the development of new theoretical, computational and technological tools for Biodiversity research at an unprecedented rate. The symposium aims to explore the impact of some of these new conceptual and methodological approaches on our current understanding of the origins and the processes that shape Biodiversity. Research on Biodiversity has multiple facets. In this symposium we will emphasize the perspective and contributions coming from the phylogenetic and phylogeographic front. The symposium will focus on a selected list of “hot topics” under the headings of Statistical phylogenetics and phylogeography, Biogeography, Time, Key Innovations, Adaptive radiations, Diversification, Community phylogenetics and Phylogenomics.

The symposium will consist of two morning sessions with invited talks and an afternoon poster session open

to participants. The symposium will close with a round table with the invited speakers on the topic “*Biodiversity in the omics era*”. The list of confirmed speakers include Frédéric Delsuc (Université Montpellier II, France), Steven W. Kembel (University of Oregon, US), L. Lacey Knowles (University of Michigan, US), Brian R. Moore (University of California, Davis, US), Daniel L. Rabosky (University of California, Berkeley, US), Isabel Sanmartin (Real Jardín Botánico, CSIC, Spain) and Ziheng Yang (University College London, UK).

The symposium will be held at the *Institute of Catalan Studies (/Institut d’Estudis Catalans/, IEC),* located at the heart of Barcelona’s old town, in the 17th century Santa Creu Hospital building.

The registration fee is 80EUR. There is no deadline for registration and poster abstract submission, but attendance will be limited to *100* *participants* and the number of posters to *30*. Both registration and poster contributions will be accepted on *first-come, first-served* basis, and will close once we reach the maximum number of contributors.

Detailed information, including conference titles, can be found on the conference website:

<http://www.phylofrontiers2010.com/> We invite you to visit the site and register for the conference and submit your contribution.

Come and join us!

The organizing committee: Miquel A. Arnedo, Marta Riutort and Julio Rozas (Biodiversity Research Institute, University of Barcelona), and Salvador Carranza, Jose Castresana and Ignacio Ribera (Evolutionary Biology Institute, CSIC-University Pompeu Fabra)

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Miquel A. Arnedo

Biodiversity Research Institute UB Departament Biologia Animal Universitat de Barcelona Av. Diagonal 645, E-08028 Barcelona, Spain Tel. +34 93 403 4808 Fax. +34 93 403 5740 email: marnedo@ub.edu

<http://www.marnedo.net> Visit the ATOL:Phylogeny of Spiders web page at: <http://research.amnh.org/-atol/files/index.html> Visit the PANCODING web page at: <http://www.pancoding.org/index.php> Miquel Arnedo <marnedo@gmail.com>

BathU SexualSelection Sep1-4

Dear friends and colleagues

“New directions in sexual selection research: unifying behavioural and genomic approaches” Bath University September 1st to 4th 2010.

Conference website: http://www.ert-conservation.co.uk/Conference_home.htm (1) Conference programme:

The final programme of speakers (38 oral presentation and 4 keynotes) can now be seen on our website: <http://www.ert-conservation.co.uk/Programme.htm> (2) Final call for registration:

The deadline for registration at the conference is Wednesday 21st July. To book your place complete the attached booking form or go to: <http://www.ert-conservation.co.uk/Registration.htm> Places have gone fast so please book your place as early as possible. Funding for accommodation, meals and registration fees, is available for delegates from eastern Europe through monies from a Framework 6 EC project called INCORE (see conference website).

We would be extremely grateful if you could forward this message to colleagues who you think might be interested in attending the conference.

We very much hope you will be able to join us in September and look forward to welcoming you to Bath.

With best wishes.

Dr Mark O’Connell, on behalf of the conference science committee.

This conference has been generously sponsored by the Genetics Society.

Fribourg AdaptationGenomics Sep2-3

Evolutionary and ecological genomics of adaptation Abstract registration extended until 10 July

Symposium: 2-3 September 2010

Fribourg, Switzerland

Organizers: Christoph Haag and Christian Lexer, University of Fribourg Laurent Excoffier, University of Bern

Confirmed invited speakers:

- * Roger Butlin (University of Sheffield, UK)
- * Adam Eyre-Walker (University of Sussex, UK)
- * Hopi Hoekstra (Harvard University, USA)
- * Magnus Nordborg (Gregor Mendel Institute, Vienna, Austria)
- * David Reich (Harvard University, USA)
- * Outi Savolainen (University of Oulu, Finland)

Natural environments differ in many biotic and abiotic aspects, and the way in which animals and plants adapt to these different environments is one of the fundamental questions of ecology and evolutionary biology. In recent years, new genetic and genomic methods have been developed, making it possible to discover the genes involved in such adaptations. This has facilitated many new exciting insights, for instance into

- * the functional mechanisms of adaptation
- * the molecular evolution of adaptively important genes
- * the genetic architecture of evolving traits
- * the convergent evolution of similar phenotypic traits by distinct mutations
- * the ecology of speciation

We organize a symposium bringing together six invited speakers including top empirical and theoretical evolutionary biologists and a number of younger researchers to discuss recent developments in this fast developing field.

Deadline for contributed talk or poster submission: *10 July 2010* Deadline for registration without presentation: 15 August 2010

For more information on program, travel, venue, registration etc. please visit: http://www.unifr.ch/biol/-ecology/adaptation_genomics/ Sponsored by: 3ème

Cycle Romand en Sciences Biologiques, Conférence Universitaire de Suisse Occidentale (CUSO), University of Fribourg, University of Bern

Christoph Haag, Christian Lexer, Laurent Excoffier
christoph.haag@unifr.ch

— Christian Lexer Associate Professor of Evolutionary Biology University of Fribourg, Department of Biology Unit of Ecology & Evolution Chemin du Musée 10, CH-1700 Fribourg, Switzerland Tel (office) +41 (0)26 300 8868 Tel (lab): +41 (0)26 300 8895 Fax: +41 (0)26 300 9698 Mobile: +41-77-4720-789 Email: christian.lexer@unifr.ch Web: <http://www.unifr.ch/biol/-ecology/lexer/index.html> christian.lexer@unifr.ch

Heraklion Biogeography Jan7-11

The 5th Biennial Conference of the International Biogeography Society Heraklion, Crete, Greece; 7-11 January, 2011

Registration opens late-August 2010.

For more information, see <http://www.biogeography.org/html/Meetings/index.html>

. The meeting is built around four successive SYMPOSIA (8th & 9th January) on broad foundational and cutting-edge topics and approaches in biogeography and macroecology, each with a suite of leading international scientists and *openings for contributed papers*:

1. Mediterranean Biogeography: Where History Meets Ecology Across Scales (Organizers: Spyros Sfenthourakis & Remy J. Petit).
2. New Perspectives on Comparative Phylogeography V Novel Integrative Approaches and Challenges (Organizers: Ana Carnaval & Mike Hickerson).
3. Biogeography and Ecology: Two Lenses in One Telescope (Organizers: Dave Jenkins & Robert E. Ricklefs).
4. Analytical Advancements in Macroecology and Biogeography (Organizers: Alexandre Diniz-Filho & Carsten Rahbek).

The meeting also has six sessions of CONTRIBUTED PAPERS (10th January) on key topics: i. Island biogeography ii. Climate change biogeography iii. Conservation biogeography iv. Palaeoecology v. Marine biogeography vii. Hot topics in Biogeography.

Dr. Robert E. Ricklefs will give a keynote lecture after receiving the Alfred Russel Wallace Award, recognizing his lifetime of outstanding contributions to biogeogra-

phy.

In addition, before the meeting, on 7th January, three WORKSHOPS will held: Spatial Analysis in Macroecology, Phylogenetic Analysis in Macroecology, and Communicating Biogeography.

On 7th & 11th January arranged FIELD EXCURSIONS will visit a number Cretes most exciting historic and biogeographic locations.

The INTERNATIONAL BIOGEOGRAPHY SOCIETY (IBS; <http://www.biogeography.org/>) is a non-profit organization, founded in 2000, with the mission to:

- Foster communication and collaboration between biogeographers in disparate academic fields.
- Increase both the awareness and interests of the scientific community and the lay public in the contributions of biogeographers.
- Promote the training and education of biogeographers so that they may develop sound strategies for studying and conserving the worlds biota.

Michael Dawson <dawsonmartin@sbcglobal.net>

Hilo Hawaii Conservation Genomics Jul26-28 3

July 1 is the online Registration Deadline for the 2010 AGA Symposium, "Conservation Genomics".

After July 1st, contact Brad Shaffer to inquire if space is still available: <mailto:hbshaffer@ucdavis.edu>

Symposium details and registration at: <http://www.theaga.org/2010> AGA meetings focus on a single topic and last for 2.5 days. This year's topic is Conservation Genomics, and will include talks by a series of genomicists and conservation biologists, including those who are already shaping this emerging discipline. Our goal is to provide a focused forum for discussion, brainstorming, and development of collaborative efforts that leverage emerging genomic resources for applications in conservation biology.

To encourage broad attendance, we have kept registration low (\$150), which includes an opening mixer and evening luau. We have negotiated very reasonable hotel accommodation in Hilo as well as the dormitory space at UH.

Please join us- Hilo is an amazing setting, and we look forward to an engaging, enlightening three days.

Any questions, contact:

Brad Shaffer <mailto:hbshaffer@ucdavis.edu>, President of the AGA, or

Anjanette Baker <mailto:agajoh@oregonstate.edu>, Managing Editor, Journal of Heredity
agajoh@oregonstate.edu

KansasCity Genomics Nov5-7

8th Ecological Genomics Symposium, Nov 5-7, 2010, in Kansas City

REGISTRATION IS NOW OPEN to attend the 8th Annual “Genes in Ecology, Ecology in Genes” Symposium on November 5, 6, and 7, 2010, in Kansas City.

The Ecological Genomics Symposium will convene in the historic Muehlebach/Marriott Hotel in downtown Kansas City Friday evening at 6:00 p.m. and conclude on Sunday at noon. For a brochure and complete information regarding poster abstract submission, registration and hotel reservations, please visit our Symposium website, <http://ecogen.ksu.edu/symp2010>. Ecological Genomics is a field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context.

We have an outstanding lineup of speakers for the 2010 Symposium and we encourage you to attend!

PLENARY SPEAKER: +Hopi Hoekstra, Harvard University, “Digging for genes that contribute to behavioral evolution”

FEATURED SPEAKERS: +Seth R. Bordenstein, Vanderbilt University, “Microbial symbiosis and mobile genetic elements” +Maitreya Dunham, University of Washington, “Comparative functional genomics in yeasts” +Audrey P. Gasch, University of Wisconsin-Madison, “Natural variation in stress sensitivity and genomic expression in *Saccharomyces cerevisiae*” +Corbin Jones, The University of North Carolina at Chapel Hill, “Genetics of host specialization in *Drosophila*: Insights into the interplay of speciation and adaptation” +John K. McKay, Colorado State University, “Evolutionary genetics of local adaptation in *Arabidopsis* and beyond” +Marilyn Roossinck, The Samuel Roberts Noble Foundation, “Plant virus biodiversity and ecology” +Michael J. Wade, Indiana University, “The plasticity load: The cost of flexibility in

a variable environment” +Anna E. Whitfield, Kansas State University, “Dissecting the molecular interplay between plant viruses and their arthropod vectors”

POSTER ABSTRACTS: Please submit your poster abstract by e-mail by Friday, October 8, 2010. Abstract submission guidelines are available on the website. Poster sessions will be held on Friday night and Saturday. Poster topics should be related to the field of Ecological Genomics. A LIMITED NUMBER OF SUBMITTED POSTER ABSTRACTS WILL BE SELECTED FOR ORAL PRESENTATIONS.

STUDENT TRAVEL FELLOWSHIPS: A limited number of fellowships will be awarded to assist graduate students to attend the Symposium. Students applying for these fellowships must submit a poster abstract for presentation. Additional guidelines and application information is available on the website. The deadline to apply is 9/21/10.

INFORMATION will be posted on our website, <http://ecogen.ksu.edu/symp2010>, as details are finalized. Please share this announcement with colleagues and students. If you have questions, please contact us at (785) 532-3482 or dmerrill@k-state.edu.

FUNDING for this symposium is provided by Targeted Excellence at Kansas State University and the National Science Foundation.

CORPORATE SPONSORS: JMP Genomics and Roche-NimbleGen.

DEADLINES: Tuesday, 9/21/10, Student travel fellowship application materials are due. Friday, 10/8/10, Registration deadline at early bird rates. Friday, 10/8/10, Poster Abstracts are due for oral presentation consideration. Friday, 10/8/10, Hotel Rooms must be reserved to receive reduced group rate. Wednesday, 10/27/10, Poster Abstracts are due if NOT being considered for oral presentation.

Ecological Genomics Institute Directors: Dr. Loretta Johnson Dr. Michael Herman Kansas State University, Division of Biology Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, <http://ecogen.ksu.edu>

ECOLOGICAL GENOMICS INSTITUTE Kansas State University Biology, 104 Ackert Hall Manhattan, KS 66506-4901 (785) 532-3482, <http://ecogen.ksu.edu>

Ecological Genomics <dmerrill@ksu.edu>

Marseilles 14thEBM Sep21-24 2

Dear All,

We are pleased to inform you that the program of the 14th Evolutionary Biology Meeting at Marseilles, Marseilles, France, 21-24 september 2010 is now available on our web site: <http://sites.univ-provence.fr/evol-cgr>
Few spots are still available for poster presentation.

Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

UOttawa RECOMB Oct9-11 2

CALL FOR POSTERS, EARLY REGISTRATION and APPLICATION FOR TRAVEL SCHOLARSHIPS

Eighth Annual RECOMB Satellite Meeting on Comparative Genomics October 9-11, 2010 University of Ottawa <http://recombcg.uottawa.ca/recombcg2010/>
Comparison of related genomes offers enormous inferential power, revealing a wealth of knowledge about genome evolution itself and about genetic function and cellular processes. As the number of fully sequenced genomes grows, so do the opportunities and challenges for computational comparative genomics. This workshop brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and novel experimental results. The program includes both invited speakers and contributed talks.

KEYNOTE SPEAKERS

Brenda J. Andrews (University of Toronto) Andrew G. Clark (Cornell University) Nicolas Corradi (University of Ottawa) Jan Dvorak (University of California at Davis) Aoife McLysaght (University of Dublin) Nicholas Putnam (Rice University)

PROGRAM

24 contributed talks selected by the program committee; see <http://recombcg.uottawa.ca/recombcg2010/>

programInfo.html POSTERS

Poster abstracts for this workshop are welcomed on any theoretical and/or empirical approach to genome-wide comparison such as genome evolution, algorithms for genome rearrangement, comparative tools for assembly, gene identification or annotation, comparison of functional networks, genomic variation in humans and model organisms, cancer genomics, duplication patterns of genes, segments and whole genomes, and comparative epigenetics.

Abstracts should be composed on the LaTeX template downloaded from <http://recombcg.uottawa.ca/recombcg2010/posters.html>. The compiled pdf of the abstract should be at most one page long, including any tables, figures, and bibliography. Send the pdf file to Eric.Tannier@inria.fr

The deadline for poster abstract submission is September 13, 2010, but early submission is encouraged. We will make acceptance decisions on posters as soon as possible after we receive them, and in any case before the early registration deadline of September 17.

CONFERENCE SITE

The workshop will be held on the campus of the University of Ottawa beside the downtown area. Ottawa is served by direct flights from New York, Philadelphia, Chicago, Washington, Detroit, London, Frankfurt and many Canadian cities. The dates of the workshop coincide with the three-day Canadian Thanksgiving weekend, around the peak time for autumn foliage colour.

EARLY REGISTRATION and ACCOMMODATION

Registration is now open at <http://recombcg.uottawa.ca/recombcg2010/register.html>

Accommodation information is available at <http://recombcg.uottawa.ca/recombcg2010/logistics.html>

TRAVEL FELLOWSHIPS

A limited number of partial travel scholarships will be available to student and postdoctoral registered participants, with first priority to those presenting papers, and second priority to those presenting posters. Deadline for applications is September 13, 2010. See <http://recombcg.uottawa.ca/recombcg2010/scholarship.html>

KEY DATES

Travel scholarship applications September 13, 2010

Poster submission deadline September 17, 2010

Notification of poster acceptance September 21

CONTACT

Address any questions to the conference chair or the program committee chair: David Sankoff

sankoff@uottawa.ca Eric Tannier Eric.Tannier@inria.fr
David Sankoff <sankoff@uottawa.ca>

WoodsHole CytochromeP450Biodiversity Oct3-7

The abstract deadline for oral presentations to the International Symposium on Cytochrome P450 Biodiversity and Biotechnology has been extended to *August 15th*

Come visit Woods Hole, a unique scientific village on beautiful Cape Cod, Massachusetts!

Original announcement:

10th International Symposium on Cytochrome P450 Biodiversity and Biotechnology, 3-7 October 2010 in Woods Hole, Massachusetts, USA.

This symposium addresses all aspects of cytochrome P450 biodiversity, biotechnology, and evolution. The overall goal of this 10th symposium is to foster a synthesis of understanding of cytochrome P450 (CYP) structural and functional evolution, and new directions

in application of this knowledge in environmental assessment, remediation, and synthesis of new potential drugs.

Sessions in this meeting include evolutionary and mechanistic comparisons among available P450 structures, functional comparisons among microbial, insect and plant P450s in synthetic and detoxification pathways, as well as bioengineering of P450 catalytic sites for technological and environmental applications.

Presentations (talks and posters) by graduate students and post-docs are strongly encouraged.

Abstract Submission and Registration are now open ##### <http://www.whoi.edu/-conferences/p450> Abstract Deadline extended to August 15, 2010

A list of plenary speakers has been posted. We hope to welcome you to Woods Hole in October!

Please share this announcement with students and colleagues.

John Stegeman and Jed Goldstone, Woods Hole Oceanographic Institution Mary Schuler and Stephen Sligar, University of Illinois, Urbana-Champaign
p450@whoi.edu

jedgold@gmail.com

GradStudentPositions

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Muenster EvolutionStressImmunity	12	ULethbridge AvianPopGenetics	19
Munich EvolutionaryProteomics	13	UManchester Evolution of social evolution	20
NewZealand EvolBiol	13	UMuenchen PlantEvolutionaryGenetics	20
NewZealand MarineMolEvol	13	UMunich PlantEvolutionaryGenetics	21
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Adelaide Australia AncientDNA

PhD and Postdoc opportunities at the Australian Centre for Ancient DNA, Adelaide, Australia

We are looking for interested graduate students, who are highly motivated and enjoy independent and unusual research in the general areas below. An interest in evolution and natural history are key requirements, and a background in any of the following would be useful: evolution, genetics, molecular biology, bioinformatics/computing, chemistry/biochemistry, palaeontology, archaeology, and anthropology.

1. Environmental Genomics (including 1-2 postdoc positions) New genomic approaches for Biodiversity studies of Australian Soils, Water, Grasses, Forensic samples and Antarctic biota A number of PhD positions are available in a large-scale project to apply high throughput sequencing approaches to the analysis of environmental samples and develop a new range of methods to perform biodiversity surveys, taxonomic discovery, and environmental impact reports. The project will employ multiplexed PCR, 2nd/3rd Gen Sequencing, Bioinformatics and Phylogenetics to develop novel systems for rapid and accurate biodiversity assessment. Key topics within the project are the analysis of Australian soils, natural and re-use water supplies, Australian native grasses, Antarctic biota, and forensic material. A strong molecular Biology and/or bioinformatics background is required. The project is a \$1M Australian Research Council-industry partnership.

1-2 postdoc positions will also be available for this project, and will carry supervisory responsibilities for the PhD projects. It is anticipated that one position will be oriented towards data generation, and another towards bioinformatics/database analysis.

2. Evolutionary Bioinformatics This project will apply the latest evolutionary bioinformatics methods to the study of ancient and modern DNA generated through new genomics and 3rd Gen sequencing data. Study species include a wide range of ancient humans, domestic animals, environmental samples, and broader evolutionary projects such as marsupial evolution, and extinct species such as thylacines, mammoths and other megafauna. The datasets will include genomic sequencing projects, SNP arrays and multigene phylogenies.

3. Ancient human DNA and Domestication genomics Several project opportunities are available to work with ancient humans, animals and plants. These projects will use advanced new genomic techniques to study ancient populations and species, and focus on evolutionary history, archaeology/anthropology, and the study of domestic/commensal animals to trace human movement, and identify and analyse genetic loci under selection. The methods used will include SNP and capture array approaches, and a strong expertise in molecular biology and bioinformatics is required. Recent studies have examined Neolithic farmers in Europe, pre-Columbian South Americans, and bovinds, chickens, pigs, and rats from around the world.

International Students wishing to study at The University of Adelaide in 2011 should check the available scholarship opportunities (<http://www.adelaide.edu.au/graduatecentre/scholarships/postgrad/international/>) as they provide payment of full tuition fees plus an annual living allowance of approximately AUD\$21,000 tax free. Note the closing date for international scholarship enrolment 31st August, 2010 or 30th October for Australian/NZ applicants. Both the Australian Department of Immigration and University of Adelaide expect international applicants to meet English Language Proficiency (ELP) requirements. The ELP is based on high scores in IELTS (International English Language Testing System) or TOEFL (Test of English as a Foreign Language). For further information please refer to <http://www.international.adelaide.edu.au/admission/> or http://www.adelaide.edu.au/publications/pdfs/inter_pgcw_en10.pdf. Expressions of interest from applicants with strong graduate marks, a good TOEFL score, and a background in evolution/bioinformatics/molecular biology are encouraged. Please contact the following supervisors and provide your CV/resume:

Prof. Alan Cooper (alan.cooper@adelaide.edu.au) Dr. Wolfgang Haak (wolfgang.haak@adelaide.edu.au) Dr. Bastien Llamas (bastien.llamas@adelaide.edu.au)

Australian Centre for Ancient DNA School of Earth & Environmental Sciences Darling Building THE UNIVERSITY OF ADELAIDE SA 5005 AUSTRALIA Telephone: +61 8 8303 3952 Facsimile: +61 8 8303 4364 <http://www.adelaide.edu.au/acad/> -

Prof. Alan Cooper ARC Federation Fellow Director, Australian Centre for Ancient DNA

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

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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>

Barcelona 2 GeneNetworkEvolution

Universitat Autònoma de Barcelona Dep of Genetics and Microbiology

We are looking for two students, preferably a biologists, to start two grants for two PhD in systems biology and/or evo-devo about:

-Gene network simulation in pattern formation, morphogenesis and morphological evolution.

or/and

-Comparative embryonic morphometrics

One of the current challenges of evolutionary biology is to understand how genetic variation leads to specific morphological variation (the g-p map) and how that process affects the direction of morphological change in evolution. Our group is devoted to address this question by using gene network models.

Programming skills or a willingness to acquire them is required.

The grants are provided by the Spanish ministry of science and innovation. One of them is for 4 years and the other is for 3 years extendable to an additional year.

The exact topic of the theses would be discussed in detail after interview.

For an outline of the groups research: http://bioinf3.uab.cat/grupgbe/index.php?option=com_content&task=view&id=64&Itemid=104 For further inquiries:

isaac.salazar@uab.cat

Genomics, Bioinformatics and Evolution Group

Article exemple:Salazar-Ciudad I, Jernvall J.A computational model of teeth and the developmental origins of morphological variation. Nature. 2010 Mar 25;464(7288):583-6.

The Autonomous University of Barcelona is a public university located 20 kms north of Barcelona centre. It

has its own “green” campus. It is the university with more PhD students (in proportion of its size) in Spain.

Isaac Salazar Ciudad <Isaac.Salazar@uab.cat>

EPFL Switzerland LandscapeGenomics

A PhD position is available at Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland, Laboratory of Geographic Information Systems (LASIG) (4 years)

Topic: Very High Resolution Digital Elevation Models (VHR DEMs) and multiscale analysis using the wavelet transform: an application to landscape genomics *Key-words*: GIS, spatial analysis, DEMs, landscape genetics, landscape genomics, natural selection, adaptation, signal processing, wavelet transform, structure tensors *Supervisors*: Dr Stéphane Joost (LASIG, EPFL); Prof Dimitri Van De Ville (Medical Image Processing Lab, EPFL & University of Geneva); Prof François Golay (LASIG, EPFL)

Description of the PhD project Digital Elevation Models (DEMs) are able to provide a diversity of geomorphometric (slope, aspect, curvature), hydro-morphometric (e.g. wetness), and also climatic (e.g.solar radiation) predictors. But DEMs are under-exploited environmental variables in landscape genetics and landscape genomics. In particular, increasingly available Very High Resolution DEMs (1 m for XY coordinates, and ~0.5 m for Z) acquired with LIDAR (Light Detection And Ranging) technology, are able to generate high-resolution habitat predictors (Andrew & Ustin 2009), and make it possible to implement a novel multiscale analysis. A recent PhD thesis (Kalbermaten 2010) showed that the application of the wavelet transform (signal processing theory) is a clever way to generalize topography.

A powerful feature of Wavelets applied to DEMs is the capacity to decompose DEMs into multiscale spaces. This permit to come closer to what happens in nature as regards the concept of scale, and to replicate at best the spatial continuum constituting landscapes.

Moreover, wavelet coefficients can be interpreted as pixel value changes (gradients) in a local neighbourhood (a window of 3x3 pixels for example) on the basis of which it is possible to construct 3 additional DEM derivatives (structure tensors): the energy of the local

gradient, the dominant orientation of local structures, and coherency (indication of isotropy/anisotropy).

The goal of the thesis is to apply the wavelet transform approach and to use the new DEM variables (second order derivatives) described hereabove in the context of different case studies (plants, wild and domestic animals) implementing the landscape genomics approach (see Hanotte et al. 2010) to detect loci possibly under natural selection (Joost et al. 2007; Manel et al. 2010). This research context is ideal to address a fundamental issue often referred as to "What is the best spatial scale to study adaptation" or "at which spatial scale does adaptation operate?"

Requirements for the position Master in Science (biology, environment, computer & communication, etc.), excellent skills in GIS and spatial analysis, excellent skills in population genetics, background in landscape ecology/landscape genetics, good mathematical background, basics in signal processing, good knowledge of statistics, initiative, high motivation, teamwork, fluency in english, french is an advantage (official language in Lausanne area).

Please send applications with CV, one-page statement of research interests, and the names and addresses of two referees as a single PDF file by email to: Stephane.Joost@epfl.ch Deadline for applications: September 1, 2010.

Start of position: as soon as possible. *Salary*: Year 1: CHF 50'500, Year 2: CHF 52'500, Year 3: CHF 54'500, Year 4: 56'500 (according to EPFL's PhD salary standards)

For further details and questions, send an email to: Stephane.Joost@epfl.ch

References - Andrew ME, Ustin SL (2009) Habitat suitability modelling of an invasive plant with advanced remote sensing data. *Diversity and Distributions*, 15, 627–640. - Kalbermatten M. (2010) Multi-scale analysis of high resolution digital elevation models using the wavelet transform. Ph.D. Thesis, EPFL, no 4610. [<http://library.epfl.ch/theses/?nr=4610>] - Hanotte O et al. (2010) Time to tap Africa's Livestock Genomes < <http://www.sciencemag.org/cgi/content/full/328/5986/1640> >, *Science*, 5986:1640-1641 - Joost S, Bonin A, Bruford, M.W., Després, L., Conord, C., Erhardt, G., Taberlet, P., (2007) A Spatial Analysis Method (SAM) to detect candidate loci for selection: towards a landscape genomics approach to adaptation, *Molecular Ecology*, 18:3955–3969. - Manel S, Joost S, Epperson BK, Holderegger R, Storfer A, Rosenberg MS, Scribner K, Bonin A, Fortin M-J (In press) Perspectives on the use of landscape genetics to detect ge-

netic adaptive variation in the field, *Molecular Ecology*
Dr Stephane Joost GIS Research Laboratory (*LASIG*) Institute of Environmental Engineering (IIE), ENAC Faculty Ecole Polytechnique Federale de Lausanne (EPFL)

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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>

ImperialCollegeLondon ComputationalBiol

GlaxoSmithKline sponsored PhD Studentship
In Computational Biology

Department of Computing, Imperial College London

PhD Studentship: Applications are invited for an EPSRC/CASE funded PhD studentship supervised by Dr. NataÅa PrÅ¾ulj at Imperial College*. *CASE studentships are awarded jointly to academic and industrial partners, and provide an exciting opportunity to work with cutting edge data and leading scientists from both research environments. The successful applicant will work both at Imperial College and at the GlaxoSmithKline (GSK) Computational Biology group at Stevenage. Eligible applicants will receive an untaxed bursary of Â£15,200 per annum, UK/EU fees and a bursary top-up provided by GSK. Details regarding student eligibility can be found at <http://www.epsrc.ac.uk/PostgraduateTraining/StudentEligibility.htm> Fixed Term for 3 years, starting October 2010.

The PhD studentship, under the supervision of Dr. NataÅa PrÅ¾ulj and in collaboration with scientists at GlaxoSmithKline in Stevenage (UK), will address the question of integrating different types of large scale biological data with the aim to redefine disease classification and relationships between diseases. Most diseases have been defined a century or more ago. The question is whether the old classification holds in the light of modern systems-level data, including genetics data (e.g. genome-wide association studies), genomics data (e.g. microarray), protein-protein interaction networks, metabolic networks, phenotypic data etc. For example, cancer types are being redefined with molecular data. Furthermore, there is evidence that many

complex seemingly unrelated diseases, such as cancer, diabetes and Alzheimer's, originate from a disruption in metabolism, raising the possibility that disease (phenotypes) can be clustered according to common mechanisms. Thus far, diseases have been classified focusing locally only on the organ the most affected by the disease. Instead, the research project will consider diseases as systems-level disorders of the entire cellular system that includes genetics, molecular interactions and metabolism, and that affect every cell of the body, rather than through just symptoms that they are presenting. Network science approach will be taken to present various slices of systems-level biological information in an integrated way that will allow mining of these complex data. This approach to biological data network integration will lead to the design of network-based mathematical models and computational tools aiming to improve disease classification. The final goal is to improve biological understanding, get insights into disease and, in collaboration with GlaxoSmithKline, improve the disease indication(s) decision for therapeutics. The student will spend a minimum of 3 months at GlaxoSmithKline during the PhD, during which time GlaxoSmithKline will cover any additional expenses (e.g., commuting).

Imperial College is ranked in the top five universities of the world, according to the 2009 Times Higher Education World University Rankings. It has particular strength in Engineering, Natural Sciences, Life Sciences and Biomedicine, and was ranked the 6th in the world in technology, the 10th in the world in natural sciences, and 17th in the world in life sciences and biomedicine in the Times Higher Education World University Rankings, October 2009. The *Department of Computing* is one of the largest computing departments in the UK and is a world leader in academic research in computer science. The department has been awarded the top rating (5*) in each of the Research Assessment Exercises undertaken by the Higher Education Funding Council for England (HEFCE). There are over sixty academic staff actively involved in research, creating a lively and stimulating atmosphere. The department also enjoys strong links with UK industry, which helps to ensure that its research and teaching is well informed and relevant to the needs of society. Imperial College London has active research in *computational, systems, and synthetic biology* and related scientific disciplines. Over 60 academic appointments were made over the past decade at the interface between the life and physical sciences. The College also has substantial high performance computing resources. The project will interface with related programs and institutes at Imperial College, including the *Institute of Systems

and Synthetic Biology*, the *Centre for Bioinformatics*, and the *Centre for Integrative Systems Biology (CISBIC)*. Informal inquiries can be directed to: Dr. Natasha PrÅ¼ulj (natasha@imperial.ac.uk).

Applicants should have at least a distinction or first in a Masters level degree in computer science, or an equivalent degree in

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Jagiellonian Exeter VU Amsterdam Wageningen Evolution Ecology

EvolDir -for announcement section
Graduate positions: Jagiellonian_Exeter_VU Amsterdam_Wageningen.Evolution Ecology

An international scientific consortium including: Jagiellonian University (coordinator), University of Exeter, VU Amsterdam and Wageningen University, is opening applications for 7 PhD positions in evolutionary biology, ecology, ecotoxicology and genetics within International PhD Studies Programme awarded to the consortium by the Foundation for Polish Science.

Proposed topics of PhD projects:

Accumulation of mutations and the robustness of genetic systems

Interaction between natural and sexual selection in adaptation to novel, stressful environment

Monitoring of metal availability thresholds causing changes in insect larval community structure in metal-contaminated stream systems

Impact of industrial pollution (heavy metals) on stoichiometry of soil-litter food webs in forests

Role of anti-competitor toxins in the origin and maintenance of diversity in structured microbial populations

Relationship between the diversity of soil microbial communities and their resistance to different stressors

Metabolic performance and susceptibility to pollution in voles: an experimental evolution approach

Full description of the program, containing a detailed description of PhD projects can be found at:

<http://www.eko.uj.edu.pl/MPD> The studentships will be funded for 4 years, starting from 1st October 2010. The students will receive stipends from Foundation for Polish Science (3000 PLN/month during stay in Poland, and 5000 PLN/month during stay abroad).

Application deadline: 8 September 2010

Programme co-financed by European Union within the Innovative Economy Operational Programme 2007-2013

Prof. Jacek Radwan Institute of Environmental Sciences Jagiellonian University ul. Gronostajowa 7 30-387 Krakow

tel. +48 12 664 6849 www.eko.uj.edu.pl/radwan Jacek Radwan <jacek.radwan@uj.edu.pl>

2600 Euros. Deadline for submission of applications is the 3rd of September 2010. Interested candidates are strongly encouraged to make informal contact with Guila Ganem (guila.ganem@univ-montp2.fr) a week before the deadline. Applicants should send a 1-2-page application letter stating research interests and date of availability, a detailed CV, and the names and contact details of at least two referees, preferably by email.

– Dr. Carole Smadja Chargé de recherche CNRS à CNRS researcher Institut des Sciences de l'Évolution (ISEM), Montpellier – Tel: +33 (0)4 67 14 46 31 Postal address: ISEM, cc065, Université Montpellier 2, 34095 Montpellier cedex 5, France Web: <http://www.carole-smadja.staff.shef.ac.uk/> Carole.Smadja@univ-montp2.fr

Montpellier Adaptive Speciation

A PhD position is available at the Institut des Sciences de l'Évolution (Montpellier, France) to work with Guila Ganem on the causal and proximal mechanisms of adaptive speciation in the house mouse (*Mus musculus*). The project combines behavioural, biochemical, chemical and genetic approaches to understand the evolution of an olfactory-based species mate recognition system. Specifically, the PhD student will test for the role of competition and sexual selection in adaptive speciation, and will participate to the identification of the odorant molecules involved in species mate recognition. A strong background in evolutionary biology is required, experience in chemical ecology and behavioural ecology is not compulsory but will be appreciated. Candidates of all nationalities can apply, but they should be proficient in spoken and written English. French skills, although helpful, are not essential.

The PhD student will be immersed in a multidisciplinary international project. Furthermore, the Institut des Sciences de l'Évolution (<http://www.isem.cnrs.fr/>) is hosted at the University of Montpellier, in the Mediterranean part of France and is part of a vast group of academic institutions in Montpellier devoted to research in Evolutionary Sciences, Ecology and Environmental Sciences and Applied Plant Sciences. Montpellier is more generally one of the most vibrant research communities in France.

The position is for three years. The student will be attached to the 'Ecole Doctorale SIBAGHE' (<http://www.adum.fr/as/ed/bsiae>). Raw monthly salary is

Muenster Evolution Stress Immunity

Graduate position: Muenster (Germany) - Evolutionary Ecology of Stress and Immunity

We invite applications for a PhD position in the group of Animal Evolutionary Ecology at the Institute for Evolution and Biodiversity, University of Muenster, Germany (<http://ieb.uni-muenster.de/>).

We are seeking highly motivated students with a background in evolutionary ecology, immunology or physiology. Experience with molecular techniques is advantageous. Successful candidates will work in the field of ecological immunology/physiology. Research goals will include the evolutionary relationship between immune defence and stress, using the red flour beetle *Tribolium castaneum* as a model organism. Working language of the lab is English.

Muenster hosts many excellent scientific institutions and is a dynamic city with a high number of students and a rich choice of social, cultural and sporting facilities (see <http://www.muenster.de/en/> for further details).

Interested candidates should send applications (preferentially as E-mail attachment) containing a CV, a list of publications (if available), a research statement and the addresses of two potential referees to:

Prof. Joachim Kurtz Institute for Evolution and Biodiversity University of Muenster Huefferstr. 1 DE-48149 Muenster Germany

joachim.kurtz@uni-muenster.de Tel. +49 251 83 24 661

Closing date is August 8th, 2010

joachim.kurtz@uni-muenster.de

Munich Evolutionary Proteomics

PhD position in Evolutionary Ecology/Proteomics on the model system *Daphnia*

A 3-year PhD position is available in the labs of PD Dr. Christian Laforsch and Dr. Georg Arnold (joined project) at the Ludwig-Maximilians-Universität (LMU) in Munich.

We are looking for an enthusiastic and well-motivated person who would like to join our laboratories to study the molecular basis of adaptation to predation stress, focusing on plastic defensive traits in the water flea *Daphnia*. A holistic proteome approach will be applied to show differences and similarities in protein expression in *D. magna* faced to vertebrate and invertebrate predators to discover the proteins controlling different defensive strategies. The main objectives of the project are: -to discover candidate proteins, which may play a critical role in building the defensive traits -to compare the expression of candidate proteins in populations with contrasting predator coexistence history -to generate peptide induced antibodies with monoepitopic specificity (iSEPIA) against a set of candidate proteins derived from holistic approaches to enable their functional analysis.

The project is embedded in the European Science Foundation project "Stressflea" - How to live in a mosaic of stressors - an ecological genomics approach on the water flea *Daphnia*.

Applicants should have a Master's or diploma degree in biology. Experience in experimental design, handling aquatic organisms, protein biochemistry, statistics and bioinformatics would be advantageous. Applicants should email a cover letter summarizing their research background and interest in the posted position, a CV, an abstract of master/diploma thesis, and contact information for two referees (everything as one PDF document) to both supervisors (laforsch@bio.lmu.de and arnold@lmb.uni-muenchen.de), by July 16. The position is available from 1st September 2010.

laforsch@zi.biologie.uni-muenchen.de

NewZealand EvolBiol

PhD Studentships in New Zealand on offer:

The Allan Wilson Centre is seeking candidates for seven PhD studentships. The titles of the projects for which candidates are sought are:

* Population-Genetic Models for the Maintenance of Genetic Variation * Discrete random models in evolutionary biology * The evolution of sex pheromone receptors and speciation in New Zealand endemic leafroller moths * Biodiversity science: bioinformatics * Mathematical and statistical analysis of SNP data * Visualising evolution * New Combinatorial and Algorithmic Tools for Network Reconstruction * Population genetics of tetrodotoxin-producing sea slugs

To make application for a studentship please contact the academic listed in the first instance. This information is at <http://www.allanwilsoncentre.ac.nz/> hamish.spencer@otago.ac.nz

NewZealand MarineMolEvol

PhD position in Marine Molecular Evolution and Chemical Ecology (New Zealand - now available).

A fully-funded, full-time PhD position is now available (starting Oct. 1st, 2010) offering an opportunity to undertake basic studies in marine molecular evolution and chemical ecology in a research project that also has biotechnological applications.

The project will provide an opportunity to work in functional molecular evolution whilst gaining generic 'biotech' skills in the development and use of recombinant yeast-based bioassays and, if all goes well, in the 'directed evolution' of ligand binding domains..

The project is a collaborative exercise between Drs Andrew Fidler and Pat Holland (Cawthron Institute, Nelson, N.Z.) and Prof. Ken McNatty (Victoria University, Wellington, N.Z.) and the PhD candidate will be enrolled at Victoria University (Wellington, New Zealand).

For more project details contact:

Andrew Fidler (andrew.fidler@cawthron.org.nz)
 CAWTHRON INSTITUTE, 98 Halifax Street East,
 Private Bag 2, Nelson 7042. NEW ZEALAND Tel +64
 3 548 2319 ext. 223 DDI +64 3 539 3223 Fax +64 3
 546 9464

Andrew Fidler <Andrew.Fidler@cawthron.org.nz>

Dr. Ralph Tiedemann, University of Potsdam, In-
 stitute of Biochemistry and Biology, Evolutionary Bi-
 ology/Systematic Zoology, Karl-Liebknecht-Str. 24-
 25, Haus 26, D-14476 Potsdam, Germany, Email:
 tiedeman@uni-potsdam.de

Ralph Tiedemann <tiedeman@uni-potsdam.de>

PotsdamU EvolutionaryBiol

PhD position in Evolutionary Biology at Potsdam Uni-
 versity

A 3-year PhD position (TVEL 13/2) is available at
 the Unit of Evolutionary Biology/Systematic Zoology
 at the University of Potsdam, starting September 1st
 2010.

The Unit of Evolutionary Biology/Systematic Biology
 has a strong focus on population genetic and speciation
 research, involving various taxonomic groups and a
 suite of molecular, morphological, and behavioural
 approaches (see [http://www.bio.uni-potsdam.de/-
 professuren/evolutionsbiologie/publikationen/-
 publikationen](http://www.bio.uni-potsdam.de/-professuren/evolutionsbiologie/publikationen/-publikationen) for recent work).

The successful applicant will work on the speciation of
 electric fish, combining molecular, electrophysiological,
 and behavioural studies. The project may involve field
 work in the tropics.

The position includes a teaching duty of 2 hours/week
 in zoology for undergraduates.

Applicants must hold a university degree (Diplom oder
 Master of Science in biology or a related discipline).
 Familiarity with modern molecular genetic techniques
 (PCR etc.), genomic data analysis and/or behavioral
 methods (including multivariate statistics) is prefer-
 able.

The University of Potsdam is an equal opportunity em-
 ployer. If equally qualified, disabled applicants will be
 preferably considered. The University of Potsdam aims
 at increasing the number of female researchers and en-
 courages qualified females to apply.

Potsdam is a beautiful city in close vicinity to the Ger-
 man capital of Berlin. Potsdam University takes an
 effort to assist its members in family-related issues and
 has repeatedly been awarded the total e-quality award.

Please send your application by email (preferably in
 a single pdf) before 16th of July 2010 to: Prof.

QueensUBelfast InsectEvolution

A PhD studentship is now available at Queen's Univer-
 sity Belfast in the Ecology, Evolution, Behaviour and
 Environmental Economics group. Please note that only
 UK students are eligible for full funding, European stu-
 dents are eligible for part funding.

The impact of disease on parental care

Primary supervisor: Dr Sheena Cotter Secondary su-
 pervisor: Prof Bob Elwood

Superficially, the raising of offspring by two parents
 appears to be a cooperative and harmonious venture.
 However, it often masks an evolutionary battle, as in
 reality families are at war: mothers and fathers would
 both prefer their partner to do more work, brothers
 and sisters are rivals for their parents' attention, and
 children want more from their parents than parents are
 willing to give. As a result, the amount of care we see
 parents delivering is the compromise that attempts to
 resolve this conflict. But what happens when condi-
 tions change?

Disease is a common threat that could change the
 amount of care that parents deliver. They may need
 to spend more effort on getting healthy and so neglect
 their children, or diseased parents may lavish extra care
 on their children because they are unlikely to survive
 to have more.

This PhD studentship will address the effects of disease
 on parental care using a combination of pathogen and
 hormonal manipulations in a model system: the bury-
 ing beetle. Also known as "gravediggers" these bee-
 tles breed on small vertebrate corpses and are almost
 unique in that both parents prepare food, feed and care
 for their offspring.

The student will receive training in: Insect rearing,
 collection and pedigrees, immune function assays, hor-
 monal manipulations, pathogen bioassays, experimen-
 tal design and statistical analysis.

Requirements: MSc. or at least a 2(i) Bachelor degree

in biological sciences

Application procedure: Informal enquiries to Dr Sheena Cotter, Tel: 01223 331861, Email: sc570@cam.ac.uk Application is via the QUB portal: <https://qolps.qub.ac.uk/home/> Closing date 23rd August 2010, interviews expected early September and start date by agreement.

Sheena Cotter PDRA Department of Zoology University of Cambridge Downing St Cambridge CB2 3EJ

Tel: +44 (0) 1223 331 861 Fax: +44 (0) 1223 336 676 webpage: <http://www.zoo.cam.ac.uk/zoostaff/-bbe/Cotter/Sheena1.htm>

sc570@cam.ac.uk

Sydney Conservation Genetics

PhD or M Phil Positions in Invasion and Conservation Genetics and Demography A/Prof W Sherwin Evolution & Ecology Research Centre, BEES, UNSW, Sydney AUSTRALIA. www.bees.unsw.edu.au/school-staff/sherwin/sherwinwilliam.html Project 1: Weeds adapting to Australia: rate and direction of evolution. With A Moles, R Frankham. As well as threatening biodiversity, introduced species also allow us to study processes of adaptation and invasion. We are measuring changes in form, function and genetic make-up of introduced species since their arrival in Australia. This position would focus on the genetical aspects of the project, using genetic approaches which include microsatellite assignment of origins, 454 sequencing, and common-garden experiments. You should be qualified in population genetics, or molecular sciences. There may be some fieldwork. Ecology qualifications are desirable.

Project 2: Resilience of small populations to periods of selection A consortium of mathematicians and biologists at UNSW has produced new theory about the way that small endangered populations might rapidly recover their responsiveness to selection. This PhD position will follow up this theoretical work by carrying out experiments in model populations of flies. There could be an additional stipend supplement for this project. You should be qualified in maths/physics/computing, or in population genetics.

Project 3: Forecasting demography of bottlenose dolphins With partners from Murdoch University we are studying ecology, threats, and genetics of Bunbury (WA) bottlenose dolphins. The PhD student at UNSW

will use these data in existing or novel programs, to evaluate population viability with different management and threats. The work involves integration between demographic, ecological, and genetical approaches There would be field-trips to Bunbury. You should be qualified in population ecology. Molecular ecology qualifications are desirable.

Project 4: Conservation of Little Penguins in New South Wales: With Dr J Sinclair. To assess the viability of an endangered population of Little Penguins in Sydney Harbour under a range of threats and management strategies. The PhD student would conduct a molecular genetic and demographic analysis on NSW penguin populations, to input into a population forecasting model. The project involves some fieldwork and molecular laboratory work. There could be an additional stipend supplement for this project.

Other projects: It is possible to negotiate other projects in this general area of research. Note that projects which are theoretical or use existing data in Sherwin's group, are much quicker to start because they can commence without application for external funding of research expenses!

PROCEDURE: (1) DISCUSS: Email letter with CV, academic record, and details of two academic referees, to A/Prof Bill Sherwin (W.Sherwin@unsw.edu.au). For further information phone: +61-2-9385-2119. Your letter should include explicit explanation of how your results are sufficient to allow application for a SCHOLARSHIP at UNSW (see below for grades required). We cannot consider other applications.

(2) PhD M/Phil CANDIDACY APPLICATION: Requirements for PhD are BSc (Hons 1), MSc, or equivalent. For MPhil, requirement is BSc. Specific areas essential and desirable are shown for each project above. Solid research and communication skills. Full NSW driver license desirable. For exact timing and details www.grs.unsw.edu.au/homepage.html (3a) PhD SCHOLARSHIP APPLICATION - LOCAL: Citizens or permanent residents of Australia/NZ, apply for APA and UPA at UNSW. You will need to have completed a research degree (eg MSc or BSc Honours research year), with results which are equivalent to 85% or higher, in order to be competitive for these scholarships. Publications in international journals may help also. Applications open Sep 2010, for study commencing in First Session in 2011. For exact application timing and details see www.grs.unsw.edu.au/scholarships/local.html (3b) PhD SCHOLARSHIP APPLICATION - INTERNATIONAL: Applicants who are NOT-citizens or permanent residents of Australia/NZ, should apply for IPRS and UIPA at UNSW. You will need to have com-

pleted a research degree (eg MSc or BSc Honours research year), with results which are equivalent to 95% or higher, in order to be competitive for these scholarships. Applications are due 31 Aug 2010, for study commencing in First Session in 2011. For exact timing and details see www.grs.unsw.edu.au/scholarships/-internationalschols.html (3c) M Phil SCHOLARSHIP APPLICATION. Local and international students can apply for a \$4000 stipend form the EERC, UNSW.

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Tallahassee CoralEvolution

Hello everyone,

I have a last-minute opening for a Master's student to begin Fall 2010. Semester start date is Aug 23, 2010 so complete applications needed, including transcripts and reference letters, etc, needs to be *received by July 23*. You must have already taken the GRE and send scores to be eligible. Unofficial copies are okay at this stage.

I have an opening in my lab for an MS students with interests in the ecology and evolution of deep-sea corals and/or in seamount ecology. Please see the FSU website www.fsu.edu for information on the university. The degree will be granted in (Biological) Oceanography through the new Dept of Earth, Ocean and Atmospheric Sciences - <http://www.eoas.fsu.edu/>. Applicants with a background in benthic invertebrates and experience in molecular methods, GIS, video survey analyses, and/or multivariate statistics will be given preference. Application is available at <https://admissions.fsu.edu/gradapp/>. Please also send me an email with your interests and a summary of your background.

Thank you for forwarding this message to potential candidates, Amy Baco-Taylor

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Amy Baco-Taylor, PhD EOAS/Oceanography 117 N. Woodward Avenue P.O. Box 3064320 Tallahassee, FL 32306-4320

Phone: (850) 645-1547 Fax: (850) 644-2581

PLEASE NOTE NEW EMAIL: abacotaylor@fsu.edu

Amy Baco-Taylor <abaco@ocean.fsu.edu>

UAarhus QuantGenetics

Applications are invited for a PhD position at the University of Aarhus, Faculty of Agricultural Sciences (DJF), Department of Genetics and Biotechnology < http://agrsci.au.dk/en/institutter/-institut_for_genetik_og_bioteknologi/ > . The position is available for three years beginning as soon as possible.

Research area and project description The area of research is quantitative genetics focusing on applications of dense marker map genotypes in animal breeding schemes. The aim of the project is twofold. First it aims at developing our understanding of the effects of genomic selection with respect to changes in allele frequencies at markers and linked loci. Secondly it aims to utilise dense marker genotypes more efficiently by optimised weighing of marker effects and use of dense marker genotypes to optimise phenotyping and genotyping strategies.

Qualifications and specific competences Applicants to the PhD positions must have a relevant Master's degree (or graduate in the very near future - documentation for final thesis and date of examination must be enclosed in the application) or equivalent.

The student must have a thorough training in quantitative genetics and statistics, and documented expertise in working in these subjects e.g. in thesis work. Experience with computer programming is an advantage.

In order to be considered for the position please remember to enclose your diplomas, grade sheets, transcripts etc.

Applicants seeking further information are invited to contact: senior researcher Peer Berg, e-mail: Peer.Berg@agrsci.dk or tel.: +45 8999 1226 or senior researcher Anders Christian Sørensen e-mail; AndersC.Sorensen@agrsci.dk or tel.: +45 89991355.

Place of Employment and Place of Work The place of employment is the University of Aarhus, and the place of work is the Faculty of Agricultural Sciences, Blichers Allé 20, 8830 Tjele, Denmark.

Salary and Terms of Employment

Salary and terms of employment are according to current agreement for state-employed academics and government circular from the Ministry of Finance regarding PhD students as well as the appointment structure of 2007 for scientific personnel at universities.

The salary level for PhD students with qualifications corresponding to a Danish Master degree is approx. DKK 288,000 per year excluding pension (corresponding to USD 48,600 / EUR 38,600 per year - depending on the rate of exchange at the actual time of employment).

Matriculation as a PhD student will be in accordance with Ministerial Order no. 18 of 14 January 2008 on the PhD Programme at Universities, and matriculation at the Faculty of Agricultural Sciences is a prerequisite for employment as a PhD student.

Deadline

All applications must be made online and received by: 15/08/2010

For further information and on-line application, see http://agrsci.au.dk/en/om_djf/jobs/phd_positions
Kind regards

Peer Berg Senior scientist Dept. of Genetics and Biotechnology Faculty of Agricultural Sciences Aarhus University Blichers Allé 20, Postboks 50 DK-8830 Tjele Tel.: +45 8999 1226 Mobile: +45 2229 1226 Email: Peer.Berg@agrsci.dk Tel.: +45 8999 1900 Web: www.agrsci.au.dk <outbind://30/www.agrsci.au.dk>

Peer.Berg@agrsci.dk

UAuckland MicrobialEvolution

PhD position in New Zealand available beginning November/December 2010, these include stipends and course fees.

We are seeking enthusiastic PhD candidates with interests in both fundamental and applied aspects of microbial ecology and evolution, biogeography and genetics to join our group in Biological Sciences at the University of Auckland, New Zealand.

We have recently been awarded funds to provide options to improve NZ wines (and thus exports). One of the roles of the Goddard group in the program is to test the hypothesis that different regions of NZ have different microbial communities and populations, and then to test some members of these communities for their

potential to contribute to novel wine attributes during the fermentation process.

This projects will integrate ecological theory (we are fundamentally testing ideas concerning species composition in space and time, and the degree to which these species are adapted to the niches in which they are found), molecular biology and genetics (including next-generation sequencing, as tools to quantify species presence and abundance and differentiate and quantify relatedness of individuals within species) and applied aspects of yeast ecology (examining the impact of candidate yeasts on wine aroma and flavour using experimental fermentation and volatile analyses).

The student will be expected to gather samples from vineyards and wineries around NZ, then use microbiology and molecular biology techniques to analyze communities and populations, then employ community ecology and population genetic analyses to test the hypotheses of interest. The PhD student will go onto examine the fitness landscapes of these isolates from different areas and niches, and also screen isolates, and interactions between isolates, for strains of potential worth to the wine industry - i.e. do any of them make interesting/different wine? This may also provide the student with GC-MS and sensory analysis experience.

This position provides a tax-free stipend of NZD\$25,000 per annum for 3 years; the successful applicant must ensure they have the correct immigration permit. You will be part of a close-knit, friendly team in the Goddard group that will interact with the other program partners in the University, Plant and Food Research (a Crown Research Institute) and Lincoln University, as well as collaborating wine companies in Auckland, Hawkes Bay, Marlborough and Central Otago.

Please send a one-page expression of interest, grade transcript and a CV to Dr Mat Goddard (m.goddard@auckland.ac.nz)

Dr Matthew R Goddard School of Biological Sciences The University of Auckland Private Bag 92019 Auckland Mail Centre Auckland 1142 New Zealand <http://www.sbs.auckland.ac.nz/uoa/science/-about/departments/sbs/>

m.goddard@auckland.ac.nz

UBarcelona ComparativeGenomics

PhD position in Comparative Genomics

I am looking for a highly motivated candidate to work on a genomic comparative project. The aim of the PhD is to study *evolutionary genomic regions* in different mammalian species. Interest in evolutionary biology, molecular biology and cell biology is required. Applicants must hold a Master's degree or equivalent in biology, molecular biology or related disciplines, with a strong background in bioinformatics. The applicants should possess excellent written and oral communication abilities.

Our group work chiefly in the fields of comparative genomics, evolution and chromosomal instability and, in particular, we are interested in the mechanisms that are driving karyotype evolution and genomic architecture in mammals. Our research activity is aimed at addressing a whole range of different evolutionary questions through a multidisciplinary approach, combining computational and experimental methods such as available genome databases and a battery of molecular, cytogenetic and cell biology, and by studying the genomes of different mammalian species.

For further information please contact Dr Aurora Ruiz-Herrera directly.

Complete application packages, including a CV (with a list of publications, if applicable), a brief (1-page) statement of research interests, and the names and e-mail addresses of two referees should be sent to aurora.ruizherrera@uab.cat

Application deadline: 1st September 2010.

Aurora Ruiz-Herrera, Ph.D. Citology and Histology Unit Dept. Cell Biology, Physiology & Immunology Universitat Autònoma de Barcelona Efidici C Campus UAB-Cerdanyola del Vallès, 08193, Spain Phone +34935812051 Fax +34935813357 aurora.ruizherrera@uab.cat

"Ruiz-Herrera, A" <aurora.ruizherrera@uab.cat>

Uiceland MolecularBasis Of ResourcePolymorphism

Molecular basis of resource polymorphism

Two Ph.D. positions are available at the University of Iceland, Institute of Biology.

We are seeking two PhD students to work on an interdisciplinary project studying the genetic and molecular mechanisms underlying the formation and rapid evolu-

tion of diverse cranial morphology in Icelandic Arctic charr (*Salvelinus alpinus*). The research group is coordinated by prof. Sigurdur S. Snorrason, and the molecular work will be performed under the supervision of Drs. Zophonías O. Jónsson, Arnar Pálsson, Sigríur Rut Franzdóttir and Valerie H. Maier which have expertise in developmental and molecular biology, genomics and population genetics.

The candidates should hold an M.Sc. degree or equivalent in biology, have a strong background in molecular biology and be highly motivated. A good ability to work in a team is essential.

The project addresses questions in developmental genetics and evolutionary genetics, concerning the origin of skeletal divergence and parallel evolution. Over the last 10 000 years Arctic charr in Iceland has evolved an extensive variation in morphology and life history. We are interested in studying the differences in development of key craniofacial elements in contrasting morphs of this non-model species.

Specifically, we are aiming at elucidating the genes underlying morphological differences in size, and skeletal and craniofacial features among Arctic charr morphs. The projects will include sampling, cloning and characterization of candidate genes, transcriptional analysis, in situ and other molecular methods. One of the two projects will also involve a study of evolutionary forces, by documenting variation in developmental genes in morphologically distinct morphs.

The University of Iceland is located in the center of Reykjavik. The laboratory shares facilities with several groups in the field of molecular biology, genetics and evolutionary biology, with state of the art equipment for these studies. The students will be part of a research environment of around 40 graduate students, post-docs and senior researchers. The student will also be part of the Graduate Program in Molecular Life Sciences at the University of Iceland <http://www.gpmls.hi.is> Start date: autumn 2010 or on agreement.

Those interested, please submit a CV, statement of research interest, and names of three referees to: Sigurur S. Snorrason (signor@hi.is).

For further information contact Arnar Pálsson (apalsson@hi.is).

– Arnar Pálsson (Ph.D) Faculty of Life and Environmental Sciences Institute of Biology University of Iceland Sturlugata 7, 101 Reykjavik, Iceland Tel: +(354) 525 4265 Fax: +(354) 525 4069 E-mail: apalsson@hi.is www.hi.is/~apalsson apalsson@hi.is

ULaval Molecular basis of behaviour variation

Our laboratory is eager to receive application from highly motivated scientists with an excellent record to apply to a Quebec government fellowship available for non-Canadian candidates to study in a Quebec-based laboratory. Doctoral fellowships are available. Furthermore, internships are available for a visit to our laboratory (3000\$/month, up to 4 months) during graduate studies in another laboratory. Pre-selection by the host university and our laboratory is mandatory.

Candidates from all over the world are invited to apply. Additionally, specific fellowships are available for candidates from Mexico, Brazil, China and Wallonie.

We are in the Department of Biology at Laval University, located in Quebec City, Quebec, Canada. Our laboratory is part of the Institute of Integrative and Systems Biology (IBIS). We study the underlying molecular and hormonal causes of variation in behaviour in vertebrates. We are interested in personality with an emphasis on the stress response and correlation among behaviours, as well as in reproductive tactics. We are also interested by the effects of the environment on development of behaviour, such as environmental enrichment in captive animals, maternal/paternal and social group effects, and endocrine disrupters. We therefore have a strong interest for phenotypic plasticity, along with the effects of genetic variation. We favour an integrative approach by linking data from the same individual: neuropeptides, neurotransmitters and their receptors (quantitative Real-Time PCR, microarrays, in situ hybridization, HPLC), hormones (EIA, HPLC), physiology and behaviour. Our model system is the threespine stickleback *Gasterosteus aculeatus*, a small fish studied in behavioural biology, which can be kept easily in the lab and whose genome is sequenced.

Laval University is one of the ten main Canadian universities. Quebec City is dynamic with all the advantages of a large city while still allowing for very easy access to wilderness and very reasonable cost of living. The chosen candidates that are successful at obtaining a fellowship will be part of the Institute of Integrative and Systems Biology. They will have access to core genomics and molecular biology facilities, lab meetings and Institute-wide group meetings, journal clubs and weekly seminars at the Institute and in the Biology

Department. Several ecological genomics laboratories are part of the Institute and the Biology department, allowing for enriched interactions with members of the other laboratories working in this field. DEADLINES: Our laboratory must receive applications before July 23, 2010. We will then proceed to select candidates that will be able to apply to the University pre-selection committee with a deadline of August 9th 2010. Candidates selected by the university will then be allowed to apply to the general competition in Fall 2010, with results given in April 2011. Start date can be between May and December 2011.

Contact me directly by email for more information about the program and opportunities in our laboratory.

Nadia.Aubin-Horth@bio.ulaval.ca

Nadia Aubin-Horth

Assistant professor

Department of Biology

Institute of Integrative and Systems Biology

Pavillon Charles-Eugene-Marchand

1030, Avenue de la Medecine

Laval University

Quebec city (Quebec) G1V 0A6

Canada

Nadia.Aubin-Horth@bio.ulaval.ca

ULethbridge AvianPopGenetics

Population Genetics of North American Forest Birds

A graduate assistantship (M.Sc.) is available in the laboratory of Dr. Theresa Burg at the University of Lethbridge in molecular ecology starting Jan 2011 or May 2011. I am looking for a highly motivated graduate student to work with me to study large-scale population divergence of resident bird species, specifically Picidae. The project involves both laboratory and field-based research and the use of high-throughput DNA-based methodologies. Students must be able to work independently and as part of a group. Candidates should have a strong undergraduate background in evolution, ecology and genetics. Prior research experience with molecular techniques and mistnetting are desirable but not required. Please consult the Graduate Studies website (<http://www.uleth.ca/graduatestudies/>) for

admissions criteria, tuition fees and other expenses.

The Biology Graduate Program at the University of Lethbridge offers research-based M.Sc. and Ph.D. degrees in a collegial setting. Our faculty and students are engaged in a variety of research projects, many in collaboration with partners in government, non-profit agencies, or industry. The students will be part of a research environment with about 60 graduate students in Biology. Our mission is to train students to be leaders in identifying and addressing biological questions at multiple levels of investigation from the molecular to the ecosystem.

Lethbridge is an attractive city of 70,000 situated in Southern Alberta, close to National Parks and Wilderness areas of the Rocky Mountains and Cypress Hills.

For more information please contact Theresa Burg at theresa.burg@uleth.ca. The deadline is Sept 15 or until the position is filled. Please send me a copy of your CV, transcripts and research statement to me, if you are interested.

Theresa Burg

<http://people.uleth.ca/~theresa.burg> "Burg, Theresa"
<theresa.burg@uleth.ca>

UManchester Evolution of social evolution

A PhD studentship is available at the University of Manchester to examine the effect of ecological factors and life-history trade-offs on social success and cheating. The project integrates concepts from ecology, social evolution and life-history evolution with a developmental genetics perspective. It provides opportunities for students to develop both theoretical and empirical/experimental skills (though the project is strongly experimentally driven).

The project will use the social amoeba *Dictyostelium discoideum* as a model organism. *D. discoideum* is an excellent model system to examine the genetic basis of cooperation and cheating because free living individuals aggregate to make a multicellular 'organism' (the 'slug') that goes through development to form a dead stalk that holds aloft a sporehead. Because different genotypes will aggregate to form chimeric slugs, competition for space in the sporehead should lead to strong selection to become viable spores rather than dead stalk cells. The aim of this studentship is to ask how nat-

ural variation in social success is maintained and how cheater spread is mitigated in *D. discoideum* in the face of this strong selection.

The project will be jointly supervised by Daniel Rozen and Chris Thompson in new state of the art laboratory facilities in the Faculty of Life Sciences (University of Manchester). The student will benefit from exposure to and training in a wide variety of different techniques, ranging from quantitative data handling, theoretical population genetics, experimental evolution and statistical analysis to genetics and molecular cell biology. Importantly, you will also work closely with Jason Wolf at the University of Bath, where additional mathematical, theoretical or data analysis training needs will be met.

The studentship would begin at either the September 2010 or January 2011 intake dates.

For application details and further information, please see <http://tinyurl.com/32odjg5> (the advertisement on findaphd.com).

Chris Thompson (Christopher.thompson@manchester.ac.uk) Daniel Rozen (Daniel.rozen@manchester.ac.uk)
for

Jason@evolutionarygenetics.org

UMuenchen PlantEvolutionaryGenetics

PhD position in Germany: Plant evolutionary genetics

I am looking for a PhD candidate interested in plant evolutionary genetics. In my lab, we are investigating the genetic basis for symbiont recognition and discrimination in *Lotus* species. A PhD position, funded by the German Science Foundation (DFG), is available immediately to work on this project. This project has both experimental and computational components and will involve functional studies on plants (inoculations with bacteria and trans-gene expression) and classical population genetics. Applicants should have a Master's degree or equivalent in biology or a related field. Previous laboratory experience and coursework in evolutionary biology and genetics are desirable.

Currently my lab is located in Munich, Germany at the Ludwig-Maximilians Universität (http://evol.bio.lmu.de/people/group_stephan/rose.l/). This fall we will be relocating to Heinrich-Heine Universität

in Düsseldorf where I will be establishing the Department of Population Genetics and join an active group of plant molecular biologists and evolutionary geneticists (<http://www.biologie.uni-duesseldorf.de/englisch>).

The closing date for applications is August 22, 2010, or when the position is filled. Applicants should send a single PDF file containing a statement of interest and previous research experience, curriculum vitae, and contact information for at least two referees to: Dr. Laura Rose (rose@bio.lmu.de).

Dr. Laura Rose Department Biologie - Biozentrum University of Munich Grosshaderner Str. 2 82152 Planegg Germany

Phone: 49 89 2180 74 150 Fax: 49 89 2180 74 104 Email: rose@bio.lmu.de

rose@zi.biologie.uni-muenchen.de

UMunich PlantEvolutionaryGenetics

PhD position in Germany: Plant evolutionary genetics

I am looking for a PhD candidate interested in plant evolutionary genetics. In my lab, we are investigating the genetic basis for symbiont recognition and discrimination in Lotus species. A PhD position, funded by the German Science Foundation (DFG), is available immediately to work on this project. This project has both experimental and computational components and will involve functional studies on plants (inoculations with bacteria and trans-gene expression) and classical population genetics. Applicants should have a Master's degree or equivalent in biology or a related field. Previous laboratory experience and coursework in evolutionary biology and genetics are desirable.

Currently my lab is located in Munich, Germany at the Ludwig-Maximilians Universität (http://evol.bio.lmu.de/people/group_stephan/rose_1/). This fall we will be relocating to Heinrich-Heine Universität in Düsseldorf where I will be establishing the Department of Population Genetics and join an active group of plant molecular biologists and evolutionary geneticists (<http://www.biologie.uni-duesseldorf.de/englisch>).

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Dr. Laura Rose Department Biologie - Biozentrum University of Munich Grosshaderner Str. 2 82152 Planegg Germany

Phone: 49 89 2180 74 150 Fax: 49 89 2180 74 104 Email: rose@bio.lmu.de

rose@zi.biologie.uni-muenchen.de

UNewBrunswick 3 ClimateAdaptation

GRADUATE POSITIONS AVAILABLE

As a collaborating group of academic and government scientists, we are seeking 5 Ph. D. students to work as a part of a multidisciplinary team conducting manipulative experiments designed to examine the effects of multiple stressors in small wetland ecosystems. The focus of this NSERC funded research program will be on the potential effects of climate change on amphibians and other aquatic organisms alone and in combination with herbicide use. This would be the 3rd in a series of experiments conducted at the Long-term Experimental Wetlands Area (LEWA), on Canadian Forces Base Gagetown in New Brunswick Canada. All positions are contingent on funding ? we will know funding decision by October 2010.

1 Ph. D. position at the University of Ottawa

A Ph. D student will be examining climate change/herbicide effects on gene expression, sexual development and metamorphosis in amphibians. They will be supervised by Dr. Vance Trudeau (University of Ottawa; see www.teamendo.ca) and Dr. Vince Palace (DFO, Winnipeg, Manitoba) and work out of The University of Ottawa Centre for Advanced Research in Environmental Genomics. Qualifications: Candidates should have a background in comparative physiology or vertebrate endocrinology, and have demonstrated experience with basic molecular biology methods (PCR, gene cloning, etc). A keen interest in climate change effects on aquatic ecosystems would be an asset to the team.

3 Ph. D. positions with the Biology Department and The Canadian Rivers Institute at the University of New Brunswick Saint John (UNB Saint John)

1. One Ph. D. student will be examining climate

change/herbicide effects on DOC and UV radiation attenuation. The student will be supervised by Drs. Nelson O'Driscoll and Jeff Houlihan (UNB Saint John). Qualifications: An M. Sc. in chemistry, biology, environmental science or a related discipline is preferred. Exceptional B. Sc. students will be considered. All candidates should have good statistical skills (i.e. are comfortable with traditional analyses such as ANOVA and regression) and be comfortable with independent laboratory and field work. 2. One Ph.D. student will examine the effects of climate change/herbicide use on planktonic and benthic invertebrate communities in these experimental ponds. The student will be supervised by Dr. Karen Kidd (UNB Saint John). Qualifications: An M.Sc. in ecotoxicology, aquatic ecology or a related discipline. The student should have experience conducting field work on aquatic systems and good statistical skills. Experience in macroinvertebrate identifications is an asset. 3. One Ph. D student will be examining the effects of climate change/herbicide stressors on primary production and plant abundance and diversity. The student will be supervised by Dr. Jeff Houlihan. Qualifications: An M. Sc. in ecology, conservation biology, botany or a related discipline is preferred. We would consider a statistics, math or computer modelling graduate if there is a strong natural history interest and background. Exceptional B. Sc. students will be considered. All candidates should have good statistical skills (i.e. are comfortable with traditional analyses such as ANOVA and regression). Experience in aquatic plant identification is an asset.

1 Ph. D. position with the Department of Physical and Environmental Sciences at the University of Toronto

One Ph. D student will be using the output from 24 Global Climate Models and four Regional Climate Models applied to Canada in conjunction with a common regression-based stochastic weather generator software to develop realistic regional climate projections under different future scenarios of climate change. The student will be supervised by Dr. Adam Fenech. Qualifications: A Masters degree in physical geography or physics with specific courses in climatology and/or meteorology. All candidates should have numerical skills, and enjoy database development and manipulation. Geographic information system experience is an asset.

Additional qualifications: The importance of candidates being effective team players cannot be overstated. Excellent verbal and written communication skills as well as interpersonal relation skills are considered vital personal attributes. This project will involve many students and senior researchers (as well as, a number of field technicians) working on the same set of 24 ponds for at least the next 3 years and therefore the ability

to collaborate effectively will be a critical, perhaps the most critical, attribute determining the success of this project. We are looking for that rare combination - the ability to think and work independently while also being a collegial, collaborative and cooperative team member.

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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>

UOslo AdaptiveDiversification

University of Oslo, Department of Biology - Centre for Ecological and Evolutionary Synthesis (CEES) PhD Research Fellow in Evolutionary Biology - (ref no 2010/9145)

The CEES is a centre of excellence for integrative biological research and is well funded. It provides a stimulating research environment, situated at the Department of Biology, with many young international and Norwegian scientists working on a variety of theoretical and empirical topics within ecology, evolution, population genetics, genomics, phylogenetics, molecular biology, and statistical methodology. The CEES is chaired by Nils Chr. Stenseth and currently employs 20 faculty members, 40 postdocs/researchers, 35 PhD students and 36 MSc students. Information about the centre can be found at: <http://www.cees.uio.no/> The fellowship is for a period of 3 years. Starting date is tentatively 15 October 2010.

Job description:

The PhD fellow will be part of a team working on the project "Tracking signatures of adaptive diversification during postglacial colonization in threespine stickleback". The project is funded by the Research Council of Norway. The overall aims of the project are to detect genomic regions and phenotypic traits under selection when sticklebacks invade fresh waters. To do this we will use a set of genetic methods, including SNP-genotyping and large-scale sequencing. Sticklebacks will be sampled in the field, based on prior information on phenotype distributions. Based on phenotypic and genotypic data the candidate will, depending on prior competence, investigate this adaptation process either using molecular genetic approaches or more sta-

tistically based methods. The PhD-candidate will work with supervisors at the CEES (L.A. VÅllestad, T.F. Hansen, K.S. Jakobsen, K. Åstbye) and international collaborators (F. Volckaert, A. Nolte).

Requirements:

Applicants must hold a MSc-degree (or equivalent) and have experience in evolutionary biology, molecular biology, molecular genetics, population genetics or quantitative genetics â preferentially with solid experience in several of these field. Good analytical skills are necessary.

For this position, we seek a highly motivated, enthusiastic person with the ambition to gain insight and publish papers in leading, international journals. The successful candidate must be prepared to spend some periods abroad for training and cooperation.

The purpose of the fellowship is research training leading to the successful completion of a PhD degree.

The fellowship requires admission to the research training programme at the Faculty of Mathematics and Natural Sciences. An approved plan for the research training, including a project outline, must be submitted no later than two months after taking up the position, and the admission must be approved within three months. For more information see: <http://www.uio.no/admhb/reglhb/personal/-tilsettingvitenskapelig/regulationstermcondition.xml>

A good command of English is required of all students attending the University of Oslo. http://www.matnat.uio.no/english/research/education/-proficiency_in_English.html Salary:

PhD Research Fellow (SKO 1017), pay grade: 48-56 (NOK 383 700 â 440 500 per year, depending on seniority/qualifications)

The application must include:

- * a cover letter including a statement of interest, summarizing the applicantâs scientific work and interests and describing how she/ he fits the requirements for the position
- * a CV including a list of published and unpublished works
- * transcripts of records, copies of certificates and grades from bachelor and master level
- * two letters from reference persons or names and addresses of two reference persons
- * copies of relevant published papers

Applicants may be called in for an interview.

Foreign applicants are advised to attach an explanation of their Universityâs grading system. Please remember that all documents should be in English or a Scandinavian language.

Closing date for applications: 20 August, 2010

The University of Oslo has an agreement for all employees, aiming to secure rights to research results a.o.

The University of Oslo has a goal of recruiting more women in academic positions. Women are encouraged to apply.

In accordance with the University of Osloâs equal opportunities policy, we invite applications from all interested individuals regardless of gender or ethnicity.

* Region: * Oslo

* Job type: * Contract

* Working hours: * Full-time

* Working days: * Day

* Application deadline: * 20 August, 2010

* Location: * Blindern, Oslo

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UPaulSabatier MolEvol

One Ph.D. position is available at the University Paul Sabatier (Toulouse 3, France), Lab. UMR 5174 “Evolution et Diversité Biologique” (CNRS grant for 3 years, 1757 euros brut/month) Sex chromosome evolution and Y degeneration within the Primates lineage.

We are seeking PhD student to work on an interdisciplinary project studying the molecular mechanisms underlying the evolution of sex chromosomes and Y degeneration in mammals (Primates). The candidates should hold an M.Sc. degree (M2R) or equivalent in biology, have a strong background in molecular and evolutive biology and be highly motivated. A good ability to work in a team is essential.

The project addresses questions in molecular evolution and evolutionary genetics, concerning the origin of sex chromosome divergence and Y degeneration in mammals, and specifically Primates (Lahn & Page, 1999; Skaletsky et al., 2003; Wilson & Makova, 2009; Charlesworth & Charlesworth, 2000; Graves, 2006). We propose a fine-scale comparative genomic approach to determine (1) the respective component of the evolu-

tionary forces (genetic drift, nature and intensity of selection...) driving the molecular evolution of sex chromosomes and the Y degeneration; (2) the specific factors involved in the evolution of the X-Y homologous gene pairs. The fine-scale approach, together with intra-specific data, would enable us to identify micro-evolutionary processes of the sex chromosomes evolution and Y degeneration. This project includes different approaches: 1. Evolutionary mode and rates. The objective of this first axis will be to compare, at a fine taxonomic scale, the molecular evolution of the X- and Y-linked genes. This comparative genomic approach would enable us to finely characterise the evolutionary mode and rate of the homologous genes pairs. 2. Selective pressure. The objective will be to characterise the selective pressure acting on each gene copy and determine whether the selection pressure have been the same throughout the X and Y evolutionary histories, the different Primate lineages and the genes. Is the nature of selection acting on the X and Y copy similar (background selection, selective sweep, balancing selection)? Is the intensity of selection different between the X and Y and among lineages?

The University Paul Sabatier is located in the South of France, near Pyrénées. The laboratory shares facilities with several groups in the field of molecular biology, genetics and evolutionary biology, with state of the art equipment for these studies. The students will be part of a research environment of around 60 graduate students, post-docs and senior researchers.

Start date: 1st of October 2010. Those interested, please submit a CV, statement of research interest, and names of 2-3 referees to: bcrouau@cict.fr For further information contact : B. Crouau-Roy (bcrouau@cict.fr) or E. Lecompte (emilie.lecompte@cict.fr)

Prof Brigitte CROUAU-ROY Université Paul Sabatier, 118 route de Narbonne, Bat. IV R3 b2 Directrice UMR CNRS 5174 "Evolution et Diversité Biologique" EDB 31062- Toulouse cedex 9, FRANCE Tel (33)5 61 55 62 59 (direct) 73 28 (secrétariat) Fax:(33)5 61 55 73 27 <http://www.edb.ups-tlse.fr>

bcrouau@cict.fr

UPrinceEdwardIsland Biogeography

MSc.Geographic ranges.UPrinceEdwardIsland

All species have limits to their geographic and ecologi-

cal distributions, but the causes of these limits remain largely unknown. While reduced dispersal, physiological limits and/or genetic constraints to adaptation are likely to play a role in determining distributional limits, more empirical research is needed to understand and predict where individual species can and cannot occur.

An MSc position in evolutionary ecology is available in the lab of Dr. Karen Samis at the University of Prince Edward Island starting Sept. 2010 (option Jan or May 2011, and potential to convert to PhD). Dr. Samis is interested in local adaption and the limits to geographic ranges, and is looking for students demonstrating an interest in plant evolution and ecology. The potential project will assess fine-scale genetic structure and phylogeography in Atlantic Canada populations of *Cakile edentula* (American sea rocket), and survey large to small-scale spatial variation in habitat, life history and fitness to assess distributional limits from both ecological and geographic perspectives. This plant is endemic to coastal beaches, tends to occur on white sandy beaches from the high tide line to the open dune and is common in its native Atlantic range from Newfoundland, Canada to Florida, USA. The project may involve a combination of range-wide field surveys, common garden experiments and DNA analysis. Potential students should have some experience with field ecology and/or molecular genetics, and have demonstrated an ability to work efficiently and independently. Preference will be given to students who are competitive for Canadian graduate scholarships, but students who are eligible for graduate funding from an international agency will also be considered. Interested students are encouraged to contact Dr. Samis for more information, and to submit a pdf file including a cover letter explaining their interest and suitability for the position, their CV and contact information for at least two references to ksamis@upei.ca.

The University of Prince Edward Island in Charlottetown, the provincial capital (www.city.charlottetown.pe.ca), is ideally suited for the study of coastal plants with numerous coastal beaches within a short drive of campus and a strong marine ecology program. The Biology Department is a vibrant community with a broad range of faculty, post-doctoral and graduate researchers focused on human health, environmental, wildlife and marine biology, and ecology and evolution. Graduate students have the opportunity to teach undergraduate labs, attend research seminars and interact with scientists in other research units on campus including the Atlantic Veterinary College, NRC and Agriculture Canada. Please see the departmental (www.upei.ca/biology) and university

website (www.upei.ca/vpacademic/graduatestudies) for more information.

Karen Samis Assistant Professor 902-620-5133
ksamis@upei.ca <http://people.upei.ca/ksamis> Dr.
Karen Samis Assistant Professor Biology Department
University of PEI 550 University Avenue Charlottetown, PE C1A 2G7 902-620-5133 ksamis@upei.ca people.upei.ca/ksamis
ksamis@grpwise.novell.upei.ca

UUppsala AvianGenomics

PhD position in speciation genomics of a non-model bird species

A 4-year PhD position in speciation genomics is available in the research group of Dr. Jochen Wolf at the Department of Evolutionary Biology in Uppsala, Sweden.

Background The study of speciation mechanisms remains one of the major challenges in fundamental biological research. The hybrid zone in Europe between Carrion Crows (*Corvus [corone] corone*) and Hooded Crows (*Corvus [corone] cornix*) is a text book example of speciation that has been studied from ecological, behavioral, and morphological perspectives. In contrast, the genetic architecture of the hybrid zone is poorly understood. The crow system represents a case of a very early phase of species divergence that requires new molecular approaches for its comprehensive description.

The project We use several approaches to understand the underlying genetic foundation of this hybrid zone and to identify the few decisive genetic differences between the two taxa. These include a candidate (pigmentation) gene approach, whole genome shotgun sequencing and digital expression analysis.

The successful applicant ideally has a strong background in bioinformatics and experience in handling large sequencing data sets. She/he will be highly involved in de novo assembly of paired end shotgun sequence reads using a combination of Illumina and Roche 454 technology to obtain a first draft of the crow genome. This draft sequence will then be used as a reference for re-sequencing several populations and to conduct population genomic analyses. Therefore, the project also requires a fundamental understanding of population genetic theory.

The candidate will also be involved in handling transcriptome data from crows that are currently being raised in a common garden setup. At a later stage in the project it will also be possible to analyze transcriptome data from a separate project on mallards (*Anas platyrhynchos*). Given the interest, the transcriptome work also offers the opportunity for the candidate to gain experience in the lab including the preparation of barcoded cDNA libraries for several sequencing platforms.

Environment

My group forms part of a recently launched Centre of Excellence, the Uppsala Centre for Evolution and Genomics (<http://www.uceg.uu.se>). It is situated in the Department of Evolutionary Biology, which excels in many aspects of genetics and evolution. The department offers an inspiring international atmosphere, with researchers from around the world. My group also closely interacts with other groups across departmental boundaries to exchange ideas about good solutions for handling next generation sequencing data (http://www.egs.uu.se/evbiol/Persons/Jochen/NGS_Club.html). We also collaborate on research projects with the Max Planck Institute of Ornithology in Radolfzell, Germany and the Max Planck Institute of Evolutionary Biology in Plön, Germany.

The Evolutionary Biology Centre is one of world's leading research institutions in evolutionary biology and encompasses a wide variety of disciplines in the biological sciences. It is situated in Uppsala in Sweden, a beautiful small city of that offers rich opportunities in cultural and outdoor activities. The culture and activities of the city are strongly influenced by the 40 000 students living there.

Application To apply, please send a letter describing your research experience and interests, a CV, and two letters of recommendation to Dr. Jochen Wolf at jochen.wolf@ebc.uu.se. The position will be filled as soon as a suitable candidate has been found. For further information visit the group's website (<http://www.egs.uu.se/evbiol/Persons/Jochen.html>) or contact me directly. Informal inquiries are welcome.

Dr. Jochen Brock Wacain Wolf Department of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden
phone: ++46 18 471 6468 fax:++46 18 471 6310 <http://www.egs.uu.se/evbiol/Persons/Jochen.html> Jochen Wolf <wolf@evolbio.mpg.de>

UWyoming 2 MolEvol

2 Ph.D. positions in computational molecular evolution/comparative genomics remain unfilled and are available immediately (fall semester) in the Molecular Biology Department at University of Wyoming. These positions are fully funded GAs.

Laramie is 2 hours north of Denver in the Rocky Mountains.

Position with David Liberles: Detecting positive diversifying selection in chordate gene families. <http://www.wyomingbioinformatics.org/LiberlesGroup> Position with Jessica Siltberg-Liberles: Characteriz-

ing the evolution of disorder in protein structure and other problems in evolutionary structural biology. <http://uwacadweb.uwyo.edu/uwmolecbio/Faculty/J.Liberless.Files/research.htm>

Applicants should have a B.S. or M.S. in computer science, mathematics, biology, chemistry, or physics. Applicants should have an interdisciplinary background, including undergraduate course work in biology and/or chemistry and programming skills.

Materials needed: CV Transcript of courses and grades Statement of research interests Contact (email) information for 3 references GRE scores recommended but not required.

Apply by email to David Liberles (liberles@uwyo.edu) or Jessica Siltberg-Liberles (jliberle@uwyo.edu) as appropriate.

David Liberles <liberles@uwyo.edu>

Jobs

AmericanMuseumNaturalHistory LaboratorySupervisor	UArizona LabTech OriginMulticellularity	33
AmericanMuseumNaturalHistory LaboratorySupervisor	UCaliforniaLosAngeles FieldAssist MonkeyEvolution	33
Barcelona GroupLeader EvolBiol	UCambridge ResAssist EvolutionCorvidIntelligence	34
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Taipei EvolBiol		

**AmericanMuseumNaturalHistory
LaboratorySupervisorAmericanMu-
seumNaturalHistory
LaboratorySupervisor**

Job: Laboratory Supervisor Institution: American Museum of Natural History Location: New York City Start Date: Immediately

The American Museum of Natural History is looking for a Laboratory Supervisor to work with a group of researchers on a broad variety of evolutionary and systematic problems.

Responsibilities and Duties: Extract and Sequence DNA. Sequence editing (maintaining database) responsible for ensuring lab supplies are on hand, maintain lab equipment, training other laboratory users such as graduate students and postdoctoral fellows.

Qualifications: BS required, familiar with lab procedures for DNA extraction, PCR amplification, cloning, and sequencing. A plus if experienced in DNA analyzing equipment (3730 DNA analyzer and BIO Mech robot), High-throughput, Basic computer skills, experience with Lab related software (sequence editing software), and sequence databases.

Interested applicants should send a cover letter detailing their experience and interests and a CV in PDF, along with the names and contact information of 3 references to Ward Wheeler at wheeler@amnh.org. Subject line MUST include reference to Lab Supervisor Position.

The position is open now.

crowley@amnh.org

Barcelona GroupLeader EvoBiol

GROUP LEADER POSITION (BARCELONA, SPAIN)

The Institute of Evolutionary Biology (IBE, www.ibe.upf-csic.es) is a research institute run by the Consejo Superior de Investigaciones Científicas (CSIC) and the Universitat Pompeu Fabra (UPF). The IBE is currently located in the CMIMA (www.cmima.csic.es) and PRBB (www.prbb.org) buildings, in Barcelona, while a building with new spaces is being prepared in the same campus.

The IBE currently consists of 18 research groups conducting basic research in many aspects of evolutionary biology. The research groups strongly interact with other groups located in the area and have access to outstanding scientific facilities both at the PRBB and the city of Barcelona, including state-of-the-art core ser-

vices such as animal facilities, bioinformatics, genomics, ultrasequencing and many others.

The IBE is recruiting outstanding scientists as group leaders, and a position is currently open under the subject “Genómica comparada y filogenia” (“Comparative genomics and phylogenetics”). The IBE would especially welcome now candidates conducting research on either phylogenetics or statistical genomics. Phylogenetics candidates should carry out research on animal biodiversity from a phylogenetic perspective with the aim of gaining further insight, not only into the tree of life itself, but especially on the evolutionary processes that gave rise to current biodiversity patterns. Ideally, candidates should take a multidisciplinary approach, using a combination of theoretical, morphological, cytological and molecular techniques to address the scientific questions in their areas of research. Statistical genomics candidates should carry out research on genetic diversity at the whole- genome scale from the population genetics, statistics and bioinformatics perspectives. Ideally, they should use state-of-the-art maximum-likelihood and Bayesian techniques for the interpretation of intra- and inter-specific patterns of diversity to infer information on the demographic and selective processes that shape them.

Those interested in formally applying must follow the instructions described in the Boletín Oficial del Estado (see detailed instructions and deadlines in: BOE, 162, 2B: 58937-58953, 2010, <http://www.boe.es/boe/dias/2010/07/05/pdfs/BOE-A-2010-10636.pdf>). If they want more information on the IBE, potential candidates may informally contact the IBE by sending a message (preferably accompanied by a brief CV and a proposed research program) to: director.ibe@csic.es

Xavier Bellés Director of the IBE

[ignacio.ribera <ignacio.ribera@ibe.upf-csic.es>](mailto:ignacio.ribera@ibe.upf-csic.es)

BroadInst ComputationalBiologist

BROAD INSTITUTE (Cambridge, MA USA) Job title: Associate Computational Biologist Group: Malaria Genome Sequencing and Analysis

OVERALL RESPONSIBILITY

We are searching to fill an associate computational biologist position for the Malaria Genome Sequencing and Analysis group at the Broad Institute. The person filling this position will assist in performing bioin-

formatic analyses on genomic and transcriptomic data from malaria parasites. She or he will work collaboratively with other bioinformatic scientists as well as wet lab biologists to interpret data and make it accessible to a large interdisciplinary group. The scope of activities may range from generating analysis pipelines that will be used many times to carrying out one off analyses to ask a specific question of a particular dataset. The broader goals of the work will be to better understand the general biology and evolution of malaria parasites, as well as determine how genomic diversity contributes to drug-resistance, immune evasion, and other etiologies that make malaria one of the most severe global threats to public health.

CHARACTERISTIC DUTIES . Perform bioinformatic analyses to extract biological meaning from 'next-generation' sequencing data and array-based genotyping and transcription data for malaria parasites . Research and identify proper approaches for interrogating data using primary literature . Work collaboratively with wet lab scientists at the Broad as well as other institutions to make data accessible and interpretable . Learn, utilize, and extend existing tools and pipelines for data analysis within the group . Submit large datasets to public archives . Perform other duties as necessitated by the position or as assigned

QUALIFICATIONS Bachelor's Degree (Master's preferred) in computer science, bioinformatics, biological sciences, or related field

Proficiency in: o Unix o Scripting languages such as Perl or Python

Working knowledge of: o Sequence analysis tools (BLAST, HMMer, etc.) o Statistical tools (R, Matlab, etc.) o Relational databases

Please apply at www.broadinstitute.org/careers and search by requisition number 314. Please reference you saw the job posting on EvoDir. We look forward to hearing from you!

Thank you, Yushen

Yushen Chang, M.S. Recruiter Broad Institute of MIT& Harvard T: 617-714-7168 F: 617-714-8993 7 Cambridge Center Cambridge, MA 02142 yushen@broadinstitute.org <http://www.broadinstitute.org/careers> Yushen Chang <yushen@broadinstitute.org>

ColoradoStateU ResAssoc MolEvol

POSITION: Research Associate II

LOCATION: Colorado State University Bioagricultural Sciences and Pest Management C129 Plant Science Building Fort Collins, CO 80523-1177

APPOINTMENT AND SALARY: Twelve-month full-time administrative/professional position. Salary commensurate with qualifications and experience.

RESPONSIBILITIES: We are seeking a highly organized microbiologist/plant pathologist with skills in molecular biology to serve as a lab manager and assist research scientists with research projects. Responsibilities as lab manager include general lab organization, and specifically: (1) ordering of supplies and equipment, (2) maintenance and care of a collection of plant pathogenic bacteria, 3) growth, care, and inoculation of plants in greenhouses and growth chambers, (4) manuscript preparation, and (5) supervision of undergraduate researchers in the laboratory. The lab manager must interact and work collaboratively with others, including postdoctoral, graduate, and undergraduate researchers at CSU and our collaborators at other institutions. The incumbent must pass various biosafety training requirements and be approved for work with federally regulated plant-pathogens. Some duties will involve weekend work hours.

QUALIFICATIONS: Bachelor's degree with more than 3 years of relevant professional experience or a recent Master's degree in Plant Pathology, Microbiology, Biology, Botany, or related field required. Experience in research data collection and reporting is also required. Preference will be given to candidates with demonstrated experience in microbiology and/or plant biology, particularly with skills in basic molecular biology techniques. Basic computer skills in word processing and spreadsheets are required, and basic skills in statistics are desired. Other desirable skills include organizational, interpersonal, supervisory experience, ability to work independently, problem solve, website development, grant writing, and bioinformatics.

AVAILABLE: September 1, 2010

APPLICATION: Send all application materials as a single PDF to Maggie.Hirko@colostate.edu. Please include: 1) a letter of interest including a brief summary outlining experience and qualifications for this position,

2) a C.V., 3) University transcripts (copies are acceptable, but originals may be required of finalists), and 4) names and contact information for three references.

Questions may be directed to Maggie Hirko (970-491-1930)

APPLICATION DEADLINE: August 15, 2010

Colorado State University is an equal opportunity/affirmative action employer and complies with all Federal and Colorado State laws, regulations, and executive orders regarding affirmative action requirements in all programs. The Office of Equal Opportunity and Diversity is located in 101 Student Services Building. In order to assist Colorado State University in meeting its affirmative action responsibilities, ethnic minorities, women and other protected class members are encouraged to apply and so identify themselves.

Colorado State University is committed to providing a safe and productive learning and living community. To achieve that goal, we conduct background investigations for all final candidates being considered for employment. Background checks may include, but are not limited to, criminal history, national sex offender search and motor vehicle history.

Maggie.Hirko@ColoState.EDU

Eagle Idaho FishPopGenetics

Job openings at the Eagle Fish Genetics Lab (IDFG) through PSMFC

JOB OPPORTUNITIES Several new positions are open in our genetics lab in Eagle, Idaho (just outside Boise). These positions (2 biologists, 1 data coordinator, and 4 technicians) are part of 2 new Bonneville Power Administration funded projects evaluating Genetic Stock Identification and Parentage Based Tagging technologies in the Snake River basin. Information about these projects can found at: <http://www.nwcouncil.org/fw/budget/2010/rme/proposalsdone.asp> All 6 positions are through the Pacific States Marine Fisheries Commission and are posted on the PSMFC website: http://www.psmfc.org/Current_PSMFC_Job_Opportunities These job openings are only open until August 1st!!!!

Please contact me with any questions. Thanks,

Matt

Matthew Campbell

Fish Genetics Manager Idaho Department of Fish and Game Eagle Fish Genetics Lab 1800 Trout Rd. Eagle, ID 83616 work (208) 939-6713 fax (208) 939-2415 matthew.campbell@idfg.idaho.gov

heiseihessian@gmail.com

GeorgetownU LaboratoryAssistantProfessor

Full-time Laboratory Assistant Professor in Biology

The Department of Biology of Georgetown University invites applications for a full-time Laboratory Assistant Professor to begin during the Fall semester of 2010. We seek an enthusiastic science educator to actively collaborate with faculty in the development and deployment of our Foundations of Biology laboratory curriculum. We especially encourage applications from science educators able to develop and offer inquiry-based, active learning pedagogy.

The successful candidate will have shared responsibility for the laboratory component of both semesters of Foundations in Biology (BIOL-103, -104), including recruitment and training of teaching assistants, meeting with students in office hours and grading. Additional responsibilities can be tailored to best fit the candidate's areas of expertise and departmental needs, but may include laboratories/discussion sections for upper-level courses, courses devoted to science pedagogy, or involvement in assessment of departmental curricular initiatives.

Applicants should have enthusiasm for science education and a PhD in biology or a Masters degree in science and/or science education. Applicants should possess excellent writing and speaking skills; be well organized and able to carry out position duties independently; have the ability to provide individual and group instruction with an awareness of diverse learning styles; be able to train and manage undergraduate and graduate TAs; and be able to teach effectively in lecture, field and laboratory contexts. This is a nine-month position with the possibility to teach in our summer school for additional compensation. Applicants should send a brief cover letter summarizing their qualifications, a curriculum vitae, and names and contact information of three references.

Learn more about the Department of Biology at <http://www.georgetown.edu/biology>

/ biology.georgetown.edu.

Potential applicants can contact Dr. Heidi Elmendorf (hge@georgetown.edu) with questions.

Applications should be mailed to Laboratory Assistant Professor Search, Department of Biology, P.O. Box 571229, Georgetown University, Washington, DC 20057-1229 or sent via email as pdf files to Ms. Niparat Pitchayanonmetr (np9@georgetown.edu). Review of applications will begin August 1, 2010 and continue until the position is filled.

Georgetown University is committed to workplace diversity as an Affirmative-Action, Equal-Opportunity Employer.

hamiltm1@georgetown.edu

Harvard ResTech EvolDevo

FULL TIME TECHNICIAN WANTED

A full-time technician/research assistant position is available in the group of Cassandra Extavour at Harvard University (Department of Organismal and Evolutionary Biology), Cambridge, MA, USA. This position will primarily assist with a project on stem cell regulation in the emerging model organism *Parhyale hawaiiensis*. For further information on the Extavour lab's work, visit www.extavourlab.com. A 12-month commitment is expected; pending satisfactory performance and availability of funding, the position may be renewed for a further one to three years.

We are seeking a well-trained and self-motivated technician with good organizational, molecular biology, management, and social skills. The successful applicant should have prior laboratory experience with molecular biology techniques, a strong work ethic, and the ability to work independently. A degree in biology or a related field would be a plus. Experience in developmental biology and/or bioinformatics is desirable but not absolutely required. The position is available immediately.

The responsibilities of the technician/research assistant will include the following: creating plasmid constructs for arthropod transgenesis, and protein expression; collection and preparation of arthropod embryos and adult tissues; assistance with maintaining arthropod cultures; preparing media and other reagents; and assistance in the daily operation and maintenance of the lab. Lab

work will include standard molecular biology procedures such as DNA and RNA extraction, PCR, qPCR, RT-PCR, molecular cloning, protein sample preparation, and Western blots.

To apply for this position, please send (1) a cover letter outlining your previous experience and explaining your interest in this position; (2) your curriculum vitae/résumé; and (3) the names of three references, as a single PDF file to extavour@oeb.harvard.edu. The subject line of your email should be "Extavour Tech Position 2010." Informal inquiries are welcome and should be sent to the same e-mail address.

The deadline for submission is 30 July 2010. Interviews will be conducted in July and August 2010.

Harvard University is an affirmative action/equal opportunity employer and applications from women and minorities are encouraged.

Dr. Cassandra Extavour Assistant Professor Department of Organismic and Evolutionary Biology Harvard University 16 Divinity Avenue BioLabs Building Room 4103 Cambridge, MA 02138 USA

Office Tel. 1 617 496 1935 Lab Tel. 1 617 496 1949/1200 Mobile 1 857 383 1443 Fax. 1 617 496 9507

extavour@oeb.harvard.edu

<http://www.extavourlab.com> Administrative Assistant to Dr. Extavour: Barbara Hanrahan Tel. 1 617 496 2132 bhanrahan@oeb.harvard.edu

extavour@oeb.harvard.edu

Orleans INRA StatisticalGenetics

A 16 month position for a statistician modeller is available at the Research Unit on Improvement, Genetics and Physiology of Forest Trees (http://www.orleans.inra.fr/les_unites/ur_agpf) at INRA Orleans (France).

Context: Integrating molecular markers in breeding programs is a challenge in forest tree breeding. To optimize breeding strategies, the "Genetics" research team at UR AGPF develops Monte-Carlo simulation programs concerning the genetic evolution of populations subjected to artificial selection. The recruited statistician will be in charge of 1) adding new methods for genotypic evaluation to the simulation program on the basis of algorithms found in the scientific literature and testing their implementation with various sets of pa-

rameters 2) the development of a graphical interface to facilitate the use of the simulation tool by breeders. The position is opened in the framework of WP3 “Designing and implementation of improved/novel tree breeding strategies” of NovelTree European research project (<http://www.noveltree.eu/index.php>). The simulation tool resulting from this work will be used in priority to optimize the poplar breeding strategies managed by the Research Unit but will also be of interest for other forest tree species.

Starting date should be as soon as possible after October 1st 2010. The application deadline will be September 1st 2010.

Job details Adapt and implement in the existing simulation program statistical routines found in scientific literature or public repositories to predict breeding values using the BLUP (Best Linear Unbiased Prediction) methodology. Participate actively to the choice of the best fitted and performing algorithms to integrate genotypic data (molecular markers) in the mixed models: particularly, the generation of IBD (identity by descent) matrices at marker and QTL. Suggest improvements to the simulation program, especially in all parts concerning statistical treatment of the data, and implement the chosen improvements. Some parts of the software will be validated by comparison with existing tools (AS-Reml, Gibbs samplers for genetic mixed models, etc.). Conceive and build an interface facilitating the use of the simulation tool by breeders, in connection with potential users.

Working Environment The successful candidate will work in the “Genetics” research team, under the co-responsibility of Leopoldo Sanchez and Helene Muranty.

Education and training Master degree in statistics

Required skills: - Expert knowledge in at least one programming language (C ++ / FORTRAN / Java) - Working knowledge of the Linux / UNIX system. - Good scientific and technical English skills.

Gross salary: 1915 euros monthly

For more details and to apply for the post, please contact H. Muranty (Helene.Muranty at- orleans.inra.fr / 33 2 38 41 78 47) or L. Sanchez (Leopoldo.Sanchez at- orleans.inra.fr / 33 2 38 41 78 14) INRA UR Amélioration, Génétique et Physiologie Forestières, 2163 avenue de la Pomme de Pin - CS40001 - Ardon, 45075 ORLEANS CEDEX 2, FRANCE

– Helene Muranty Chargee de Recherches Tel : 33 (0)2 38 41 78 47 - Fax : 33 (0)2 38 41 78 79 UR INRA Amélioration Genetique et Physiologie Forestieres, 2163 av-

enue de la Pomme de Pin - CS40001 - Ardon, 45075 ORLEANS CEDEX 2, FRANCE

Helene.Muranty@orleans.inra.fr

SeoulNatIU MicrobialPhylogeny

Two Faculty Positions at Seoul National University School of Biological Sciences, Korea

The School of Biological Sciences invites applications for two tenure-track faculty positions to preferably begin March 2011 in the areas of 1) Microbiology and its related areas and 2) Phylogeny/Ecology of eukaryotic microorganisms. The responsibilities of these positions include both research and teaching. These positions are open to qualified individuals regardless of nationality. The applicants should have a Ph.D., or equivalent degree along with postdoctoral experience. An attractive start-up package will be provided for successful applicants. Also, governmental research grants are applicable for faculty research. The School offers an excellent environment for collaborative research and is equipped with state of the art research facilities. Additional Departmental information is available at website:<http://biosci.snu.ac.kr>. Interested applicants should send a CV including lists of publications and future research topics by email to Chair, Prof. Jung-Hye Roe (ckm81@snu.ac.kr) in PDF format. Consideration of applications will continue until the positions are filled.

Bruce Waldman <waldman@snu.ac.kr>

SouthAfrica Meerkats

Field volunteer needed to work on Meerkats or Slender mongoose (at Kalahari Meerkat Project), South Africa

Begin: immediately, or whenever possible (for 6 to 12 months) We are looking for two volunteers interested in working as field assistant for a minimum of 6 months on a project on meerkats, and a project on slender mongoose, investigating aspects of communication and cognition. You will be based at the Kalahari Meerkat Project (run by Cambridge University UK and Zurich University Switzerland), located on a game re-

serve (Kuruman River Reserve) in the South African Kalahari close to the Botswana border. Your main work will be to collect the basic data (behavioural, spatial, faeces, etc), perform experiments, and progress or maintain habituation of the partly habituated groups of meerkats or slender mongoose.

Biology/zoology/veterinary students with a BSc/Vordiplom or equivalent are preferred as candidates. Applicants must have an interest in working in the field and show a high patience with the animals. Tasks involved include radio-tracking the groups, do habituation work at their sleeping burrow as well as following them during foraging, behavioural observations, if possible to weigh them, GPS recordings, and perform experiments such as playbacks. You will need an international driver's license (Bs license).

Volunteers are paid a monthly allowance to cover their food, and accommodation will be provided for free. Flight to South Africa (and home) will have to be organized by the applicant, but we will pay the inland traveling (bus from Johannesburg to Kuruman or Upington return, and the pickup from Kuruman or Upington to the study site) as well as 400 US\$ towards the international flight.

If you are interested in this position, please send a CV and a short letter stating your motivation to apply, and two names acting as referees to:

marta.manser@ieu.uzh.ch Prof Marta Manser Animal Behaviour Institute of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstr. 190 8057 Zurich Switzerland Tel. 0041 44 635 52 82

Beke Graw <bekegraw@gmx.de>

SwedishU Agric Field Assist Brown Thornbills

Field assistant position to study nest predation and life-history evolution in Brown Thornbills in Australia

For the upcoming breeding season (Oct.-Dec. 2010) we are looking for a highly motivated volunteer to join our field project investigating nest predation in Brown Thornbills *Acanthiza pusilla*. The study population is located at Trevallyn Reserve next to Launceston, Tasmania (Australia).

Our project researches the influence of nest predation

and habitat quality on life-history strategies. The project of Dr. Michael Griesser is based at the Swedish University of Agricultural Sciences and is a collaboration with Dr. Erik Wapstra at the University of Tasmania.

The work of the volunteer will be to help in carrying out field experiments, locating nests, assisting the ringer in catching and banding of birds, and data management. We will work 5-6 days per week in the field. Observe that temperatures at the beginning of the breeding season can be below zero degree.

Qualifications: (1) BSc in Biology, Ecology or similar qualification (2) Previous field experience (3) Ability to work in small teams and sociable personality (4) Knowledge in observing & handling birds would be a plus (5) Driving licence would be helpful

This is an expenses paid field assistant position, covering accommodation, food and travel expenses of up to 800 Euro to and from Launceston.

Applications - including a CV, a letter of motivation (1 page) and the name of two referees - should be sent to: Nicole Schneider (Nicole.Schneider@ekol.slu.se) and Michael Griesser (Michael.Griesser@ekol.slu.se)

Applications received until 15th July 2010 will be given full consideration.

Nicole Schneider Department of Ecology Swedish University of Agricultural Sciences PO Box 7044 75005 Uppsala Sweden

nick.schnei@googlemail.com

Taipei EvolBiol

Positions: Evolution, Ecology, Microbial Diversity and Bioinformatics

The Biodiversity Research Center (BRC), Academia Sinica, Taipei, Taiwan (see homepage at <http://-biodiv.sinica.edu.tw/>), invites applications for tenure track positions in terrestrial ecology, marine ecology, evolution, microbial diversity and bioinformatics. The rank is open, though junior scientists are preferred. Candidates with a research interest in ecology, microbial diversity, evolutionary biology, or bioinformatics are encouraged to apply. Candidates with good post-doctoral research experience are preferred. BRC is in an expansion mode, with many tenure-track openings. The center is strong in marine biodiversity and molecu-

lar and genomic evolution and has set up a sequencing core with one 454 and two Solexa machines. The center wishes to strengthen research in ecology (especially terrestrial ecology, wetland and coral reef ecosystems), microbial diversity, molecular and genomic evolution, and bioinformatics. The positions will be open until filled; however, the first review will be conducted in the last week of August. An applicant should submit the names and e-mail addresses of three references along with CV (including a list of publications), 3-5 representative papers (pdf files), and a statement of past achievements and future research interests to Ms. Jennifer Jia-Yu Chen (jennyc26@gate.sinica.edu.tw).

wli@uchicago.edu

UArizona LabTech OriginMulticellularity

Dear colleagues, please note the available position below for a laboratory technician.

A Laboratory Technician position is available in the laboratory of Dr. Richard E. Michod (<http://www.eebweb.arizona.edu/Michod/>) in the Department of Ecology and Evolutionary Biology at the University of Arizona, Tucson (<http://www.eebweb.arizona.edu>). We are looking for a motivated, enthusiastic and independent individual with a biological science background (molecular / cell biology is preferable). Responsibilities will include: (1) Daily management of the laboratory, comprising tasks such as ordering materials, maintaining cell culture stocks, preparing reagents and glassware and providing a supportive role for researchers in the lab. (2) Contributing to research projects as required. The main project currently requiring an assistant involves the identification of genes implicated in the origin of multicellularity in the volvocine green algae.

Attributes deemed necessary for this position are good organizational and time management skills and a good work ethic. Although molecular biology skills are preferred, the necessary training will be provided.

The starting date is flexible and the salary range for full-time employment is between \$22,000 and \$26,000 p.a. depending on prior experience. A probationary period applies.

To apply please use the University's online application system on the University of Arizona human resources site (<http://www.hr.arizona.edu/job>) or contact Dr P.

Durand at pdurand@email.arizona.edu for enquiries.

pdurand@email.arizona.edu

UCaliforniaLosAngeles FieldAssist MonkeyEvolution

Field assistant position, Evolution of social strategies in wild capuchin monkeys

Position Description: The Lomas Barbudal Capuchin Project has been running for 20 years, and (funding permitting) will continue for many years to come. Each year we accept about 6 interns who stay a full year and participate in data collection. The project currently monitors 11 social groups of monkeys. Virtually all monkeys are well habituated, and their genetic relationships are known, as well as social histories dating back several years in most cases. The primary focus of research currently is life histories, particularly male migration strategies and female counter-strategies to infanticide.

Application instructions are on the following website: <http://www.sscnet.ucla.edu/anthro/faculty/sperry/-jobs.html> Please read the detailed guide to working on the monkey project BEFORE applying or contacting the project, as this will answer virtually all questions. Applicants are also strongly encouraged to read the book "Manipulative Monkeys: The Capuchins of Lomas Barbudal," which is a popular science book documenting not only the first 15 years of scientific research, but the life style of researchers working at this site.

Salary/funding: None. However, the field manager position (which pays a real salary in addition to room and board) is always someone selected from the pool of former or current interns. We are applying for grants to allow small stipends in addition to paying living and transportation expenses, but currently we do not have such funds. Support provided for internship/volunteer positions (travel, meals, lodging): Room and board are provided, though interns must feed themselves when away on vacation. Upon completion of the 1-year contract, interns qualify for a travel refund of up to \$1000 for their plane fares. Assistants must buy their own medical insurance.

Term of Appointment: Minimum one year, due to the long training investment. Start dates are flexible, but we need people to start immediately (August and every

couple months thereafter.) Applications are accepted at any time, and we fill positions as they become available.

Contact Information:

Susan Perry Dept. of Anthropology, Box 951553, UCLA Los Angeles, CA 90095-1553 USA Telephone Number: 310-267-4338 Website: <http://www.sscnet.ucla.edu/anthro/faculty/sperry> E-mail Address: sperry [at] anthro.ucla.edu

UCambridge ResAssist EvolutionCorvidIntelligence

UCambridge.ResAssist.Jackdaws

Department of Experimental Psychology, University of Cambridge

BBSRC-Funded Research Assistant: Intelligence and Culture in Wild Corvids

Salary Scale: Grade 5, point 34 to 38 (£23,566 - £26,523 per annum).

A BBSRC-funded research assistant post at the University of Cambridge with Dr Alex Thornton is available from 1 October 2010. The project will investigate intelligence and culture in wild jackdaws (*Corvus monedula*). Specifically, the work will use observational data and field experiments to examine the fitness consequences of individual variation in cognitive abilities and the effects of social learning on the development of individual and group behaviour. The position would be ideal for graduates seeking research experience before embarking on a PhD or keen birdwatchers with strong interests in evolution and cognition. The successful candidate will spend the majority of their time conducting fieldwork in and around Madingley village, 4 miles from Cambridge.

Limit of Tenure applies: the post is available for up to five years.

Required experience / knowledge

Essential: - Relevant BSC, or equivalent, to a high level in an appropriate subject (e.g. biological science/zoology, psychology). - Ability to organise time and work independently - Fieldwork experience - Strong computer skills - Good knowledge of research methods and theory in some or all of the following areas: behavioural ecology, evolutionary biology, experimental

psychology

Desirable: - An MSc, or equivalent, in an appropriate subject - Ornithological fieldwork experience - Bird ringing experience - Full driving license - Strong communication skills

How to apply

Informal enquiries can be addressed to Dr Alex Thornton (jant2@cam.ac.uk).

Further particulars and forms are available from <http://www.psychol.cam.ac.uk/pages/posts.html> or from the Departmental Administrator, Department of Experimental Psychology, University of Cambridge, Downing Street, Cambridge, CB2 3EB, UK.

Quoting reference number PJ006908, applicants should send the following: (i) a full CV including the contact details of two referees; (ii) a cover letter outlining how they meet the requirements of the job and why they wish to work on jackdaws (2 sides A4 maximum); and (iii) a completed CHRIS 6 (Parts 1 and 3 only), available at: www.admin.cam.ac.uk/offices/hr/forms/-chris6/. Please send these to the Departmental Administrator, via email to: reception@psychol.cam.ac.uk, or by post to the address above.

The closing date for applications is 13 August 2010, and interviews with short-listed candidates are scheduled for 27 August 2010.

- Dr Alex Thornton Large Animal Research Group Department of Zoology University of Cambridge Cambridge CB2 3EJ

Alex Thornton <jant2@cam.ac.uk>

UCLondon EvolutionaryBiol

UNIVERSITY COLLEGE LONDON Department of Genetics, Evolution and Environment

Chair in Evolutionary and Population Biology

Dear all,

The Department of Genetics, Evolution and Environment at University College London is seeking to fill a Chair (full professorship) in Evolutionary and Population Biology. The job ad has appeared in the latest issue of Science (July 9th) and is pasted below.

We are looking for excellent candidates; we are open with respect to approaches used (theory, bioinformat-

ics, experimentation), level of investigation (cellular to ecosystems) and career stage (successful mid-career scientists or established leaders in their field).

The closing date for applications is 3rd September 2010.

The Department of Genetics, Evolution and Environment brings together scientists with interests in evolutionary, population and environmental biology, genetics, systems and theoretical biology and human genetics. The Department offers a dynamic and stimulating multi-disciplinary research environment and is part of a variety of cross-departmental and cross-institutional groupings within UCL and the wider London research landscape. From spring 2011, the department will be housed in re-furbished lab and office space on UCL's campus in the centre of London.

For more information on the Department, please visit our website (<http://www.ucl.ac.uk/gee>). For informal enquiries, please email the Head of Department, Prof. Andrew Pomiankowski (a.pomiankowski@ucl.ac.uk).

Best regards, Max

++

Advertisement in Science July 9th

Chair in Evolutionary and Population Biology

The appointment will be full time on the UCL Professorial grade. The salary range will be negotiable on the professorial scale but not less than £61,713 per annum, inclusive of London Allowance.

We invite applications from world class research scientists using theoretical or experimental approaches, with no restriction on organism or level of biological organisation studied. The appointment is part of a major initiative to strengthen and diversify research activity in evolutionary, population and environmental biology in newly refurbished laboratories within UCL.

The successful candidate will be expected to play a leadership role in this initiative and promote interaction across the diverse disciplines represented in the Department, the Division of Biosciences and across UCL, as well as co-ordinate efforts to respond to national and international funding initiatives. Furthermore, the successful candidate will play an important part in developing existing and new postgraduate training programmes and contribute to undergraduate teaching.

The successful candidate will have an international reputation in an area of Evolutionary and Population Biology and a track record of running a successful research group, securing competitive funding over a number of years and publishing high impact original research ar-

ticles.

For further details about the vacancy and how to apply online please go to <http://www.ucl.ac.uk/hr/jobs/> and search for Reference Number 1127113.

Informal enquiries may be made to Professor Andrew Pomiankowski, tel: +44 (0)20 7679 7413; email:a.pomiankowski@ucl.ac.uk. Queries regarding the application process should be addressed to Nick McGhee, tel: +44 (0)20 7679 8878; email:n.mcgee@ucl.ac.uk.

Closing Date: 3rd September 2010. Interview Date: Week commencing 11th October 2010.

We particularly welcome female applicants and those from an ethnic minority, as they are under-represented within University College London at this level.

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London 4 Stephenson Way London NW1 2HE, UK

Phone: +44-20-76795095 (internal 25095)

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UdeMontreal EvolutionaryModelling

Département de sciences biologiques Faculté des arts et des sciences

Tenure-Track Position for an Assistant Professor in Ecological Modeling

The Department of Biology invites applications for a tenure-track position for an Assistant Professor specializing in Ecological Modeling.

Responsibilities

Teach undergraduate, graduate and postgraduate courses, supervise graduate students, conduct independent research, produce publications, and contribute to the life and administration of the University. Upon arrival, the priority will be to develop an undergraduate course in ecological modeling.

Interested candidates are strongly encouraged to consult the Department's Web site: www.bio.umontreal.ca
. Requirements

* Ph.D. in ecological modeling or a related field * Postdoctoral research experience is an asset * Strong publication record in international journals with high visibility * Innovative research program in ecological modeling of ecosystems. Interest in modeling the distribution and/or flow of contaminants, nutrients, genes or organisms at various levels in aquatic or terrestrial ecosystems. Candidates are expected to complement theoretical modeling with experimental or field validation. * Interest in interdisciplinary research and openness to collaboration with members of the Department * Excellent aptitude for teaching in higher education and incorporating new technologies * A good working knowledge of French is required. French being the teaching language on campus, candidates who do not speak French should acquire an adequate knowledge of it within a reasonable period after the appointment.

Salary

The Université de Montréal offers a competitive salary and a complete range of fringe benefits.

Starting Date

After January 1, 2011 (subject to budget approval)

Candidates' file, including a curriculum vitae, copies of 3 recent publications or research, a description of their research program (2 pages maximum), and their teaching philosophy should be sent by September 15, 2010. Three confidential letters of reference, from the thesis supervisor, postdoctoral research director, and employer should be sent under separate cover to the same address.

Madame Bernadette Pinel-Alloul, Directrice
Département de sciences biologiques Université
de Montréal C.P. 6128, succ. Centre-ville Montréal
(Québec) H3C 3J7

The Université de Montréal selection process allows all regular professors in the Department to have access to submissions unless the candidate explicitly states in her or his covering letter that access to the file should be limited to the selection committee. This restriction on accessibility will be lifted if the candidate is invited for an interview.

In compliance with Canadian immigration requirements, priority shall be given to Canadian citizens and landed immigrants. The Université de Montréal upholds the principles of employment equity and welcomes applications from women, ethnic and visible minorities, aboriginals and people with disabilities.

Dr. Bernadette Pinel-Alloul Directrice, Professeure titulaire GRIL, Département de Sciences biologiques Université de Montréal C.P. 6128, Succ. Cen-

tre ville Montréal, Qué. Canada, H3C 3J7 Tél: 514-343-6878; 514-343-6784 (bureaux) Fax: 514-343-2293 (département); 514-343-6216 (GRIL) Courriel: bernadette.pinel-alloul@umontreal.ca

Pinel-Alloul Bernadette <bernadette.pinel-alloul@umontreal.ca>

UEdinburgh 3 Evolution

The School of Biological Sciences, University of Edinburgh, has created three new positions to further enhance our capacity in evolutionary biology and infectious disease research. The School is one of the UK's largest and most highly-rated life sciences departments, providing an innovative environment for research and teaching with a strong emphasis on interdisciplinary research. The School is part of the College of Science and Engineering.

Readership in Evolutionary Medicine. You will be an outstanding scientist with the breadth of vision, the ability and energy to give strong academic leadership at the interface of infection, immunity and evolution. An inspirational researcher with an international reputation, you will have an established track record of publication and funding. You will join a large group of researchers associated with the Wellcome Trust Centre in Development for Immunology, Infection and Evolution. This offers a unique interdisciplinary research environment. You will contribute to a vision for the further development of interdisciplinary approaches at the interface of infection, immunity and evolution. You will also pursue excellence in teaching within the spectrum of undergraduate and postgraduate degrees offered in the School. <http://www.jobs.ed.ac.uk/> vacancy ref 3013132 Deadline 17th Sept 2010. Informal enquiries to David Gray, Head of IIR, d.gray@ed.ac.uk or Josephine Pemberton, Head of IEB, j.pemberton@ed.ac.uk

Lectureship in Behaviour and Evolution This new lectureship will extend our research and teaching in behaviour and evolution. Working in a large and multidisciplinary group of evolutionary biologists, you will have an outstanding opportunity to develop your own research and teaching programme in a well-supported environment. You will have a PhD in a relevant area of biology and a strong research record in the evolutionary aspects of behaviour. <http://www.jobs.ed.ac.uk/> vacancy ref 3013131 Deadline 23rd August 2010 Infor-

mal enquiries to Josephine Pemberton, Head of IEB, j.pemberton@ed.ac.uk

Teaching Fellow in Zoology and Evolution You will enhance our undergraduate programme in whole organism biology. Responsible for the design, planning and delivery of a high-quality teaching programme, you will be encouraged to develop a personal programme of scholarship and research activity. The position provides an excellent opportunity to develop your career in a well-supported multidisciplinary environment. You will have a PhD in a relevant area of biology and undergraduate teaching experience. <http://www.jobs.ed.ac.uk/> vacancy ref 3013153 Deadline 25th August 2010. This post is fixed term for 3 years. Informal enquiries to Josephine Pemberton, Head of IEB, j.pemberton@ed.ac.uk

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Prof. J.M. Pemberton Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road EH9 3JT

tel 0131 650 5505 fax 0131 650 6564 <http://wildevolution.biology.ed.ac.uk/> The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

J.Pemberton@ed.ac.uk

UEdinburgh ResTech EvolutionSoaySheep

A research technician position is available for three years on an ERC-Advanced Grant 'Wild Evolutionary Genomics' with Professor Josephine Pemberton, in which Soay sheep sampled over the last three decades on St Kilda will be genotyped on a SNP chip to investigate the quantitative genetics of fitness. Initially, working with the grant holder and a postdoc, the technician will prepare DNA samples for submission to a genotyping subcontractor. Subsequently, the technician will conduct further laboratory work on QTL candidates. Previous experience of molecular laboratory work (DNA preparation, PCR and sequencing) is required.

Apply online by August 24th 2010 at <http://www.jobs.ed.ac.uk> where the reference no is 3013134.

Informal enquiries to: Professor Josephine Pemberton Institute of Evolutionary Biology School of Biological

Sciences University of Edinburgh West Mains Road EH9 3JT

tel 0131 650 5505 fax 0131 650 6564 j.pemberton@ed.ac.uk <http://wildevolution.biology.ed.ac.uk/> – The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

J.Pemberton@ed.ac.uk

UHull EvolBiol

Dear Evoldir members,

A lectureship in Evolutionary Biology is available at the Department of Biological Sciences, University of Hull, UK. Please see below for further details.

The Department of Biological Sciences has an international reputation in Evolutionary Biology, Functional Ecology and Biomedical Science, and seeks to appoint a strongly motivated biologist ready to make a contribution to our Evolutionary Biology research group <http://www2.hull.ac.uk/science/biological_sciences/research/evolutionary_biology.aspx> . The focus of the group is on the molecular analysis of population subdivision and speciation patterns, with a strong integration of population genetic, phylogenetic, behavioural and quantitative genetic approaches to address evolutionary and ecological questions. Current research examines the varied processes that shape individual, population and species diversity. Most importantly, this knowledge is translated into research-driven teaching that benefits students at all levels.

Applications are invited from suitably qualified individuals (who hold a PhD in a relevant subject) with a proven ability to attract funding to support their own program of research. Applicants should have a high quality publication record, and be ready to share their ideas and skills with our students through excellent teaching at both undergraduate and postgraduate level.

Salary range £30,747 - £43,840 pa

For more information about the Department, please see the departmental homepage (http://www2.hull.ac.uk/science/biological_sciences.aspx). For full details on how to apply, see the current vacancies area of the main university home page (follow link from the Departmental homepage, <http://www2.hull.ac.uk/>

science/biologicalsciences/vacancies/lecturer.aspx)

Please feel free to contact me for informal enquiries,

Best wishes

Lori Handley

Dr Lori Lawson Handley Lecturer in Evolutionary Biology Evolutionary Biology Group Department of Biological Sciences Cottingham Road Kingston-upon-Hull HU6 7RX, UK

email l.lawson-handley@hull.ac.uk Tel 0044 (0) 1482 462061 Website http://www2.hull.ac.uk/science/biological_sciences.aspx L.Lawson-Handley@hull.ac.uk

UMichigan EvolBiology

Ecology and Evolutionary Biology University of Michigan

The Department of Ecology and Evolutionary Biology at the University of Michigan invites applications for three tenure-track positions (open rank) in evolution, one of which will be in the area of computational biology. We seek outstanding individuals with research and teaching interests in evolutionary biology or evolutionary ecology. These searches are part of a hiring initiative to expand the evolution program, which includes a coordinated university-wide effort of integration with the computational sciences. Areas of research include evolutionary or ecological genetics and genomics, computational evolutionary biology, evolutionary theory, phylogenetics, and evolution of morphology, function, and behavior. Also strongly encouraged are research programs that take advantage of the outstanding collections of the Museum of Zoology, Herbarium, and Museum of Paleontology. For further information, see <http://eeb.lsa.umich.edu>. To apply, please begin at www.lsa.umich.edu/eeb/apply/-evolsearch, and arrange to have three letters of recommendation submitted through the same website. Review of applications will begin on 15 September 2010.

Women and minorities are encouraged to apply and the University is supportive of the needs of dual career couples. The University of Michigan is an equal opportunity/affirmative action employer.

“Knowles, L” <knowlesl@umich.edu>

UWisconsinParkside Biostatistics

Lecturer, Biology

The Biology department at the University of Wisconsin-Parkside invites applications for a 9-month lecturer position to begin August 2010. The position will teach lecture and laboratory courses in biostatistics for B.S. students in Biological Sciences major, Molecular Biology and Bioinformatics major and the Applied Health Sciences majors. Teach General Education courses in biology and the possibility to teach a special biology course in an area of expertise.

Provide additional duties such as student advising, and curriculum development. Attend departmental meetings and hold regular office hours. Provide outreach services to the Department, University or Community as related to expertise.

Knowledge, Skills and Abilities: * Broad knowledge of biology and biostatistics to undergraduates. * Ability to effectively communicate with students. * Ability to staff and colleagues both verbally and in writing. * Ability to teach lecture and laboratory sections of biostatistics. * Ability to teach general education courses in biology. * Knowledge in scientific methods. * Sensitivity to, or experience in, working with a diverse, multicultural population. * Ability to engage in appropriate instructor-student relationships and interactions and collegial conduct. * Ability to use a computer or a teaching laboratory bench. * Ability to sit and stand for extended periods of time. * Ability to lift and manually operate equipment and supplies for teaching.

Qualifications: Required: * Master's in biology (or biology-related field) or ABD with planned completion of a Master's degree by September, 2010 in biology (or biology-related field). * Graduate experience in statistics or related expertise in biostatistics. Preferred: * Ph.D in Biology or related field or ABD with planned completion of a Ph.D. degree by September, 2010 in biology (or biology-related field). * Experience teaching biostatistics. * Experience teaching a broad range of biology courses. * Experience with college-level teaching. * Experience teaching students of diverse and multicultural backgrounds. * Experience in scientific reasoning. * Experience in biodiversity Salary: Salary is commensurate with qualifications and experience. The University of Wisconsin System provides a liberal benefits package, including participation in a state pension

plan.

Review of Applications: Applications received by July 7th, 2010 are ensured full consideration; position is open until filled.

To Apply: Interested candidates should submit the following, preferably in electronic format: * a cover letter outlining their qualifications for the position, * curriculum vitae * statement of teaching philosophy * three letters of recommendations including the contact information from persons who are willing to serve as references and who can attest to the qualifications required for this position

Email submissions: aiello@uwp.edu

Mail submissions: Katy Aiello, Search Committee Department of Biological Sciences University of Wisconsin-Parkside Kenosha, WI 53141

Gregory C. Mayer Dept. of Biological Sciences University of Wisconsin-Parkside 900 Wood Road Kenosha, WI 53141-2000 USA 262-595-2074 office 262-595-2056 fax mayerg@uwp.edu <http://uwp.edu/~mayerg/>

mayerg@uwp.edu

WageningenU Biosystematics

Wageningen University & Research Centre Full Professor Experimental Biosystematics

Location: Wageningen, the Netherlands Wageningen University is looking for candidates for a Full Professorship Experimental Biosystematics. The focus of the chair is on the mechanisms underlying the processes of speciation and domestication, studied at the species and intra-species level. The scope of the research is the study of evolutionary processes leading to patterns of biodiversity from a comparative perspective and will include both plant- and animal-related topics. Vacancy number PSG-BIOSYS-0002.

For more information www.jobsat.wur.nl

Robin.vanVelzen@wur.nl

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BarcodeLife conference host

The Consortium for the Barcode of Life (CBOL; www.barcodeoflife.org) has received many expressions of interest from institutions interested in hosting the Fourth International Barcode of Life Conference in the fall of 2011. If your institution would like to submit a proposal to host the conference, please send me a message identifying your institution and the proposed conference chair. I will send you the guidelines for preparing your conference proposal. Proposals will be due 1 September and CBOL's Executive Committee plans to select the conference host by 1 October 2010.

Expressions of interest must be received by Monday, 26 July 2010.

Thanks in advance for your interest in the next barcode conference.

Best regards,

David E. Schindel, Executive Secretary

Consortium for the Barcode of Life 202/633-0812; fax 202/633-2938; portable 202/557-1149
Email: SchindelD@si.edu CBOL WEBSITE: <http://www.barcoding.si.edu> Office and overnight delivery address:

National Museum of Natural History Room CE-119
10th & Constitution Avenue, NW Washington, DC 20560

Postal mailing address:

National Museum of Natural History Smithsonian Institution P.O. Box 37012, MRC-105 Washington, DC 20013-7012

"Schindel, David" <schindeld@si.edu>

Bat evolution video

Dear Folks,

following the line of work that our group began a year ago we have added a new video that we believe can help in tasks related to teaching evolution. You can see it at: <http://webs.uvigo.es/plantecology/divulgacion.en.html> The new video illustrates the

changes that have had occur in the shape of skull in different lineages of the family of bats Phyllostomidae, related to the transition to different types of diet from an insectivorous ancestor.

This video was created for free use as teaching material. If anyone is interested, can download a version freely.

I hope you enjoy it.

PD: We appreciate that this information will be spread where you consider being helpful.

Luis Navarro

Luis Navarro phone 1: (+34) 986 812619 Depto. Biología Vegetal phone 2: (+34) 647 343097 Facultad de Ciencias fax: (+34) 986 812556 As Lagoas-Marcosende email: lnavarro@uvigo.es Universidad de Vigo 36200-Vigo <http://webs.uvigo.es/plantecology> Spain

Luis Navarro <lnavarro@uvigo.es>

Bone homogenizer

Dear Evoldir members,

We are considering buying a disrupter/homogenizer for the homogenization of wood and bone samples. There are several different models available on the market but we have yet to find one that specifically states that it is suitable for wood/bone samples. We're interested in bench-top models that can process up to 24 samples at once (preferably in an eppendorf tube format). Any advice anyone can offer on suitable or tried-and-tested equipment/models for the automated disruption/homogenization of wood and bone samples will be gratefully appreciated.

Thanks

Paul

Paul Bloor Profesor Especial Coordinador Grupo de Especies Silvestres Instituto de Genética Universidad Nacional de Colombia Entrada Calle 53 con Cra 37 Edificio 426 Código Postal 111321 Bogotá D.C - COLOMBIA
pbloor@gmail.com

coalescent web site down

Dear Colleagues,

I was hoping that someone could provide a contact for the person(s) who administer the www.coalescence.dk web site or pass a message along.

I was hoping to use the simulators there for some exercises in a workshop held this week. To my discomfort, the animators are down. When you click on the links you get permission denied or "forbidden"!

Also, I do not know who to thank but the animations are an excellent resource! That web site is very valuable for teaching and I appreciate the effort that went into building the animators!

Sincerely, Matt

Matthew B. Hamilton, PhD Associate Professor
Georgetown University Department of Biology,
Reiss 406 37th and O Streets NW Washington,
DC 20057 202-687-5924 (office) 202-687-5662 (fax)
<http://www9.georgetown.edu/faculty/hamiltm1/>
hamiltm1@georgetown.edu

Deep-sea shrimp samples

Dear evoldir members,

I have just started my PhD at the University of the Azores and I am trying to get as many samples I can of two deep-sea shrimp species for molecular studies. The species I am interested in are **Acantheephyra pelagica* and **Acantheephyra eximia* from any part of the Atlantic and Mediterranean sea. Please, let me know if you have any samples of these species that you may be willing to share for molecular studies or if you know anyone with access to this kind of samples.

Thank you for your time and my best regards,

Diana Catarino

Attention: New address!

Diana Catarino PhD Student DOP - University of the Azores
Rua Prof. Dr. Frederico Machado, nr 4 9901-862 Horta Faial Portugal

Ph: +351.292200400 Fax: +351.292200411 e-mail:
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Divergence to MutationRate answers

Recently, I posed the following question to the Evoldir community:

I would like to calculate a mutation rate per site, per generation, from a mtDNA control region divergence rate reported in the literature in units of divergence per million years. In my calculation, I am assuming that each species diverges at an equal rate, and I have a generation time of 5 years. The reported divergence rate is 4.8% per million years. To get the mutation rate, I divide 0.048/1,000,000, multiply by 5 for my generation time and divide by 2 to account for the fact that I have two lineages going different directions. This gives me a lineage-specific mutation rate of 1.2×10^{-7} per-site, per-generation.

That seems like an awfully slow rate for the control region. Where am I going wrong? I feel like my math is off somehow but I can't figure out where.

I think the consensus is that (a) there are a lot of caveats to calculating a mutation rate this way, but mathematically it is correct, and (b) 1.2×10^{-7} is well within the range of control region evolution. Specific responses to the question are listed below.

—

The rationale behind your estimate of mutation rate (strictly speaking substitution rate) looks correct to me.

A problem, though, might arise from equating short- and long-term evolutionary rates. There is an extensive literature on the slowing down of substitution rates over longer evolutionary timescales.

For example, mutation rates estimated from pedigrees on human mtDNA are at least an order of magnitude higher than phylogenetic estimates. Similar conclusions have repeatedly been reached for microorganisms. One likely reason behind this discrepancy stems from purifying selection acting in the long term.

Best wishes

Dr François Balloux

—

in 1.2×10^{-7} per-site, per-generation, is this % or base pairs... or something else?

When I see your calculation, you just transformed 4.8 % per my to 0.048 /1.000.000 and I dont know if what you are really looking for is substitutions per generation (meaning, you have to account for the length of the sequence in focus)? But perhabs I am also wrong

It looks like you are starting with a relatively low divergence rate (4.8%) to begin with in your calculations. For example, some of the control region work that I have done have 14.27% substitution per site per million years.

1.) There are different rates in different lineages so you really need to use a rate specific to your lineage.

2.) I am not sure where you are getting the rate, but if it is already in 4.8% per million years, it should be the rate for that branch [i.e., you would not have to divide by 2] - but double check where those figures came from...

3.) Your math looks ok, I think it looks low just the way you provide it.... 1.2×10^{-7} per-site is really 12% per million generations, with 5 years per generation you are back to your 2.4 % per million years (but to reiterate you may not have to divide by 2).

The 4.8% per million does seem slow for the control region, but again it depends what species that figure came from. I have found a lot of errors in published literature, so i would caution you against using previous numbers without checking where they came from.

I can't comment on whether this is a reasonable rate for the control region. In fact nobody could, because you didn't say what species you are working with. Presumably animals, which have a region called "control region", but are they humans, lizards, butterflies, horse-shoe crabs, or what?

Another problem is that what you are calculating is not the mutation rate, which is the rate at which a site actually changes from one base pair to another, but the substitution rate, which is the mutation rate multiplied by the fixation probability for that region in those organisms. The two are commonly confused in everyday language, but they are only equal for neutral mutations.

1×10^{-7} seems actually pretty HIGH to me, compared to rates for COI and cytb (we usually estimate a rate

of about 1×10^{-8}). Maybe for the d-loop this is normal? You might look at Ho et al's paper in MBE (Mol. Biol. Evol. 22(7):1561-1568. 2005), for a discussion of mutation rates and clocks in general. It looks like for the d-loop in mammals they find rates between 10 and 40% per million years (or 1×10^{-7} per YEAR)

I guess it all depends on what kind of rate was reported in the literature exactly: If the reported rate is units of divergence per million years 'per site' your calculation is correct. If it was units of divergence per million years 'for the mtDNA control region as a whole' (so not per nucleotide site), you would need to further divide your rate by the number of nucleotide sites in that region to get the per-site rate. This means that your rate would become even slower.

I don't know what rate values to expect from the mtDNA control region,

— / —

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>

EncyclopediaOfLife Fellowship

The Encyclopedia of Life (EOL) is now accepting applications for its 2011 Rubenstein Fellows competition.

This international program seeks to support and extend the impact of original biodiversity research by postgraduates, graduate students, and other early career scientists. Rubenstein Fellows funds provide partial support for up to one year so that biodiversity research, databases, and media can be effectively translated into rich, online resources available through the Encyclopedia of Life. Fellows must work in collaboration with a research mentor and may encourage collaborative and synthetic work with a community of colleagues.

Fellows and mentors also help EOL to develop effective strategies for engaging and supporting the scientific community.

For more information on the program and to download the application package, please visit <http://www.eol.org/content/page/fellows> . Applications must be submitted via email to fellows_program@eol.org no later than 15 September 2010.

Questions regarding the EOL Fellows competition should be directed to the EOL Fellows Coordinator at fellows_program@eol.org.

Leo Shapiro <lshapiro@eol.org>

GeneticsSelectionEvolution paper

Hi,

Does anyone have a PDF of:

Largiader CR, Estoup A, Lecerf F, Champigneulle A, Guyomard R (2001) Microsatellite analysis of polyandry and spawning site competition in brown trout (*Salmo trutta* L.). *Genetics Selection Evolution*, 33, 205-222.

Thanks,

Roseanne Miller PhD. student School of Biological Sciences University of Aberdeen Tillydrone Avenue Aberdeen, AB24 2TZ

“Miller, Roseanne Judith” <r.miller@abdn.ac.uk>

Heiser tribute

TRIBUTE: To a remarkable biologist for his contributions to Evolution

We offer a tribute to a remarkable evolutionary biologist, whose life's work and publications set the stage for our current understanding of the roles of hybridization and introgression in nature and in the evolution of crops and weeds. Here we summarize briefly not only his achievements and their influence on current paradigms, but how we can learn today from the model he exemplified for research and student mentoring. As in the Sherlock Holmes mysteries he loved, this scientist's full identity follows the initial clues. Enjoy the discovery!

Born in 1920 in rural Indiana, this scientist's first paper on sunflowers (*Helianthus*) appeared in the very first 1947 volume of *Evolution* (SSE), immediately preceding one by Ernst Mayr on ecological speciation; his last papers, on the North American origins of domesticated sunflowers were published in 2008 (*Intl J. Plnt.*

Sci., Genet. Crop Resour. Crop Evol., PNAS). In his first paper, he argued that introgressive hybridization between a pair of annual sunflowers increased the variability of the two species, yet each remained distinct. Later, as a Distinguished Professor at Indiana University, he followed and valued greatly the contributions of new advances in genomics to our understanding of the role of introgression in the evolution of sunflowers, other plants, and also animals as in long-term studies of finches. The person we seek to honor is Charles B. Heiser, a member of the National Academy of Sciences whose diverse accomplishments are reflected in four notable presidencies: The Society for the Study of Evolution (1974), American Society of Plant Taxonomists (1967), Botanical Society of America (1980) and the Society for Economic Botany (1978). So what can we learn from his life about science, living life fully, and sharing it with others?

Response: think broadly and critically, delve deeply, be open to new perspectives, and share what you learn. Together with the nearly 60 graduate students he advised directly at Indiana University, Heiser explored or tested hypotheses of plant evolutionary biology in at least 30 tropical and temperate genera of 14 different families (most notably sunflowers in the Asteraceae and peppers in the Solanaceae). He thus imagined life's diversity broadly in his research efforts and their application, pursuing not only many studies of hybridization and polyploidy in relation to plant evolution, reproductive isolation, and taxonomy (e.g. *Aster*, *Asclepias*, *Capsicum*, *Claytonia*, *Helianthus*, *Solanum*), but also conducting thorough investigations of the evolutionary origins and uses of cultivated plants in these genera and others (southwestern *Proboscidea*, or devils' claw; bottle gourds and their pollination; Quinoa and amaranths). His research contributed to the development of the domesticated naranjilla 'orange' of Ecuador (*Solanum quitoense*), the loofah bath sponge (*Luffa operculata*), and the cultagen *Pepperomia* 'Tena.' Of many awards (details in the upcoming *Pl. Sci. Bull.* 56 (3), ASPT), the international commendation from the National Institute of Ecuador for Agricultural Research for research in Ecuador was especially important to him.

As exemplified by his work with Jorge Soria in Ecuador, Heiser also shared what he learned with the students he mentored, his many collaborators, and a larger audience of science-interested readers through books and speaking engagements. His own most influential mentors hailed from his PhD. Institution, U.C. Berkeley (i.e., G. Ledyard Stebbins, his advisor in 'spirit and deed,' *Ann. Mo. Bot. Gard.* 59: 370), and from Washington University in St. Louis, MO where he majored

in English, took his first botany class, and completed his MA. There his mentors were Robert Woodson (who shared his vast knowledge of botany and *Asclepias*) and Edgar Anderson (brilliant author of early papers on hybridization and introgression, topics Heiser later reviewed for the larger botanical community). Anderson stimulated Heiser's first studies of sunflower hybridization, encouraging what became a lifelong interest in how plants intersect with people. His pioneering work on weedy, hybridizing sunflowers, and their importance in nascent North American agriculture, became the subject of one of six books he published for science-interested audiences. His books drew from extensive research on the evolution of domesticates from their wild relatives, and indeed on the origin of agriculture itself, as evident in his popular textbook, *Seed to Civilization*. Heiser's excellent writing, outreach to the public, and his role in mentoring students earned him both the prestigious Raven Outreach Award, from the American Society of Plant Taxonomists, and the 2004 Garden Globe Award for 'best talent/writing.'

Charles B. Heiser died at his home in Bloomington, IN on 11 June 2010, just short of his 90th birthday, from complications of a stroke, but his

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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>

Hiring survey

Some time ago we asked newly hired, tenure-track or equivalent, permanent faculty members to take a survey indicating the number of publications, grants, years as postdocs, etc. they had at time of hire. We would like to thank the many readers of Evoldir that participated in this survey.

If you are interested in the published results you can find them at the *Israel Journal of Ecology and Evolution* 55(4): 381-392. Although this is not an open-access journal, the publisher has kindly allowed open access to a number of articles in this volume that would be of interest to undergraduate students, graduate students, and postdocs pursuing academic careers in ecology or evolutionary biology.

Our article is followed by two excellent responses, Darwin was correct and so were Marshall et al. (2009)

by Roy Turgington and Life history and multi-level selection in academe by Douglas Morris. Finally, in the IJEE soapbox Robert Holt provides thoughtful reflection on some general issues for anyone entering ecology or evolution as a profession. All of these articles can be found free at the link below.

<http://www.sciencefromisrael.com/app/-home/issue.asp?referrer=3Dparent&backto=journal,1,13;homemainpublications,2,5>; Best regards,

Jon Marshall

Jonathon C. Marshall, Ph.D. Dept. of Zoology Weber State University 2505 University Circle Ogden, UT 84408

Phone (801) 626-6587

Faculty Page: <http://sites.google.com/site/drmarshallwebsite/Research> Page: <http://jcmarshall.blogspot.com/>

jonathon_c_marshall@hotmail.com

Holocene shells DNA isolation

Dear all

I would like to isolate DNA from holocene shells which were obtained by boring with a drill in a lagoon area. Those shells were estimated to be about 8500 years old and the quantity available is about 20 mgr. I would greatly appreciate if anyone with a similar experience could provide feedback. The applications needed are pcr/sequencing. I am not sure if there's any DNA left in those samples and moreover if the starting material would be enough for the isolation procedure.

Thanks everyone Vasilis Papatotiropoulos

Vasilis Papatotiropoulos <vpapasot@gmail.com>

Hybridization with multilocus data

Evoldir community:

I have a microsatellite dataset comprising both sexual diploid taxa and a set of asexual individuals (both diploid and triploid) that we think are hybrids between various combinations of these sexual diploids.

I'm looking for a method that would allow me to assess these hybridization scenarios with some sort of optimality approach (ML, Bayesian, etc.), using the allele frequencies of the potential parents and their putative hybrid offspring as input data. I'd be happy with software that could handle the diploids-only scenario (both diploid parents and hybrids), but if such methods exist for the analysis of triploid hybrids and their putative diploid parents that would be great.

I've dug around a bit, and both NewHybrids (Anderson and Thompson 2002) and GenoDive (Miermans) may offer some of these functions. I'd appreciate any comments from EvoDir users regarding these programs or (especially) others that come to mind.

Thanks! James – James Beck Department of Biology Duke University Durham, NC 27708 <http://www.duke.edu/~jbb31/> “It’s cold outside, but brightly lit. Skip the subway, let’s go to the overground...” U2 (Zooropa) 1993

jbb31@duke.edu

Lemey seminar July16

Philippe Lemey will be giving a free online seminar on Friday July 16 at noon PDT on

“Phylogenetic diffusion models and their applications in viral epidemiology”

Abstract: Emerging infectious diseases continue to appear all over the world, and importantly, they have also risen significantly over time after. Having the potential to quickly adapt to new hosts and environments, RNA viruses are prime candidates to emerge as global threats to human health. Their rapid rate of evolution, however, also turns viral genomes into valuable resources to reconstruct the spatial and temporal processes that are shaping epidemic or endemic dynamics. In this seminar, I will highlight recent developments in phylogenetic diffusion models that tie together sequence evolution and geographic history in a coherent statistical framework. Both discrete and continuous phylogeographic models have recently been implemented in a Bayesian statistical approach. I will position this approach among other popular phylogeographic methods, and then focus on applications in viral molecular epidemiology to demonstrate their use. Finally, I will hint at future extensions that may provide entirely new opportunities for phylogeographic hypothesis testing.

For more information on how to attend this and other seminars, visit phyloseminar.org.

ematsen@gmail.com

Micro genotyping

Dear all, We have developed a suite of microsatellite markers, and are hoping to find a good quality, relatively inexpensive institution to genotype our samples for us. We plan to start small (~ 150 individuals, ~ 20 msats), but hope to expand in the future. Can anyone recommend some good places to look/contact. I thought I remembered this being asked before, but can't seem to find it in the archive (neither mine nor evodir's). Thank you all for any help you can give us.

tripp

–

Kenneth S Macdonald III New Mexico State University Dept of Fish, Wildlife& Conservation Ecology Box 30003, MSC-4901 Las Cruces, NM 88003-8003

Phone: 575.646.5022 email tripp@nmsu.edu

“Heck, we’re invertebrates, my boy! As a whole, we’re the movers and shakers on this planet! Spineless superheroes, that’s what we are!” - Father Worm

Micro touchdown dropout answers

Hello, all–

Several months ago I posted a question on microsatellite dropout with touchdown programs, and realized that I have yet to put the replies together and send them out to the list. Better late than never, I suppose! Thanks to all who replied.

There didn't seem to be a consensus position: some people noticed dropout, some didn't, many seem to run touchdown programs with great success. No one could point me to a paper, so the phenomenon may not be published. Seems like it may vary considerably with

DNA source and genotyping technology. My original question is below, followed by the replies:

Initial question:

Is there anything published on the frequency of allele dropout when using touchdown programs to amplify microsatellites?

Years ago, I tested some microsats (for crabs, I believe) with a touchdown program and with a range of single-annealing temp programs. When I ran the PCRs out on a BaseStation, it was obvious that in a significant number of instances the touchdown program resulted in homozygotes, while the single-temp programs showed heterozygotes. It appeared that in heterozygotes, sometimes the smaller-length alleles were being preferentially amplified with the touchdown program, and the larger alleles were dropping out. Taking this as a cautionary tale, I've always been careful to run microsats with optimized single-temp programs. Other than that, I never really followed up on it. I note now that it is not uncommon to see papers that use touchdown PCR to amplify microsats, and am curious if a) there is anything published on the matter, and b) anyone else has had noticed dropout (or not!) in program comparisons.

Carolyn Tepolt carolyn.tepolt@gmail.com

Replies:

Unfortunately I don't know of any publications that discuss this issue but thought I'd drop you a line since I have experienced the same thing myself. It's been exactly as you describe with the larger of the two alleles dropping out with a touchdown but not with its own single temp. It's a shame since it was a good way of getting lots of loci with varying Tm's going in a multiplex. I guess it makes a bit of sense though since with a touchdown, the amplification gets going right at the extreme limit of its Tm range. This would tend to favour more easily amplified fragments ie the shorter ones. It's amazing really that such a small advantage can make such a big difference but I guess since it happens early in a reaction, the advantage is exponential.

As an aside, I got around this by having multiple Tm's in a reaction ie alternate cycles of two (or maybe three, I can't remember for sure) different temperatures, but with no touchdown between them. This helped a lot, presumably because at the upper temp, the other loci didn't amplify at all so the allele length advantage was removed. It was a bit of fiddling around but meant I could keep my multiplex together and not have to subsequently pool. I would give this a whirl if I found myself in this situation again. Good luck.

N.Aitken niccy.aitken@canberra.edu.au

We didn't notice any significantly greater null-allele problem with an optimized touchdown program vs. optimized single-temp program; in fact we noticed the opposite, but some of this may be due to our study.

For work described in a manuscript currently in revision, we used touchdown while amplifying loci in extracts from pericarps of Quercus acorns, for which the DNA may be somewhat degraded. We used undiluted extracts, and amplified three separate multiplex panels totalling 10 loci, using touchdown programs optimized for our species and tissue. To quantify error rates we re-genotyped a number of pericarps once or twice and found that, on average, even in very good samples about 1.7% of loci would be heterozygotes on one run and homozygotes on another. For this paper, we were assigning these pericarps to source trees, so I wrote an R program to handle the potential impact of null alleles upon assignment probabilities within a likelihood context.

It seems that the large majority of our null alleles were due to issues with pericarp DNA; for us the optimized touchdown programs (plus not diluting our extracts) gave better results than optimized single-temp programs.

Doug Scofield dgscofield@ucla.edu

I almost always use touchdown, as it saves on months of optimisation. Overall, it has given larger peaks for the same samples. I have been using it for parentage, so I know when there is a null allele. Null alleles have not been a problem so far (except with 1/7 loci), despite 3 loci having large size ranges.

I am also keen to know if Qiagen multiplexing kits have any influence on dropout rates. I'd imagine they should as they are designed to amplify different microsats of vastly different lengths in a single PCR.

Patrick Hamilton p.b.hamilton@exeter.ac.uk

I have learn and use touch down prc protocol for amplification of genes allèles with unspecific primers prior to cloning and sequencing

— / —

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>

PSB Microbiome Manuscript deadline

The submission deadline for manuscripts to be considered for the “Microbiome Studies” special session of the Pacific Symposium on Biocomputing has been extended to 26 July. For more information, please see: <http://psb.stanford.edu/cfp-microbiome.html> James A. Foster, U. Idaho Jason Moore, Dartmouth Medical School “James A. Foster” <foster@uidaho.edu>

PSB MicrobiomeStudies due

Just a quick reminder, manuscripts to be considered for the (refereed and pubmed indexed) special session at PSB 2011 on “Microbiome Studies” are due 7/18.

Details are here: <http://psb.stanford.edu/cfp-microbiome.html> james a. foster university of Idaho

foster@uidaho.edu

Question on GMYC

Hi,

I'm trying to do the clustering on the phylogenetic tree of 695 bacterial *phoB* proteins, but I have a couple of questions for applying the GMYC model using R:

1. When I apply the single threshold method the summary is listed as below

method: single likelihood of null model: NaN maximum likelihood of GMYC model: NaN likelihood ratio: NaN result of LR test: NaNNA

number of ML clusters: 76 confidence interval: NA-NA

number of ML entities: 481 confidence interval: NA-NA

threshold time: -0.0023826

Why the likelihood other parameters are NAN? When I apply the multiple threshold model, after a long list of likelihood (maybe), it shows an error... Does it have something to do with the bootstrap value equal to zero or the memory issue?

2. After I plot the test (`plot(test1)`), the clustered tree is demonstrated. However, because the tree is very compact with low resolution, you cannot differentiate the 695 genomes at all, how can I output the clusters and entities and parse them by myself?

3. If I want to construct a phylogenetic tree with high confidence before I do the clustering, can I just bootstrap a tree using UPGMA method using MEGA? or do I need to use the maximum likelihood method to search the tree space, say, using PAUP?

Many thanks in advance!

Best wishes,

shan

– Shan Li Bioinformatics UNC Charlotte

Shan Li <lishan989@gmail.com>

RoyalSociety OriginOfSpecies

Royal Society Publishing has just published ' Origin of species: 150 years later' compiled and edited by Hans Ellegren. See - <http://rstb.royalsocietypublishing.org/site/2010/speciation.xhtml> for further details or you can go straight to the issue contents which are freely available online until the end of July 2010 at <http://rstb.royalsocietypublishing.org/content/365/-1547.toc> The print issue is available at the special price of £47.50. You can order this online via the above web page (enter special code TB1547 when prompted) or, alternatively, you can contact debbie.vaughan@royalsociety.org

All Royal Society content (65,000+ articles dating back to 1665) is FREE to access until 30th July 2010 (<http://royalsocietypublishing.org/seefurther>)

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RoyalSociety ViralEmergence

Royal Society Publishing has just published New experimental and theoretical approaches towards the understanding of the emergence of viral infections compiled and edited by Santiago F Elena and Rémy Froisart. See - http://rstb.royalsocietypublishing.org/site/2010/emerging_viruses.xhtml for further details or you can go straight to the issue contents which are freely available online until the end of July 2010 at <http://rstb.royalsocietypublishing.org/content/365/1548.toc> The print issue is available at the special price of £47.50. You can order this online via the above web page (enter special code TB1548 when prompted) or, alternatively, you can contact debbie.vaughan@royalsociety.org

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SmallScaleSNPs answers

Dear all,

Thank you for all the replies I received regarding methods for small scale SNP genotyping. It seems a common problem in evolution and ecology studies so I'll summarise the replies I got in this email. To save space I'll not acknowledge people individually (unless when quoting their entire emails) but thank you all so much for sending me the suggestions!

The most obvious one is restriction enzyme (PCR-RFLP / CAPS): If the SNP is in a restriction site, you can simply PCR across it, digest, and run on a gel.

<http://www.ncbi.nlm.nih.gov/projects/genome/probe/doc/TechCAPS.shtml> I was also recommended the following tool for selecting restriction enzymes for CAPS:

<http://pgrc.ipk-gatersleben.de/snp2caps/> If the SNP isn't in a restriction site, one may be engineered:

<http://www.ncbi.nlm.nih.gov/projects/genome/probe/doc/TechDCAPS.shtml>

Apart from restriction digestion, the most popular methods are allele-specific PCR (AS-PCR) and related: two allele-specific primers can be designed to complement the SNP at the 3' end. There are many variations to this, e.g. labeling the two allele-specific primers with different fluorescent dyes; making the two primers different lengths; running two separate reactions with the reverse primers at different locations so each allele-specific product is of different length; etc.

This could also be made medium-throughput:

Multiplex SNP-SCALE: a cost-effective medium-throughput single nucleotide polymorphism genotyping method

Kenta, T; Gratten, J; Haigh, NS, et al. (2008) MOLECULAR ECOLOGY RESOURCES 8 (6) 1230-1238

David Remington kindly shared some experience in primer design for AS-PCR:

'My strategy would be to use Primer3 or something similar to design the primers to ensure you get something as well-behaved as possible. You would use the sequence for containing one of the two versions of the SNP, fixing the location of the SNP-specific primer and letting the program pick the second primer. If the SNP-specific primer has problems (e.g. too much internal base pairing), you can try making the SNP-specific primer the reverse primer rather than forward. Then use the other SNP allele in the template sequence and try the corresponding primer with the new 3' base, and specify the 2nd primer the program found for the first version to see if that is still acceptable. This may get tricky, and you might have to try a bunch of combinations, different 5' starting points for the SNP-specific primer, etc. As a last resort, you can relax the program's parameters slightly and see if you get something workable.

'I usually try for Tm close to 60 degrees (the Primer3 default) and use a touchdown cycle starting annealing at 62 and stepping down to 55 or 52 over the first 7-10 cycles. That helps take care of the possibility of additional mismatch sites causing problems. If you need to pick less-than-optimal primers based on self-complementarity, etc, doing a hot start on your PCR can reduce problems with primer dimers. One nice thing about this approach is that you're not very limited in where the 2nd primer goes, since all you need to do is see the band on a gel. It could be 200 bases away or 1200.

'I haven't tried the following, but you could even use 2 different 2nd primers for the two different allele-specific reactions to give you different product lengths. Then you could mix them together after PCR and run in the same lane on the gel. It would essentially look like a length polymorphism.'

And Pirmin Nietlisbach shared his own method:

'The discrimination among SNP states is achieved through the competition of two reverse primers with their 3'-end complementary to either SNP state and being of differing length. One advantage of this method is that it can be combined with microsatellite typing or typing of several SNPs in the same multiplex PCR. I am currently working on a manuscript on this method, which I probably could send you sometime next week if you are interested (let me know). I attach you a paper, that also used almost the same method. The method does need some optimization, but I am not aware of a method that does not (even sequencing may pose some problems and potentially require cloning, if heterozygotes are not obvious in the electropherogram). However, careful primer design should keep optimization time to a minimum. It worked well for me when I designed primers in a way that the reverse primers had a 1-2 C lower melting temperature and higher concentration than the forward primer.

'This should keep competition between the two allele-specific reverse primers high. I did not introduce deliberate mismatches into the primer sequence as Li et al. did (attached paper). However, as I was working

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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>

Software coalescentSimulation

Dear all,

We are pleased to announce the release of msms (<http://www.mabs.at/ewing/msms/>). Msms is a coalescent simulation program for a structured population with selection at a single diploid locus. The program includes the functionality of the simulator ms to model population structure and demography, but adds a model for deme- and time-dependent selection using forward simulations. The program can be used, e.g., to study

hard and soft selective sweeps in structured populations or the genetic footprint of local adaptation. The implementation is designed to be easily extendable and widely deployable. The interface and output format are compatible with ms. Performance is comparable to ms, even with selection included.

An open access publication is in press as an application note in "Bioinformatics". Source code and manuals are provided at the web site of the program <http://www.mabs.at/ewing/msms/>. Users are encouraged to subscribe to the news mailing list at: <https://lists.sourceforge.net/lists/listinfo/ms2-news>. Greg Ewing and Joachim Hermisson The Mathematics and Bio-Sciences Group University of Vienna Max F. Perutz Laboratories Dr. Bohrgasse 9 A-1030 Vienna, Austria gregory.ewing@univie.ac.at

Software

LVBphylogenysoftware,release2 3

Dear all,

LVB 2.3 has been released. LVB uses parsimony to reconstruct phylogeny from nucleotide multiple alignments.

LVB 2.3 is available for Mac OS X 10.6, and as C source code which may be compiled for Linux or other systems. Download it here:

<http://biology.st-andrews.ac.uk/cegg/lvb.aspx> Compared to LVB 2.2, LVB 2.3 has:

- Potentially better results. It follows each round of simulated annealing by a round of hill-climbing. It also performs a greater number of searches (re-starts).
- Improved ease of use. The user no longer has to say anything about the desired length of the analysis. LVB makes a 'reasonable' decision about when to stop.

I would be interested to hear any surprises - pleasant or unpleasant - about LVB's performance in comparison with other parsimony programs, particularly if you can send me full details of both analyses and the input alignment (which I will not re-distribute without permission).

Thank you and best regards,

Daniel Barker db60@st-andrews.ac.uk

- Daniel Barker <http://bio.st-andrews.ac.uk/staff/>

db60.htm The University of St Andrews is a charity registered in Scotland : No SC013532

db60@st-andrews.ac.uk

julie.turgeon@bio.ulaval.ca

Software New Version FLOCK Program

FLOCK is designed to unravel genetic structure within a collection of genotypes, whether pure or admixed. It is assumed that pure, “source”, samples are not available. The program may be used to solve the “number (K) of populations” problem, separate pure and admixed specimens into K groups (K is known), picture structural relationships between samples. FLOCK is a non- Bayesian method and therefore differs substantially from previous clustering algorithms. Its working principle is repeated re-allocation of all collected specimens (total sample) to the k subsamples. The number of re-allocations until convergence typically stands between five and ten. The method was published as:

Duchesne P, Turgeon J (2009) FLOCK: a method for quick mapping of admixture without source samples. *Molecular Ecology Resources* 9: 1333-1344

A new version (2.0) is currently available. FLOCK now signals by red printing all P Values that exceed the Bonferroni corrected threshold (0.05/ number of runs) so that runs that are not validated by allocation number tables are easily identified. Also, FLOCK 2.0 may be run for a sequence of values of k in a single batch process. A separate output file, named the plateau record, is now automatically generated to facilitate plateau analysis, a powerful tool to estimate K.

FLOCK 2.0 can be downloaded at:

http://www.bio.ulaval.ca/no_cache/departement/-professeurs/fiche_des_professeurs/professeur/11/13/
Julie Turgeon (julie.turgeon@bio.ulaval.ca)

and

Pierre Duchesne (pierre.duchesne@bio.ulaval.ca)

Département de biologie

Université Laval

Québec, Québec

CANADA G1V 0A6

Software tinyFLP update

We are happy to announce an update of our tinyFLP software for automatic binning of AFLP data. The software is now in version 1.11; we have included several bugfixes and recommend to switch to this version, available under

<http://sourceforge.net/projects/tinyflp/> The new download policy at sourceforge now allows also users from Sudan, North Korea, Syria, Iran and Cuba to retrieve the software - you're welcome!

–
Dr. Wolfgang Arthofer

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http://www.uibk.ac.at/ecology/forschung/-molecular_ecology.html.de Wolfgang Arthofer
<Wolfgang.Arthofer@uibk.ac.at>

Subsampling frozen tissue

Hello all.

I am trying to sub-sample some frozen tissue. I would like it to stay frozen, and have been searching for an easy way of obtaining a core to be put directly into a 2ml cryo tube. Does anyone have a recommendation about good frozen tissue corers out there, or some other way of quickly “stamping” out a suitably sized tissue sample from a -80 frozen sample.

Thank you for the help.

Anders.

Anders.Goncalvesdasilva@csiro.au

PostDocs

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Adelaide Australia AncientDNA

PhD and Postdoc opportunities at the Australian Centre for Ancient DNA, Adelaide, Australia

We are looking for interested graduate students, who are highly motivated and enjoy independent and unusual research in the general areas below. An interest in evolution and natural history are key requirements, and a background in any of the following would be useful: evolution, genetics, molecular biology, bioinformatics/computing, chemistry/biochemistry, palaeontology, archaeology, and anthropology.

1. Environmental Genomics (including 1-2 postdoc positions) New genomic approaches for Biodiversity studies of Australian Soils, Water, Grasses, Forensic samples and Antarctic biota A number of PhD positions are

available in a large-scale project to apply high throughput sequencing approaches to the analysis of environmental samples and develop a new range of methods to perform biodiversity surveys, taxonomic discovery, and environmental impact reports. The project will employ multiplexed PCR, 2nd/3rd Gen Sequencing, Bioinformatics and Phylogenetics to develop novel systems for rapid and accurate biodiversity assessment. Key topics within the project are the analysis of Australian soils, natural and re-use water supplies, Australian native grasses, Antarctic biota, and forensic material. A strong molecular Biology and/or bioinformatics background is required. The project is a \$1M Australian Research Council-industry partnership.

1-2 postdoc positions will also be available for this project, and will carry supervisory responsibilities for the PhD projects. It is anticipated that one position will be oriented towards data generation, and another towards bioinformatics/database analysis.

2. Evolutionary Bioinformatics This project will apply

the latest evolutionary bioinformatics methods to the study of ancient and modern DNA generated through new genomics and 3rd Gen sequencing data. Study species include a wide range of ancient humans, domestic animals, environmental samples, and broader evolutionary projects such as marsupial evolution, and extinct species such as thylacines, mammoths and other megafauna. The datasets will include genomic sequencing projects, SNP arrays and multigene phylogenies.

3. Ancient human DNA and Domestication genomics
Several project opportunities are available to work with ancient humans, animals and plants. These projects will use advanced new genomic techniques to study ancient populations and species, and focus on evolutionary history, archaeology/anthropology, and the study of domestic/commensal animals to trace human movement, and identify and analyse genetic loci under selection. The methods used will include SNP and capture array approaches, and a strong expertise in molecular biology and bioinformatics is required. Recent studies have examined Neolithic farmers in Europe, pre-Columbian South Americans, and bovinds, chickens, pigs, and rats from around the world.

International Students wishing to study at The University of Adelaide in 2011 should check the available scholarship opportunities (<http://www.adelaide.edu.au/graduatecentre/scholarships/postgrad/international/>) as they provide payment of full tuition fees plus an annual living allowance of approximately AUD\$21,000 tax free. Note the closing date for international scholarship enrolment 31st August, 2010 or 30th October for Australian/NZ applicants. Both the Australian Department of Immigration and University of Adelaide expect international applicants to meet English Language Proficiency (ELP) requirements. The ELP is based on high scores in IELTS (International English Language Testing System) or TOEFL (Test of English as a Foreign Language). For further information please refer to <http://www.international.adelaide.edu.au/admission/> or http://www.adelaide.edu.au/publications/pdfs/inter_pgcw_en10.pdf. Expressions of interest from applicants with strong graduate marks, a good TOEFL score, and a background in evolution/bioinformatics/molecular biology are encouraged. Please contact the following supervisors and provide your CV/resume:

Prof. Alan Cooper (alan.cooper@adelaide.edu.au) Dr. Wolfgang Haak (wolfgang.haak@adelaide.edu.au) Dr. Bastien Llamas (bastien.llamas@adelaide.edu.au)

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Prof. Alan Cooper ARC Federation Fellow Director,
Australian Centre for Ancient DNA

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

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

Barcelona GenomicsBioinformatics

POSTDOCTORAL POSITIONS IN GENOMICS AND BIOINFORMATICS Two openings are available to work on the project entitled “Evolutionary and functional analysis of polymorphic inversions in the human genome”, selected for 5-year funding through an ERC Starting Grant from the European Research Council. This project aims to improve our understanding on the impact of inversions in the human genome at multiple levels by combining methods of different disciplines, such as next-generation genomic techniques, bioinformatics, population genetics, and molecular evolution. Successful candidates will form part of a young, very dynamic, and interdisciplinary research team located at the Institute of Biotechnology and Biomedicine (IBB) of the Universitat Autònoma de Barcelona (UAB).

The IBB is a multidisciplinary and international center located at the heart of the beautiful UAB campus, which has been designated Campus of International Excellence in biomedicine. It is located in Bellaterra, a small residential town just 20 km away from Barcelona and with excellent public transportation connections.

Available positions: We are seeking highly motivated individuals with a PhD degree and research experience in the following relevant fields:

1. Postdoc expert in high-throughput genomics and molecular biology techniques. The main role will be to develop new methods to genotype inversions and study the distribution of these inversions in human populations with the help of a technician. Experience in next-generation sequencing techniques will be highly valued.
2. Postdoc with strong background in bioinformatic

analysis of DNA sequences. This person will be responsible of the study of the functional consequences of inversions by merging all the available information in the human genome (annotation, expression levels, etc).

Conditions: Salaries will be very competitive according to profile and experience of candidates. Duration of contracts will range from 1 to 4 years.

Starting date: All positions are available from October 2010.

Application: Send a CV and a one-paragraph summary of previous research experience to Mario Cáceres (mcaceres@icrea.cat).

mcaceres@icrea.cat

Boston ButterflyComparativeGenomics

Post-doctoral Position at Boston University

A postdoctoral position is available immediately to work with Sean Mullen on an NSF-funded project to examine the comparative genomic basis of butterfly wing pattern variation.

Butterflies display a massive array of color patterns, but much of this diversity appears to be a result of variation in the elements of a conserved wing pattern ground plan. Consistent with this hypothesis, emerging research is revealing that the genetic basis of color pattern mimicry is conserved, at least among closely-related species. Current work in the lab is aimed at identifying the genes responsible for color pattern mimicry in *Heliconius*, *Limnitis*, and *Papilio* butterflies using a novel strategy that utilizes bulk segregant analyses paired with Illumina sequenced RAD tags, fine mapping, BAC contig sequencing, SNP discovery via genome resequencing, and array-based SNP genotyping.

Toward this end, the lab is currently searching for a post-doc with a strong background in evolutionary genomics and/or bioinformatics to assist with analysis of large genomic and population genomic datasets. Significant opportunities exist for collaborative interactions with the lab of Marcus Kronforst at Harvard University as well as with other members of the broader *Heliconius* butterfly community.

To apply, send a CV, a description of research interests and experience, and the names, addresses, phone num-

bers, and e-mail addresses of three references to Sean Mullen at smullen@bu.edu or at this address: Department of Biology, Boston University, 5 Cummington St., Boston MA 02215, USA.

Boston University is an Equal Opportunity/Affirmative Action Employer.

mkronforst@cgr.harvard.edu

ClemsonU MolPhylogeographics

A Post-Doctoral Position is available in the lab of Dr. Peter Marko at Clemson University in the areas of phylogeography and population genetics. The lab's research focuses on the use of molecular phylogeographic data to understand the historical development of and contemporary maintenance of species distributions (<http://www.clemson.edu/-biosci/faculty/marko/lab/index.html>). The Post-doc will work collaboratively with the senior scientist and graduate students on the population structure and biogeography of tropical and/or temperate marine species.

The successful candidate will be involved with data collection and analysis of large sequence data sets, some gathered with "next-generation" methods. Candidates should have a background in population genetics or phylogeography; recent PhDs with limited empirical experience but with strong theoretical backgrounds are also encouraged to apply. In addition to the primary research responsibilities, duties will include assisting graduate students, preparation of papers for publication, and the organization and curation of large sequence datasets. The start date for the position is flexible and funding is available for at two years.

For more information contact Peter Marko at [pmarko\(at\)clemson.edu](mailto:pmarko(at)clemson.edu). Informal inquiries about the research area and projects are welcome. To apply, send a CV, a description of your research interests and your PhD research, and contact information for three references to the above email address.

Peter Marko <pmarko@clemson.edu>

DukeU ComputationalEvolutionaryBiol

A 2-year postdoctoral appointment is available in the Rodrigo lab at Duke University beginning in October 2010 or later. The research would be in the broad area of computational evolutionary biology, with specific projects in evolutionary genetics, phylogenomics, or statistical phylogenetics. This position would suit someone who has knowledge of molecular sequence analysis, phylogenetics, population genetics, computational statistics, and can program in Java or other high-level languages. Knowledge of next-generation sequencing technologies, the coalescent, Bayesian MCMC methods, and R would be an advantage.

Please contact me by email to discuss:
a.rodrico@nescent.org. Thanks

Allen Rodrigo

a.rodrico@nescent.org

EAWAG Switzerland EvolutionaryBiol

Dear Colleagues,

evolutionary biologists and ecologists are also invited to apply for the position advertized below.

best wishes, jukka jokela

2-Year Postdoctoral Fellowship

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based but internationally active research institute within the domain of the ETH (Swiss Federal Institute of Science and Technology). It is committed to the ecologically, economically and socially responsible management of water.

In honor of its 75th anniversary in 2011, Eawag, the Swiss Federal Institute of Aquatic Science & Technology, announces a new opportunity for highly qualified individuals to apply for a

2-Year Postdoctoral Fellowship

to conduct research in any field in the area of aquatic science and technology. Eawag focuses on cutting-edge research that is driven by the needs of society and leads to significant advances in the aquatic sciences. Innovative approaches and technologies for the sustainable management and use of water are developed through collaborations among natural and social scientists and engineers.

Selection of the postdoctoral fellow will be based on his or her academic record and a concise proposal for a research project that is relevant to research activities conducted at Eawag. The postdoctoral fellow will be hosted within one of Eawag's 12 Research Departments < http://www.eawag.ch/about/-organisation/orgchart/index_EN > . Those interested in applying for this position should contact the Head of the Research Department most relevant to his or her research before September 16, 2010 to determine whether the Department would be willing to act as a host for the project. All applications must include a letter of endorsement from a Head of one of Eawag's Research Departments.

The selection decision will be made in early December 2010. It is anticipated that the starting date for the postdoctoral fellowship will be between February and May 2011. An earned Ph.D. degree is required for the postdoctoral appointment.

Applications must include

- * a brief letter of application stating the title of the proposed postdoctoral project and identifying the Research Department that will host the project
- * a curriculum vitae including a list of publications
- * a concise research proposal (not to exceed 5 pages including references)
- * a letter of endorsement from the Head of one of Eawag's Research Departments
- * names and contact information for three academic references

Please send the application as one single PDF file to Sandra Egler, Human Resources Department, recruiting@eawag.ch, indicating reference number 107002.

The deadline for applications is October 14, 2010.

Jukka.Jokela@eawag.ch

EmoryU AdaptiveEvolution

Postdoctoral positions are available in the Department of Biology, Emory University, Atlanta, GA. The Long-

term goals of our research are to elucidate the mechanisms of the spectral tuning of visual pigments and adaptive evolution of dim-light and color vision.

Selected References:

Yokoyama, S., Tada, T., Zhang, H. and Britt, L. (2008) Elucidation of phenotypic adaptations: molecular analyses of dim-light vision proteins in vertebrates. *PNAS* 105: 13480-13485. Yokoyama, S. (2008) Evolution of dim-light and color vision pigments. *Annu. Rev. Genomics Hum. Genet.* 9: 259-282.

Tada, T., Altun, A. and Yokoyama, S. (2009) Evolutionary replacement of UV vision by violet vision in fish. *Proc. Natl. Acad. Sci. USA* 106: 17457-17462. Altun, A., Yokoyama, S. and Morokuma, K. (2009) Color tuning in short wavelength-sensitive human and mouse visual pigments: Ab initio quantum mechanics/molecular mechanics studies. *J. Phys. Chem. A* 113: 11685-11692.

We are looking for recent graduates who are well versed in experimental molecular genetics. If you are interested, please send CV to Shozo Yokoyama (syokoya@emory.edu).

Shozo Yokoyama <syokoya@emory.edu>

GeorgiaInstTech EvolutionHostParasite

Postdoctoral Position in Evolutionary Ecology of Host-Parasite Interactions

A postdoctoral position focusing on the evolutionary ecology of host-parasite interactions is available in the laboratory of Meghan Duffy at the Georgia Institute of Technology. The successful candidate for this position will be expected to carry out independent research contributing to our understanding of the evolution of hosts and parasites, and how rapid evolution influences ecological host-parasite dynamics. There will also be the potential to develop additional projects building on the strengths, interests, and expertise of the successful candidate. Research will involve using *Daphnia** and their microparasites as a model system, and will involve a combination of field work and lab experiments. Experience in 1) disease ecology and/or 2) evolutionary ecology is expected. Experience working with *Daphnia** would be beneficial, but is not required.

More information on the Duffy Lab can be found at:

<http://duffylab.biology.gatech.edu> Georgia Tech was recently named one of the Top 15 Places to Work in Academia by The Scientist magazine, and Atlanta is consistently ranked among the top ten places for young professionals.

The start date for this position is flexible. Funding is available for at least two years, but is contingent on satisfactory progress in year one. Interested individuals should send a CV, a brief description of research and professional goals, and the names and contact information for 3 references to Meghan Duffy by e-mail (duffy@gatech.edu).

Review of applications will start on 1 September 2010 and will continue until the position is filled.

Meghan Duffy, Ph.D. Assistant Professor School of Biology Georgia Institute of Technology 310 Ferst Drive Atlanta, GA 30332-0230 Phone: (404) 894-8426 Fax: (404) 894-0519 duffy@gatech.edu

New webpage address: <http://duffylab.biology.gatech.edu> duffy.ma@gmail.com

Harvard ButterflyPopulationGenomics

Post-doctoral Position at Harvard University

A postdoctoral position is available immediately to work with Marcus Kronforst on the population genomics of butterflies. A major project in the lab is focused on identifying the genetic basis of adaptive color pattern variation and color-based mate preference in *Heliconius* butterflies and then elucidating the mechanisms by which the developmental process translates this DNA sequence variation into morphological and behavioral variation. In pursuit of these goals, the lab is currently searching for a post-doc with a strong background in bioinformatics/computational biology to assist with analysis of large genomic and population genomic datasets. In addition to assisting with the current *Heliconius* genome project, this post-doc will lead efforts in the lab focused on analysis of full genome resequencing data (assembly, automated polymorphism identification & scoring, population genetic analyses, etc.). This post-doc will also be responsible for some lab work on the side (DNA/RNA extractions, PCR, sequencing library prep, etc) as well as collecting butterflies in Latin America. Significant opportunities exist for collaborative interactions with the lab of Sean

Mullen at Boston University as well as with other members of the broader Heliconius butterfly community.

Potential applicants can find out more about the lab at: <http://www.people.fas.harvard.edu/~mkronfor/-index.html> To apply, send a CV, a description of research interests and experience, and the names, addresses, phone numbers, and e-mail addresses of three references to Marcus Kronforst at mkronforst@cgr.harvard.edu or at this address: FAS Center for Systems Biology, Harvard University, 52 Oxford St., Cambridge MA 02138, USA.

Harvard University is an Equal Opportunity/Affirmative Action Employer.

mkronforst@cgr.harvard.edu

Harvard EvoDevo

POSTDOCTORAL POSITION AVAILABLE

A Postdoctoral Researcher position is available in Cassandra Extavour's group at Harvard University (Department of Organismal and Evolutionary Biology), Cambridge, MA, USA. The Postdoctoral Researcher will participate in a variety of projects on stem cell regulation in the emerging model organism *Parhyale hawaiiensis*. The project will make use of use transgenesis, live imaging, experimental embryology, and transcriptomics to explore cell fate decision in wild type, regulative, and self-renewing developmental contexts. For further information on the Extavour lab's work, visit www.extavourlab.com. A 12-month commitment is expected; pending satisfactory performance and availability of funding, the position may be renewed for a further one to three years.

A Ph.D. in developmental biology, stem cell biology, evolutionary developmental biology or related fields is required. Applicants should also possess strong skills in molecular biology, microscopy, and microdissection (of embryos and tissues in a 50-300 um size range). Experience working with large data sets, bioinformatics and next-generation sequencing analysis is desirable but not absolutely required. Applicants should be enthusiastic, creative, organized, and highly motivated. Excellent communication skills and a strong publication record are expected. The position is available immediately.

To apply for this position, please send (1) a cover letter outlining your previous experience and explaining

your interest in this position; (2) your curriculum vitae/résumé; and (3) the names of three references, as a single PDF file to extavour@oeb.harvard.edu. One of your letters of reference should be from your Ph.D. supervisor. The subject line of your email should be "Extavour Postdoc 2010." Informal inquiries are welcome and should be sent to the same e-mail address.

The deadline for submission is 30 July 2010. Interviews will be conducted in July and August 2010.

Harvard University is an affirmative action/equal opportunity employer and applications from women and minorities are encouraged.

Dr. Cassandra Extavour Assistant Professor Department of Organismic and Evolutionary Biology Harvard University 16 Divinity Avenue BioLabs Building Room 4103 Cambridge, MA 02138 USA

Office Tel. 1 617 496 1935 Lab Tel. 1 617 496 1949/1200 Mobile 1 857 383 1443 Fax. 1 617 496 9507

extavour@oeb.harvard.edu

<http://www.extavourlab.com> Administrative Assistant to Dr. Extavour: Barbara Hanrahan Tel. 1 617 496 2132 bhanrahan@oeb.harvard.edu

extavour@oeb.harvard.edu

Lisbon EvolBiol

dear and reputable members of the evoldir,

the portuguese foundation for science and technology (FCT) is about to award several dozens postdoctoral fellowships (~1,500 not taxable euros per month, renewed no prob for up to 3 years but 6 years are possible if duly justified).

i would like to invite recent, and not so recent, ph.d.'s (the "desirable" 5-years after the pd.d. are not a hard cutoff)– in applied mathematics, statistics, and computer science, as well as biologists with a strong interest and potential in computational population genetics, genomics-era data mining, and statistics for phylogenies to contact me asap so we can apply for these funds together.

i have six cutting-edge ready-to-go projects already written down and backed by very strong preliminary results that interested applicants and i can propose to FCT as postdoc-research topics.

two projects are in genomics-era data mining, three are

in computational population genetics, and one in statistics for phylogenies.

the specifics of the proposals will be discussed with candidates whose CV will be deemed appropriate and then applications will be finalized and submitted.

preparing the formal application and submitting it will require from the postdoc applicant that he/she enters CV-related info in the FCT site and not much more.

the nearest submission deadline is september 6th 2010 (to start on January 2011 or later).

therefore interested researchers please email your CV, names of two+ references, and some informal lines describing relevant experience with widely used popgen and phylogenetics programs, C and unix-shell proficiency, etc, via email to

marcos a antezana (maantezana@fc.ul.pt) and

marcos.antezana@gmail.com

best to you all

marcos

Lyon Evolution of MitoticSpindleShape

Lyon/France. Evolution of the Mitotic Spindle Shape

In the context of a Human Frontiers Science Program (HFSP) grant, a post-doctoral position is open in our group for 3 years to study the evolution of the mitotic spindle shape using the diversity of nematode embryos. This interdisciplinary project involves two other groups based in Dresden/Germany and Harvard/US and combines biophysics and cell biology, with evolutionary biology. To carry out this study we will develop techniques to apply molecular methods, and quantitative light- and electron microscopy to a number of non-model organisms throughout the nematode phylum. Our goal is to develop a comprehensive model of how the mitotic spindle is shaped through evolution by mutation, selection, drift, and cellular biophysics.

Candidates should have research skills/experience in some or all of the following: molecular biology, cell biology, genetics, imaging, programming and bioinformatics, *C. elegans* biology.

In addition, ideal candidates will be highly motivated and have a strong interest for evolutionary questions.

Travel between the three groups and close collaboration will be an integral part of the project.

The lab is located in the Laboratory of Molecular Biology of the Cell (LBMC) at Ecole Normale Supérieure (ENS) de Lyon / France <http://www.ens-lyon.fr/LBMC/ENG/web/nav/> in a friendly and very enthusiastic scientific environment.

Interested candidates should email Marie DELATTRE (marie.delattre@ens-lyon.fr) with a CV (with at least two references) and cover letter indicating your research interests, background, and motivation for applying.

Marie DELATTRE, PhD LBMC-ENS Lyon 46 allée d'Italie 69007 LYON 00 33 4 72 72 89 30

[marie delattre <marie.delattre@ens-lyon.fr>](mailto:marie.delattre@ens-lyon.fr)

MichiganStateU Drosophila EvolutionaryGenetics

A postdoctoral position is available to study the genetic architecture of wing shape in *Drosophila melanogaster* in the lab of Ian Dworkin (<https://www.msu.edu/~idworkin/>) at Michigan State University. The successful candidate will utilize a combination of genetic and genomic approaches to identify polymorphisms associated with variation for wing shape, and in particular to aid in the development and implementation of methods to describe the shape trajectories of these genetic effects, and how these genetic effects interact with the environment. The initial genetic associations will then be validated using a combination of genetic associations, linkage, and mapping in large natural populations of *Drosophila*, to address the genetic contributions in the wild. This is part of a larger project to understand the relationship between genetic and phenotypic variation and evolutionary change using the *Drosophila* wing as a model organ. The position is part of a collaborative project involving Ian Dworkin (Michigan State University), David Houle (Florida State University), and Isaac Salazar-Ciudad (Universitat Autònoma de Barcelona).

Primary responsibility of this position will be in performing and validating the genetic associations, including phenotyping, genotyping and analysis of the genetic associations. The winning candidate will also collaborate with a larger team to compare models to empirical results, aid in refining the model, and use it to make evolutionary predictions, which will be tested empirically using artificial selection on wing shape. Prefer-

ence will be given to candidates with a PhD in quantitative or statistical genetics, the statistical analysis of shape (geometric morphometrics) or *Drosophila* developmental genetics, with some experience in statistical programming (i.e. using R, SAS or Matlab); and a desire to fuse developmental, genetic and evolutionary approaches to fundamental questions about the relationship between genotype and phenotype.

The position is for an initial period of two years, and may be extended for an additional two years. The Post Doc will be among an exciting group of Evolutionary biologists (<http://eebb.msu.edu/index.php>), and associated with the larger BEACON center for the study of Evolution in action (<http://www.beacon.msu.edu/>), providing an exciting and dynamic working environment.

Applications should be submitted as a single pdf file and include a curriculum vitae, a summary of research accomplishments and future research objectives, and the names and contact information for at least two professional references (and preferably three). Review of applications will begin July 30th, 2010 and continue until a suitable candidate is identified. Application materials should be sent electronically to Ian Dworkin (idworkin "at" msu "dot" edu).

Michigan State University is an Affirmative action/Equal opportunity employer.

Ian Dworkin Assistant Professor Zoology, Genetics, EEBB and BEACON. Michigan State University idworkin "at" msu "dot" edu

ian.dworkin@gmail.com

Montpellier PetrelKinRecognition

Postdoc position (24 months) available immediately in Montpellier, France

We are looking for interested junior researcher, who is highly motivated for an unusual research challenge:

Chemical characterisation of individual and species olfactory signatures in petrels (procellariiformes seabirds).

The candidate should be able to integrate himself in different scientific and cultural environments. She/he has some background in gas-chromatography and mass spectrometry techniques preferably for analysing volatiles organic compounds. Candidates with a back-

ground in insect chemical communication systems are also welcome. The candidate should be ready to travel to Kerguelen Islands, subantarctic, for fieldwork. Consequently, an interest and motivation to work both in a laboratory (for gas-chromatography and mass spectrometry), and in the field (in Subantarctic, to collect samples and perform behavioural experiments), are needed. The candidate should have some experience in field work in the wild (conceiving behavioural experimental protocols, sampling protocols etc). A good knowledge in bio-molecular work for genetics is also welcome. The first step of the project starts from the data recently obtained by one of our PhD student. The compounds produced by the uropygial gland (the main gland in birds), and those found on feathers show that in petrels it exist a chemical badge identifying species, sex, and individual. We are interested in analysing now the actual odour of the birds, sampling the air around the individual, and to show whether i) the individual, species, and sex badges still exist, ii) it exist a "family odour" identifying kin related birds. The second step of the project will be based on the data about the petrels' Major Histocompatibility Complex (MHC) that one of our postdoctoral students is currently obtaining. The candidate will try to link the personal odour of a bird with its MHC characteristics, to explore the hypothesis that MHC drives petrels' mate choice as it happens in mice.

Please contact the following supervisor and provide your CV/resume:

Dr. Francesco Bonadonna

Behavioural Ecology Group CNRS - CEFÉ, UMR 5175 1919, route de Mende F-34293 Montpellier phone: +33 (0)4 67 61 34 31 fax: +33 (0)4 67 41 21 38 e-mail: francesco.bonadonna@cefe.cnrs.fr <http://www.cefe.cnrs.fr/ecomp/> Francesco BONADONNA <francesco.bonadonna@cefe.cnrs.fr>

NatInstHealth MD VectorEcologyEvolution

Vector Ecology & Evolution Post-Doctoral Position Available at NIH. A post-doctoral position is available in the International Studies of Malaria and Entomology Section, Laboratory of Malaria and Vector Research at NIH/NIAID. We study mosquito ecology, population genetics, and mosquito-pathogen interactions from an evolutionary perspective using diverse approaches and

methodologies. Recently, we have focused on the dry season ecology, behavior, and physiology of anophelines in the Sahel; on the evolutionary forces that underlie speciation in *An. gambiae*; and on mosquito mating behavior. We are looking for a highly motivated, independently-thinking individual, who wants to design and conduct field and/or laboratory studies on disease vectors. A Ph.D. in entomology, ecology, behavior, quantitative/population genetics, or related field and at least one first-author publication are required. Experience in field biology, molecular biology, parasitology, and statistical analysis is desirable. No more than 5 years since completion of Ph.D. degree. To apply, please send CV, statement of research interests, reprints of recent papers, and names of three references to Tovi Lehmann (E-mail: tlehmann@niaid.nih.gov) by August 15, 2010.

Additional information can be found in: <http://lehmannlab.freehostia.com/> Tovi Lehmann Laboratory of Malaria and Vector Research, NIAID, NIH 12735 Twinbrook Parkway, Room 2W-09-C Rockville MD 20852 Email: TLehmann@niaid.nih.gov Phone: 301-451-1059 Fax: 301-480-2038 <http://lehmannlab.freehostia.com/> "Lehmann, Tovi (NIH/NIAID) [E]" <tlehmann@niaid.nih.gov>

Netherlands BirdAdaptation to light

To assess the impact of artificial light on flora and fauna a large-scale project has been funded by STW, Philips and the NAM. The project will be carried out jointly by the Nature Conservation and Plant Ecology Group at Wageningen University (NCP-WU) and the Animal Ecology Department of the Netherlands Institute of Ecology (NIOO-KNAW), in close collaboration with the Netherlands Society for Research on Flora and Fauna (VOFF), Philips Lighting and the NAM.

For this project we are looking for

2 post-docs & 2 PhD students Job description: The two post-docs will be responsible for the day to day running of the project, especially the collection and analysis of the data from a large scale experiment on 40 different sites. After a base line year, these sites will be randomly assigned to different light treatments. Flora and fauna around these sites will be monitored by the VOFF. The two PhD students will carry out in-depth projects on the impact of artificial light, closely linked to the large scale project.

Post-doc 1 (based at the NIOO-KNAW, vacancy number ESG ECO-0034) will coordinate, integrate and analyze the animal group surveys of the large scale experiment and will co-supervise PhD project 1 on the effects of artificial light on reproduction and survival in birds. (S)he will furthermore carry out part of the bird inventory survey and participate in smaller-scale experiments.

Post-doc 2 (based at the WUR, vacancy number ESG ECO-0030) will analyze the spatial patterns of the vegetation structure and phenology in the large-scale experiment and will co-supervise PhD project 2 on the effects of artificial light at different trophic levels. (S)he will furthermore participate in smaller scale experiments.

PhD student 1 (based at the NIOO-KNAW, vacancy number ESG ECO-0035) will carry out research on effects of artificial lights on reproduction and survival in birds, both as part of the large scale experiment and in separate smaller scale experiments.

PhD student 2 (based at the WUR, vacancy number ESG ECO-0031) will carry out research on the effects of artificial light on organisms at different trophic levels using moths as a model group, both as part of the large scale experiment and in small scale experiments.

Requirements Post-docs: We are looking for enthusiastic candidates with a PhD in Ecology or equivalent, experience with large scale data sets, statistical analysis methods and affinity for field work, as evidenced by publications, good social skills and a thorough knowledge of the Dutch flora and fauna.

Appointment Post-docs: The appointment will be on a temporary basis for a maximum of 4 years. The gross salary starts at 2.379,- per month, scale 10, Collective Agreement for Dutch Universities (CAO-Nederlandse Universiteiten). Start date 1 October, or shortly thereafter.

Requirements PhD students: We are looking for enthusiastic candidates with a MSc in Ecology or equivalent and experience with experimental work in the field and a good knowledge of the Dutch flora and fauna.

Appointment PhD students: The appointment will be on a temporary basis for a maximum of 4 years and with a probationary period of 18 months. The gross salary starts at 2.042,- per month in the 1st year, and will gradually increase to a maximum of 2.612,- per month in the 4th year, scale P, Collective Agreement for Dutch Universities (CAO-Nederlandse Universiteiten). Start date 1 October, or shortly thereafter.

Information: Additional information about these positions are available upon request from Prof. Mar-

cel E. Visser (m.visser@nioo.knaw.nl or 026-4791253) and from Prof. F. Berendse (F.berendse@wur.nl 0317-484973) or Dr. Elmar M. Veenendaal (Elmar.veenendaal@wur.nl 0317-483815). More information about the NIOO can be found at www.nioo.knaw.nl, about the WUR at www.wur.nl and the VOFF at www.voff.nl.

Applications: Please send your application including complete curriculum vitae and names of three referees to Gerda Giesen at NIOO-KNAW, P.O. Box 40, 6666 ZG Heteren, The Netherlands (g.giesen@nioo.knaw.nl). The closing date for application is 16 August 2010, and the interviews will take place early September.

“Visser, Marcel” <M.Visser@nioo.knaw.nl>

Nice France CaenorhabditisEvolution

POSTDOCTORAL POSITION: Developmental plasticity and evolution of the germ line in *Caenorhabditis* nematodes (IBDC, Nice, France)

A postdoc position is available in the lab of Christian Braendle to study the plasticity and evolution of the germ line in *Caenorhabditis* nematodes. The basic project aims are to mechanistically dissect the plastic adjustment of germ line proliferation and differentiation in response to changing environments, and to characterize evolutionary variation of such plasticity. Approaches will involve quantitative analyses of germ line development in different environments, developmental genetics, intra- and interspecific comparative analyses, and mapping of natural genetic variation in reproductive plasticity.

The successful candidate will be highly motivated and participate in the detailed planning of the project. The position is initially for one year and the start date is flexible (salary is around 2300 à 2500 Euros depending on experience). The position is funded by the French National Center for Scientific Research (CNRS) and open to all nationalities.

The IBDC is an international research institute hosting 15 teams working on diverse topics in developmental, cell and cancer biology. The institute, located in the city centre, has excellent research facilities and provides an interactive scientific environment.

To apply, send a summary of your research motiva-

tion and interests, CV, names and contact information for three references to Christian Braendle (braendle@unice.fr) in a single PDF file. For more information, please visit: <http://www.unice.fr/ibdc/> or contact me by e-mail.

Recent Publications:

Braendle C, Baer C & FÃ©lix MA 2010 Bias and evolution of the mutationally accessible phenotypic space in a developmental system PLoS Genetics, e1000877.

Braendle C & FÃ©lix MA 2008 Plasticity and errors of a robust developmental system in different environments. Developmental Cell, 15: 714-724.

Braendle C, Milloz J & FÃ©lix MA 2008 Mechanisms and evolution of environmental responses in *Caenorhabditis elegans*. Current Topics in Developmental Biology 80: 171-207.

Christian Braendle Institute of Developmental Biology and Cancer CNRS UMR 6543 University of Nice Sophia-Antipolis, Parc Valrose Batiment des Sciences Naturelles, etage 7 06108 NICE cedex 2 FRANCE Tel +33 (0) 4 92 07 68 97 Fax +33 (0) 4 92 07 64 03 braendle@unice.fr <http://www.unice.fr/ibdc> Christian Braendle <Christian.Braendle@unice.fr>

NorthCarolinaStateU CompStatistical MolEvol

Multiple postdoctoral positions will be available at the Bioinformatics Research Center at North Carolina State University. The starting dates for these positions are flexible and the duration will be two years with the possibility of renewal. Dr. Eric Stone and Dr. Jeff Thorne are collaborating to study the impact of protein tertiary structure on protein-coding sequence evolution, to reconcile population genetics and interspecific evolution, and to rigorously predict which non-synonymous variants are most likely to have health-related effects. In addition, a position related to the statistical alignment of protein tertiary structures is available. This topic involves a collaboration between Dr. Abel Rodriguez of the University of California - Santa Cruz, Dr. Scott Schmidler of Duke University, and Jeff Thorne.

Candidates for these positions should be statistically inclined and comfortable with computer programming and molecular evolution. Most importantly, candidates should be willing and able to function in a highly collaborative environment.

Informal inquiries about these positions are welcome and should be addressed to Eric Stone (eastone2@ncsu.edu) and/or Jeff Thorne (thorne@statgen.ncsu.edu). A CV along with contact details for 3 referees will be necessary for applicants.

Sincerely,

Eric Stone and Jeff Thorne Bioinformatics Research Center North Carolina State University Raleigh NC 27607

thorne@statgen.ncsu.edu

OhioStateU AphidGenomics

The soybean aphid is a serious invasive insect in North America, having first appeared in 2000. However, very little is known in regards to molecular interactions between insect and plant, specifically the genomics of adaptation during the invasion as well as the evolution of soybean aphid populations that have overcome resistance in host plants. The release of the pea aphid genome provides an extraordinary resource for understanding aphid adaptation, and recent soybean aphid molecular resources developed by our laboratory and other collaborators will provide a framework for understanding the genetic factors involved in aphid adaptation. This position will specifically focus on the genetic and transcriptomic interactions among soybean aphids, bacterial endosymbionts and soybean hosts. Additional work will include comparative evolutionary genomics between the soybean aphid and other important aphid species. Candidates for this position should have a strong record of accomplishment in the areas of evolutionary genetics and genomics, molecular biology, and insect-host plant interactions, with emphasis on transcriptomics, gene expression and next-generation sequencing technologies. Lab experience with gene expression, molecular biology techniques and bioinformatics is preferred. A desire and willingness to learn new techniques and work in a team is essential.

Applicants with a Ph.D. in biology, entomology, genetics/genomics, or molecular biology are encouraged to apply. Start date is flexible, although availability of Summer/Autumn of 2010 is preferred.

For further information please contact:

Andy Michel Assistant Professor Dept. of Entomology Ohio Agricultural Research and Development Center The Ohio State University Ph: 330-263-3730

michel.70@osu.edu

OxfordU EvolutionToolUseInCrows

OXFORD UNIVERSITY: 3-year postdoc on tool use and culture in crows

Postdoctoral Research Associate Tool use in New Caledonian crows

salary range: 28,983 – 35,646 GBP p.a. (incl. discretionary range to 38,951 GBP p.a.)

A three-year postdoctoral position is available, from August 2010 onwards, to work on the ecological and social context of tool use in New Caledonian crows (*Corvus moneduloides*). The post is funded as part of a 5-year BBSRC David Phillips Fellowship to Dr Christian Rutz, and will be based at the Department of Zoology, University of Oxford, UK. The post-holder will be responsible for coordinating and conducting fieldwork in New Caledonia, South Pacific. The research project will chart the ecology and behaviour of wild, free-ranging crows, using detailed field observations, systematic surveys, and novel biologging technologies. In addition, specific hypotheses will be examined in controlled experiments with wild and captive subjects. This is an exceptional opportunity to conduct topical field research on animal tool use and culture in a high-profile study system, and to take a leading role in a prolific and expanding research project.

The successful candidate will have a PhD in behavioural ecology, ecology, evolutionary biology or a related subject, and experience in conducting independent field research, preferably in remote study locations. Proven skills in writing and publishing papers in leading scientific journals are essential. Experience of supervision in a research context, and working as part of a multi-disciplinary team are desirable. Previous field-ornithological experience, or a background in animal-cognition research, are not essential.

Informal inquiries (with CV) should be addressed directly to Dr Christian Rutz (christian.rutz@zoo.ox.ac.uk).

Further particulars and application forms are available from <http://www.zoo.ox.ac.uk/jobs> or from the Personnel Office of the Department of Zoology, University of Oxford (Tinbergen Building, South Parks Road, Oxford OX1 3PS, UK; phone: +44(0) 1865 271190; email: recruit@zoo.ox.ac.uk). Quoting reference num-

ber AT10013, applicants should send to the above address: (i) a completed application form; (ii) a CV with contact details of three referees; and (iii) a cover letter explaining point-by-point how they meet the selection criteria for the post (as specified in the further particulars) and why they wish to conduct research on New Caledonian crows.

The closing date for applications is 30 July 2010, and interviews with short-listed candidates are scheduled for 10 August 2010 (or will take place soon thereafter). This is a re-advertisement, and applicants from the previous round do not need to re-apply.

Dr Christian Rutz BBSRC David Phillips Fellow

Department of Zoology University of Oxford South Parks Road Oxford OX1 3PS, UK

+44/1865/271179 christian.rutz@zoo.ox.ac.uk
www.zoo.ox.ac.uk Christian Rutz
 <christian.rutz@zoo.ox.ac.uk>

RutgersU ComputationalGenomics

Postdoctoral Position in Computational Genomics at Rutgers University

A postdoctoral position is available in Kevin Chens lab at Rutgers University. While there is no specific project associated with this position, weve been working on problems related to the evolution of small RNAs, transposable elements and gene regulation, especially in humans. Please visit the lab web site for more details:

<http://genfaculty.rutgers.edu/kcchen> The position can begin as early as Fall 2010.

If youre interested, please send a CV to

kcchen@biology.rutgers.edu

Were located on the New Brunswick campus of Rutgers University which is within commuting distance (by car or train) from Manhattan.

Kevin Chen <kcchen@Biology.Rutgers.Edu>

SangerInst BacterialPopulationGenomics

Pathogen Genomics at the Wellcome Trust Sanger Institute

The Sanger Institute is a genome research institute primarily funded by the Wellcome Trust. We use large-scale sequencing, informatics and analysis of genetic variation to further our understanding of gene function in health and disease and to generate data and resources of lasting value to biomedical research. The Pathogen Genomics group is focused on the study of species associated with the major infectious diseases of global importance to human and animal health, such as malaria, pneumonia and diarrhoea. Through collaboration with international scientists we aim to bring greater understanding of the mechanisms of infectious disease, and inform the development of disease prevention strategies. We are looking to recruit motivated individuals to work within a dynamic group at the Institute that continues to invest in leading edge technologies to address important scientific questions.

Three Post Doctoral Fellows: Bacterial population analysis

£27, 450-34,402

We wish to recruit talented individuals with a proven record in research to become active members of a team studying the evolution and structure of bacterial pathogen populations. Activities will involve the processing and analysis of large data sets, primarily DNA sequence, but also incorporating relevant phenotypic and clinical information. Successful applicants will be required to apply up-to-date methods in genome assembly and comparison, variation detection and phylogenetics to study the genetics and biology of a range of important bacterial pathogens. It is expected that the work will lead to high-profile publications and presentations. The ideal candidate will have a PhD in one of the following fields: phylogenetics, bacterial genetics, disease epidemiology, mathematical modelling. Applicants should also be familiar with programming languages, such as PERL or Python, for handling and processing large data sets.

Interested parties should email CV and covering letter to Stephen Bentley (sdb@sanger.ac.uk)

Stephen Bentley Senior Scientist Pathogen Genomics Wellcome Trust Sanger Institute

Associate Editor Microbiology Journal

Honorary Lecturer University of Liverpool

sdb@sanger.ac.uk

SeoulNatlU EvolutionDiseaseResistance

Post-Doctoral Fellow: Evolution of Resistance to Chytridiomycosis in Amphibians Seoul National University, Korea

We are seeking to appoint a Post-Doctoral Fellow to work on a three-year project on “Responding to the Amphibian Disease Crisis: Mapping Spread of a Pathogenic Fungus and its Immunological Effects on Infected Populations” funded by the National Research Foundation of Korea and the Seoul National University Brain Fusion Program.

The Post-Doctoral Fellow will conduct research on how chytrid fungus affects Asian amphibian populations. The research will track the spread of the pathogen to naive populations and examine selection for evolutionary responses in MHC genes that may confer immunity on infected individuals. The amphibian chytrid fungus only recently was discovered infecting frogs in Korea, its first documented appearance in mainland Asia. This provides a good platform for addressing basic and applied questions in disease ecology and conservation biology.

The project involves collaboration between the College of Veterinary Medicine and the School of Biological Sciences at Seoul National University. The successful candidate will have ample opportunities to interact with Korean colleagues and with our international collaborators in Australia, New Zealand, and the United States.

Experience in molecular biology with a strong interest in evolution is desirable. Research will be conducted in well-equipped, modern laboratory facilities.

Seoul National University is one of the leading universities in Asia and ranks 24th internationally in Life Sciences & Biomedicine (Times Higher Education, 2009). The campus is set in a mountain reserve on the outskirts of Seoul and offers excellent opportunities for outdoor activities as well as the full range of cultural activities of an exciting highly urbanized city. Subsidized housing and meals are available on campus.

Applications should include a curriculum vitae, names of three referees, university transcripts, and a brief statement of research interests and goals. Submissions by email are encouraged.

For more information, please contact Prof Bruce Waldman, email: waldman@snu.ac.kr; telephone +1 512 782 9905 (USA) or +82 10 8686 2121 (Korea); FAX +1 425 871 2891.

Bruce Waldman School of Biological Sciences Seoul National University 599 Gwanak-ro, Gwanak-gu Seoul 151-747 South Korea

<http://biosci.snu.ac.kr/professor/484> Bruce Waldman <waldman@snu.ac.kr>

StellenboschU Bioinformatics

Postdoctoral positions available in the Department of Genetics (14 June 2010)

Two postdoctoral positions are available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the project title “Genetic improvement of the abalone *Haliotis midae*.”

Haliotis midae, known locally as ‘perlemoen’, occurs along the shores of South Africa and is the only one of the five endemic species that is commercially exploited. *Haliotis midae* displays a very slow growth rate, taking two to five years to reach market size. This is an obstacle for profitable farming and global competitiveness. In order to increase the productivity and the profitability of the commercial abalone industry, a research program has been designed which makes use of modern technology currently applied to other aquaculture species. Two key outputs of this program for which two postdoctoral positions are available include: 1) The production of a transcriptome sequence of *Haliotis midae* utilizing next generation sequencing technologies including the Illumina Genome Analysis platform and the GS FLX platform and utilizing this for amongst others marker development. 2) The generation of comprehensive linkage maps and identification of QTLs utilizing microsatellite and SNP markers.

The successful candidate will be primarily responsible for: 1) Bioinformatic data analysis within this framework. This will include developing an in-depth understanding of tailored genomic analytical software packages for EST, transcriptome and gene expression analysis in order to conduct research and provide post-graduate students with bioinformatics support; keeping abreast of new developments in the areas of bioinformatics, transcriptome analysis and abalone research; the maintenance of a comprehensive sample tracking

system; assisting laboratory staff and students with their research data output requirements. 2) Linkage and QTL mapping analysis within this framework. This will include utilizing currently available marker and data resources as well as initializing further linkage and QTL mapping design; providing postgraduate students with data analysis support; keeping abreast of new developments in the areas of linkage mapping, QTL mapping and abalone research in general; the maintenance of a comprehensive sample tracking system.

Minimum requirements: 1) PhD with specialization in Biotechnology, Bioinformatics, Genetics, Genomics or a closely related discipline. Candidates should have a strong computational background (DNA sequence analysis, evolutionary genetics/biology and gene expression data analysis) and proficiency in relevant software packages. 2) PhD with specialization in Biotechnology, Genetics, Genomics or a closely related discipline. Candidates should have a strong computational background (DNA sequence analysis, linkage mapping, QTL mapping) and proficiency in relevant software packages.

Recommended requirements: Proven experience with SNP analyses (bioinformatic or mapping analysis). Project management experience; excellent organizational and communication skills; proven ability to set deadlines and meet milestones.

These positions are available for 2 years with the possibility of extension. Commencement of duties as soon as possible but no later than November 2010.

Interested researchers are requested to send their CV including details of at least 2 references to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za or Dr Aletta Bester-van der Merwe at aeb@sun.ac.za

EXTENDED Closing date: 16 July 2010.

roodt@sun.ac.za

UBologna MarinePopulationGenetics

“GRADUATE/POST-DOCTORAL RESEARCH POSITION

Research Centre for Environmental Sciences in Ravenna University of Bologna (Italy)

We are seeking to recruit an enthusiastic and highly motivated Graduate/Postdoctoral researcher to work at the laboratory of Ecological and Environmental Genet-

ics in Ravenna (University of Bologna, Italy).

Main research topics include evolutionary biology and population genetics of marine species. The successful applicant will be involved in a new research project aiming to assess the relative importance of hydrogeographic barriers, anthropogenic barriers and species' life history traits in determining genetic discontinuity zones and boundaries of species distribution along the Italian and neighbouring Mediterranean coasts by means of intra- and inter-specific analysis of genetic structuring. The project will investigate levels of divergence and genetic structuring in marine species having different life history traits and will try to understand the distribution patterns of diversity to plan effective strategies to preserve and manage coastal marine biodiversity. With this aim a multi-markers (mitochondrial DNA and microsatellites), multi-species (e.g. molluscs, teleosts) and multi-scales (regional to local) innovative approach will be used.

The position is a full time contract (net salary range 13000-15000 Euro per annum) available immediately for two years in the first instance, with the possibility after review to extend the contract for one or two years.

Activities will be carried on under the supervision of Dr. Federica Costantini (www.ecology.unibo.it/page/federica.htm) and Prof. Marco Abbiati (www.ecology.unibo.it/page/marco.htm < <http://www.ecology.unibo.it/page/marco.htm> >).

Candidates should have a working knowledge of English, good communication, teamwork and organisational skills as well as to be able to work independently.

A strong background in molecular genetics laboratory techniques is required. Main duties include:

- sampling activities and management of tissues samples,
- DNA extraction,
- PCR amplification of mitochondrial / nuclear loci
- sequencing
- database management,
- troubleshooting during laboratory analyses.

Candidates should have a Master's Degree in biological science or related fields.

The closing date for the application is August 31st 2010.

The position will be filled from October 1st, 2010.

For consideration, please email applications (including a cover letter outlining main research interests, a complete CV, a reference letter and contact info for two referees) to federica.costantini@unibo.it

Federica Costantini, PhD Laboratory of Applied Ecology Corso di Laurea in Scienze Ambientali University of Bologna Via S. Alberto 163 I-48100 - Ravenna Italy”.

Thank you in advance, Sincerely Federica Costantini

– Federica Costantini, PhD

Laboratorio di Ecologia sperimentale Centro Interdipartimentale di Ricerca per le Scienze Ambientali in Ravenna Università degli Studi di Bologna via S. Alberto, 163 48100 Ravenna

tel: +39 0544 937401 fax: +39 0544 937411 e-mail: federica.costantini@unibo.it skype username: fedalpha

Pagina WWW: <http://www.ecology.unibo.it> <http://www.ecology.unibo.it/page/federica.htm> Federica Costantini <federica.costantini@unibo.it>

UBourgogne InflammatoryResponseEvolution

A one-year postdoc position is available at the Université de Bourgogne (BioGéoSciences, CNRS), Dijon, France, starting October 1st 2010.

The position is funded by the Région Bourgogne. The postdoc will be part of a large research project aiming to assess the costs and benefits of the inflammatory response in young and old individuals. The model organisms will involve laboratory mice and domestic birds (canaries, zebra finches). The candidate should have a good background in evolutionary biology and a good skill for laboratory work.

Applicants should send a full CV and the names of three potential referees to Bruno Faivre (bruno.faivre@u-bourgogne.fr) and Gabriele Sorci (gabriele.sorci@u-bourgogne.fr).

Closing date: August 30th 2010.

–

Stéphane Garnier

Equipe Ecologie Evolutive UMR CNRS 5561 Biogéosciences Université de Bourgogne 6 Bd Gabriel 21000 Dijon - France

stephane.garnier@u-bourgogne.fr Tel: +33 (0) 3 80 39 90 58 Fax: +33 (0) 3 80 39 62 31

Stephane Garnier <stephane.garnier@u-bourgogne.fr>

UChicago HumanEvolution

Postdoctoral Positions at The University of Chicago.

Two postdoctoral positions are available in Yoav Gilad's lab at the department of Human Genetics at the University of Chicago. The Gilad lab focuses on studying genetic and regulatory differences between humans and our close evolutionary relatives. We pursue a wide range of projects under this umbrella, including comparative genomic studies, studies of regulatory interactions and mechanisms, and studies of variation in gene regulation, which underlie variation in ultimate physiological phenotypes (such as variation in immune response). Please visit the lab web site (<http://giladlab.uchicago.edu/Index.html>) for more details. Postdoctoral fellows are expected to work on whatever they find interesting.

At the University of Chicago, members of the Gilad lab benefit from the unique research and training environment provided by the Human Genetics department. In particular, they collaborate with Jonathan Pritchard, whose research focuses on understanding the regulatory landscape in humans and on developing methods to detect natural selection from variation data, as well as with Anna Di Rienzo, a population geneticist who focuses on genetic variation in humans. Gilad also works closely with statistical geneticists Matthew Stephens and Dan Nicolae, who have outstanding expertise in the analysis of high-throughput data. Thus, Dr. Gilad and his trainees have a nearly unparalleled opportunity to interact with a wide range of researchers with expertise pertinent to their research.

Apply by sending an email to Yoav Gilad (gilad@uchicago.edu). Start date is flexible. Applications will be considered until the positions are filled.

yoav.gilad@gmail.com

UEdinburgh SoaySheep EvolutionaryGenetics

A postdoc is available for three years in the first instance (extendable to five) on an ERC-Advanced Grant

'Wild Evolutionary Genomics' with Professor Josephine Pemberton in the Institute of Evolutionary Biology, University of Edinburgh. Soay sheep sampled over the last three decades on St Kilda will be genotyped on a SNP chip to investigate the quantitative genetics of fitness. Initially, you will organise the preparation and submission of DNA samples to a subcontractor for genotyping. Subsequently, you will QC data received, analyse it in relation to project objectives and draft manuscripts from the study. Candidate quantitative trait loci may also require further molecular laboratory work. A technician will be available to support the lab work. You should have or will shortly obtain a PhD in a relevant field. Previous experience of molecular laboratory work (DNA preparation, PCR and sequencing) and statistical analysis, preferably in the area of quantitative genetics are required.

Apply online by August 1st 2010 at <http://www.jobs.ed.ac.uk> where the reference no is 3013053. Interviews are likely to be held in the week beginning 23rd August.

Informal enquiries to: Professor Josephine Pemberton
Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road EH9 3JT

tel 0131 650 5505 fax 0131 650 6564
j.pemberton@ed.ac.uk <http://wildevolution.biology.ed.ac.uk/> Josephine Pemberton
<J.Pemberton@ed.ac.uk>

UFlorida Biological Informatics

The Florida Museum of Natural History, University of Florida is offering an NSF-funded postdoctoral position in biological informatics. The successful candidate will work on data integration and data interoperability, and will support the development of ontologies and web services. Project activities will involve interaction with several informatics teams working on a variety of phyloinformatics and biodiversity informatics tools, e.g., TreeBASE, Global Name Architecture, PhyloWS, NeXML, CDAO and many others.

The candidate must have a PhD in biology, computer science, computational biology or related fields. A strong background in data management and analysis is highly desirable. The position is available for 2 years with the possibility of extension. Commencement of duties negotiable but the sooner the better.

For more information contact Nico Cellinese at ncellinese@flmnh.ufl.edu. To apply, send a CV, a description of your research interests and your PhD research, and contact information of at least two references to the above email address.

Nico Cellinese, Ph.D. Assistant Curator, Herbarium & Informatics Adjunct Assistant Professor, Department of Biology

Florida Museum of Natural History University of Florida 354 Dickinson Hall, PO Box 117800 Gainesville, FL 32611-7800, U.S.A. Tel. 352-273-1979 Fax 352-846-1861

Nico Cellinese <ncellinese@flmnh.ufl.edu>

UGeorgia Cuticular Protein Evolution

UGeorgia. cuticular proteins

Two NIH-funded postdoctoral positions are available to learn more about the functions of cuticular proteins (CPs) in *Anopheles gambiae* at the University of Georgia, Athens.

An. gambiae devotes almost 2% of its protein coding genes to structural cuticular proteins. These proteins are the main constituents of structures that form the interface between the insect and its environment. We have already learned that some of these genes are found on chromosomes in clusters of almost identical genes; others are single copy. Analysis of these clusters challenged standard evolutionary models of gene duplication. (Cornman and Willis, 2008. Extensive gene amplification and concerted evolution within the CPR family of cuticular proteins in mosquitoes. *Insect Biochem. Molec. Biol.* 38:6612-676.)

Comparison of the cuticular protein complement in *Anopheles* to that in other arthropods raises some intriguing evolutionary questions. Why should mosquitoes have about 50% more CP genes than *Drosophila*, and about 5 times more than *Apis*? Is CP gene number related to life style or taxonomic position? Should identification of orthologs require shared expression patterns in addition to sequence similarity? Do common mechanisms account for the gene amplification seen in different CP families in different insects? What is the source of the CP gene families that are found exclusively in arthropods?

We already know the temporal expression patterns of all and the spatial expression patterns of many of the CP genes in *Anopheles*. Some of this work, in the context of what is known about CPs of other species is discussed in: Willis, 2010. Structural cuticular proteins from arthropods: Annotation, nomenclature, and sequence characterization in the genomics era. *Insect Biochem. Molec. Biol.* 40:189-204.

Future work has the following goals:

To learn whether expression of CP genes of adults can change in response to a blood meal or desiccation using next generation sequencing.

To locate carefully selected individual CPs in the cuticle using secondary antibodies labeled with colloidal gold on ultrathin sections.

To use RNAi technology to establish the necessity of specific CPs.

To determine the extent to which different CPs have different affinities for chitin and/or deacetylated chitin and for each other using tandem mass spectrometry to identify proteins serially extracted by increasing strength of solubilizing agents.

To use these results to understand the evolutionary processes at work in shaping the cuticulome of different insects.

Applicants must have a background in basic molecular techniques and a desire to move beyond annotation and gene identification to learn how particular proteins function to construct this formidable vector.

For further information contact Judy Willis: jhwillis@cb.uga.edu. To apply send her your CV, contact information for three references and a cover letter explaining your interest in this area of research.

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

Judy Willis <jhwillis@cb.uga.edu>

UKansas Drosophila Genitalia Variation

The Macdonald lab at the University of Kansas seeks postdoctoral applicants to study the genetic basis of morphological variation in *Drosophila* genitalia. This NIH-funded project aims to characterize the QTL and QTN responsible for variation in the shape of the pos-

terior lobe, a structure that appears to be under sexual selection. The project will expand on our previous work (*Genetics* 1999, 153:1683) as well as classic genetic studies by Jerry Coyne and Cathy Laurie to resolve the loci underlying between-species variation for this trait (see *Evolution* 1983, 37:1101 and *Genetics* 1996, 142:1129). In addition we will employ association mapping, and a panel of multiparent advanced intercross lines being created as part of another NIH grant, to identify the loci contributing to intraspecific trait variation within *D. melanogaster*.

The position requires a record of published, peer-reviewed research in areas related to population/quantitative/statistical genetics, and would suit an individual who is comfortable with microscopy and dissection. A basic knowledge of analytical methods (e.g. Unix, Perl, R) would also be helpful given the large genotype/phenotype datasets we typically deal with.

If interested, please contact Stuart Macdonald (sjmac@ku.edu) and include a CV and a statement describing your interest in the position.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu web: <http://web.ku.edu/~sjmac/> sjmac@ku.edu

ULaval Evolutionary Systems Biology

Postdoctoral, PhD and undergraduate long-term and short-term positions:

`ULaval.Evolutionary.Systems.Biology`

Our laboratory is eager to receive applications from highly motivated scientists with an excellent record to apply to a Quebec government fellowship available for non-Canadian candidates to study in our laboratory. Doctoral (\$25,000 a year for 3 years) and postdoctoral fellowships (\$35,000+ for one year) are available. Furthermore, internships are available for a visit at our laboratory (\$3,000 CDN/month, up to 4 months) during their undergraduate or graduate studies in another laboratory. Pre-selection by the host university and our laboratory is mandatory.

Candidates from all over the world are invited to apply. Additionally, specific fellowships are available for candidates from Mexico, Brazil, China and Wallonie.

Our laboratory studies the evolution of gene and protein networks using the budding yeasts as models. Potential projects include the study of gene duplication and divergence, the evolution of phenotypic divergence among species and the study of reproductive isolation. We are also interested in the quantitative genetics of noise and response dynamics of signalling networks. We are using proteomics tools such as mass spectrometry, fluorescence microscopy, and mutant library screening using robotics and protein-protein interaction technologies such as PCA. We also have access to next-generation sequencing technologies for gene expression studies and genotyping.

We are in the Department of Biology at Laval University, located in Quebec City, Quebec, Canada. Our laboratory is part of the Institute of Integrative and Systems Biology (IBIS).

Laval University is one of the ten main Canadian universities. Quebec City is dynamic with all the advantages of a large city while still allowing for very easy access to wilderness and very reasonable cost of living. The chosen candidates who are successful at obtaining a fellowship will be part of the Institute of Integrative and Systems Biology. They will have access to core genomics and molecular biology facilities, lab meetings and Institute-wide group meetings, journal clubs and weekly seminars at the Institute and in the Biology Department. Several ecological genomics laboratories are part of the Institute and the Biology department, allowing for enriched interactions with members of the other laboratories working in this field.

DEADLINES: Our laboratory must receive applications before July 23, 2010. We will then proceed to select candidates that will be able to apply to the University pre-selection committee with a deadline of August 9th 2010. Candidates selected by the university will then be allowed to apply to the general competition in Fall 2010, with results given in April 2011.

Contact me directly by email for more information about the program and opportunities in our laboratory.

Christian.landry@bio.ulaval.ca

Christian Landry, PhD

CIHR New Investigator

Département de Biologie

Institut de Biologie Intégrative et des Systèmes

Université Laval

Québec (Québec) G1V 0A6

Canada

<http://www.bio.ulaval.ca/landrylab/en/pmwiki.php>

Christian Landry <Christian.Landry@bio.ulaval.ca>

ULaval Molecular basis of behaviour variation

Our laboratory is eager to receive application from highly motivated scientists with an excellent record to apply to a Quebec government fellowship available for non-Canadian candidates to do research in a Quebec-based laboratory. Post-doctoral fellowships are available (1 year, 35,000 CAN\$). Internships are also available for a visit to our laboratory (3,000 CAN\$/month, up to 4 months). Pre-selection by the host university and our laboratory is mandatory.

Candidates from all over the world are invited to apply. Additionally, specific fellowships are available for candidates from Mexico, Brazil, China and Wallonie.

We are in the Department of Biology at Laval University, located in Quebec City, Quebec, Canada. Our laboratory is part of the Institute of Integrative and Systems Biology (IBIS). We study the underlying molecular and hormonal causes of variation in behaviour in vertebrates. We are interested in personality with an emphasis on the stress response and correlation among behaviours, as well as in reproductive tactics. We are also interested by the effects of the environment on development of behaviour, such as environmental enrichment in captive animals, maternal/paternal and social group effects, and endocrine disrupters. We therefore have a strong interest for phenotypic plasticity, along with the effects of genetic variation. We favour an integrative approach by linking data from the same individual: neuropeptides, neurotransmitters and their receptors (quantitative Real-Time PCR, microarrays, in situ hybridization, HPLC), hormones (EIA, HPLC), physiology and behaviour. Our model system is the threespine stickleback *Gasterosteus aculeatus*, a small fish studied in behavioural biology, which can be kept easily in the lab and whose genome is sequenced.

Laval University is one of the ten main Canadian universities. Quebec City is dynamic with all the advantages of a large city while still allowing for very easy access to wilderness and very reasonable cost of living. The chosen candidates that are successful at obtaining

a fellowship will be part of the Institute of Integrative and Systems Biology. They will have access to core genomics and molecular biology facilities, lab meetings and Institute-wide group meetings, journal clubs and weekly seminars at the Institute and in the Biology Department. Several ecological genomics laboratories are part of the Institute and the Biology department, allowing for enriched interactions with members of the other laboratories working in this field. DEADLINES: Our laboratory must receive applications before July 23, 2010. We will then proceed to select candidates that will be able to apply to the University pre-selection committee with a deadline of August 9th 2010. Candidates selected by the university will then be allowed to apply to the general competition in Fall 2010, with results given in April 2011. Start date can be between May and December 2011.

Contact me directly by email for more information about the program and opportunities in our laboratory.

Nadia.Aubin-Horth@bio.ulaval.ca

Nadia Aubin-Horth

Assistant professor

Department of Biology

Institute of Integrative and Systems Biology

Pavillon Charles-Eugene-Marchand

1030, Avenue de la Medecine

Laval University

Quebec city (Quebec) G1V 0A6

Canada

<http://wikiaubinhorth.ibis.ulaval.ca/Main.Page>

Aubin-Horth Nadia <Nadia.Aubin-Horth@bio.ulaval.ca>

ULeeds AntGeneticDiversity

Postdoctoral Research Assistant position, University of Leeds Project: Genetic diversity and the neurobiology of division of labour in ants

A 24 month, fixed-term, EC-funded Postdoctoral Research Assistant position is available in the research group of Dr. William Hughes at the University of Leeds. The project will investigate the neurobiology of division of labour in genetically diverse ant colonies and

is in collaboration with Dr. Marc Seid (University of Scranton and Smithsonian Tropical Research Institute). The discovery and characterization of neuromechanisms that mediate genotypic differences in behaviour is a premier paradigm in biology today. The difficulty in finding defined answers rests in the complexity of confounding factors (environment, individual behavioural flexibility, genotypic variation and polygenetic traits) and the limited sample size for comparison. This project will use social insects to overcome these issues. It will use leaf-cutting ants as the model species, because the colonies of these ants contain genetically diverse individuals and exhibit genetic influences on behavioural specialization. Microsatellite genotyping will be used to characterize the genotypic make-up of behaviourally specialized ants. The neuroanatomical and neurochemical differences between these ants will then be examined to establish the neuromechanisms underpinning genetic variation in division of labour. Ant brains will be assayed utilizing serial sectioning for brain morphology and immunocytochemistry for direct measurement of biogenic amine analysis. This project will help reveal the neuromechanisms governing genotypically derived behaviours.

You should have a first degree and PhD in a relevant subject, an excellent publication/results record for your career stage, and research experience in neurobiology. You should be hard working, self-motivated and able to work both independently and as part of a team. Research experience with social insects, animal behaviour and molecular ecology would also be advantageous.

The position is available from 1 September 2010, comes with a generous salary (euro 54,300-euro 81,400 gross per annum, depending on experience) and travel allowance. The position is open to all nationalities, but some nationality/geographic restrictions apply. For further details or to apply, please contact Dr. William Hughes (email: w.o.h.hughes@leeds.ac.uk) including a CV and cover letter outlining your experience. Applications will be considered through July until the position is filled.

W.O.H.Hughes@leeds.ac.uk

ULosLagos Chile 2 EvolutionaryImpact of SalmonidInvasions

2 Fixed-term Research positions on Evolution and Im-

fact of Salmonid Invasions Closing date: 1st August 2010

Genetics, Aquaculture & Biodiversity Laboratory University of Los Lagos (Osorno Chile) Falkland Islands Government Environmental Planning Department Falkland Islands Development Corporation (Stanley - Falkland Is.)

Applications are sought for two fixed (2 year) research positions available from August 2010 aimed at monitoring and assessing the evolutionary impact of exotic salmonids on native galaxiid fishes in Chile and the Falkland Islands. As part of a DEFRA-funded Darwin Initiative Post-Project Award (EIDPO041; www.biodiversity.cl), all suitably qualified candidates will be considered but preference will be given to Chilean and Falkland Island citizens.

Applicants should send a cover letter and CV with contact details of two potential referees to: Dr. Gonzalo Gajardo (ggajardo@ulagos.cl) or Dr. Carlos Garcia de Leaniz (c.garciadeleaniz@swansea.ac.uk) for the position in Chile, and to Nicholas Rendell (NREndell.planning@taxation.gov.fk) or Dr. Carlos Garcia de Leaniz (c.garciadeleaniz@swansea.ac.uk) for the position in the Falkland Islands by 1st August 2010.

1 Protecting galaxiids from salmonid invasions in Chile Salary: Chile\$ 10,000,000 -12,000,000 per annum Required qualifications: BSc or equivalent in Biology or Life Sciences. Experience in sampling aquatic ecosystems. Excellent oral and written communication skills in Spanish and English. Ability to work independently as part of a larger team. Ability to combine laboratory work with field sampling. Desirable qualifications: Driving licence. Experience working with salmonids and/or galaxiids. Postgraduate qualifications. Scientific publications. Experience working on fish reintroductions and/or captive breeding programmes

2 Protecting galaxiids from salmonid invasions in the Falklands Islands Salary: pounds 20,000-22,000 GBP per annum Essential qualifications: BSc or equivalent in Biology or Life Sciences. Experience in sampling aquatic ecosystems. Excellent oral and written communication skills in English. Ability to work independently as part of a larger team. Ability to combine laboratory work with field sampling. Desirable qualifications: Driving licence. Experience working with salmonids and/or galaxiids. Postgraduate qualifications. Scientific publications. Experience working on fish reintroductions and/or captive breeding programmes.

Carlos Garcia de Leaniz

"GarciaDeLeaniz C." <C.GarciaDeLeaniz@swansea.ac.uk>

ULouvainlaNeuve ButterflyEvolution

A two-year postdoctoral position is available at the Biodiversity Research Centre, Earth and Life Institute, University of Louvain-la-Neuve (UCL) in Belgium (<http://www.uclouvain.be/en-bdiv.html>). Focus will be on the functional significance of a suite of adaptive phenotypic traits (dispersal-related morphology and physiology and communication-related pheromone traits) in the laboratory and the field for two butterfly model species *Pararge aegeria* and *Bicyclus anynana*. The framework of this position is a collaborative 5-year project by the teams of Profs. Hans Van Dyck, Nicolas Schtickzelle and Caroline Nieberding. The project aims for a better understanding of the role and mechanisms of plasticity for present and future adaptation and survival under climate change in a series of model organisms.

The post doc will work in a highly active and integrated academic environment of three collaborating research teams, including faculty, other postdocs and PhD students. The work will focus on behavioural manipulations of the abiotic or biotic environments in the field or in the lab, and lab experiments using quantitative genetics. The successful applicant will have the opportunity to develop additional questions related to the main research program.

We are looking for a strongly motivated candidate with a PhD in the field of Evolutionary Biology and Ecology. Experience in behavioural and/or chemical ecology, quantitative genetics, life history trade-offs analysis and strong written and oral communication skills are a plus. Salary ranges between 2000-2200 euros netto per month plus benefits (health insurance, â) which are included in the Belgian system. The successful applicant must not have stayed in Belgium more than 24 months out of the last three years. For practical information concerning salaries, benefits, insurances and conditions of eligibility please contact Mrs. D. Socquet at UCL (dominique.socquet@uclouvain.be; +32 (0) 10 47 2720). Applications will be reviewed starting from August 25th until the position is filled. Anticipated start date is January 1st 2011 but can be negotiated. Our University is an Equal Opportunity/Affirmative Action Employer, and is in a French-speaking region, but the language for meetings and scientific interac-

tions is English. For background information about our university, see <http://www.uclouvain.be/en-index.html>

Application should be sent to Hans Van Dyck (hans.vandyck@uclouvain.be), Nicolas Schtickzelle (nicolas.schtickzelle@uclouvain.be) and Caroline Nieberding (caroline.nieberding@uclouvain.be) and include the following: (1) a cover letter describing your research interests and qualifications, (2) a full CV, (3) contact information (email, phone number) of minimum 2 referees, and (4) pdfs of up to three representative publications. Please include « post-doctoral application » in the subject line of the e-mail. Informal inquiries are welcome.

We also have a vacancy for another two-year postdoc position on the evolvability of dispersal-related traits in heterogeneous environments

Caroline Nieberding <caroline.nieberding@uclouvain.be>

ULouvainlaNeuve EvolvabilityPlasticity

A two-year postdoctoral position is available at the Biodiversity Research Centre, Earth and Life Institute, University of Louvain-la-Neuve (UCL) in Belgium (<http://www.uclouvain.be/en-bdiv.html>). Focus will be on the evolvability of a suit of plastic traits related to dispersal and the link between evolvability of plasticity and adaptation to heterogeneous environments, using the approach of experimental evolution in lab-controlled conditions in the spider mite *Tetranychus urticae* Koch and the unicellular eukaryotic ciliate *Tetrahymena thermophila*. The framework of this position is a collaborative 5-year project by the teams of Profs. Hans Van Dyck, Nicolas Schtickzelle and Caroline Nieberding. The project aims for a better understanding of the role and mechanisms of plasticity for present and future adaptation and survival under climate change in a series of model organisms.

The post doc will work in a highly active and integrated academic environment of three collaborating research teams, including faculty, other postdocs and PhD students. The work will focus on the lab-analysis of the slope and range of variation of plasticity in various GxE matrices and its functional significance in terms of adaptation and adaptability. The successful applicant will have the opportunity to develop additional questions related to the main research program.

We are looking for a strongly motivated candidate with a PhD in the field of Evolutionary Biology and Ecology. Experience in behavioural ecology, quantitative genetics, life history trade-offs analysis, statistics and strong written and oral communication skills are a plus. Salary ranges between 2000-2200 euros netto per month plus benefits (health insurance, â) which are included in the Belgian system. The successful applicant must not have stayed in Belgium more than 24 months out of the last three years. For practical information concerning salaries, benefits, insurances and conditions of eligibility please contact Mrs. D. Socquet at UCL (dominique.socquet@uclouvain.be; +32 (0) 10 47 2720). Applications will be reviewed starting from August 25th until the position is filled. Anticipated start date is January 1st 2011 but can be negotiated. Our University is an Equal Opportunity/Affirmative Action Employer, and is in a French-speaking region, but the language for meetings and scientific interactions is English. For background information about our university, see <http://www.uclouvain.be/en-index.html>

Application should be sent to Hans Van Dyck (hans.vandyck@uclouvain.be), Nicolas Schtickzelle (nicolas.schtickzelle@uclouvain.be) and Caroline Nieberding (caroline.nieberding@uclouvain.be) and include the following: (1) a cover letter describing your research interests and qualifications, (2) a full CV, (3) contact information (email, phone number) of minimum 2 referees, and (4) pdfs of up to three representative publications. Please include « post-doctoral application » in the subject line of the e-mail. Informal inquiries are welcome.

We also have a vacancy for another two-year postdoc position in behavioural/chemical ecology.

Caroline Nieberding <caroline.nieberding@uclouvain.be>

UMarseille PostGenomicSpeciation

2 years Post doc position speciation at post genomic era the candidate should have a robust bioinformatics back ground. contact Pierre Pontarotti

Pierre Antoine Pontarotti

Directeur de Recherche CNRS

UMR 6632 Université de Aix Marseille/CNRS . Equipe Evolution biologique et Modélisation <http://sites.univ-provence.fr/evol/> Pierre.Pontarotti@univ-provence.fr

UNebraska HighAltitudeAdaptation

POST-DOCTORAL POSITION in Evolutionary Genetics and Genomics University of Nebraska, Lincoln, NE

A post-doctoral position is available in the Storz lab at the University of Nebraska. This is one of several positions associated with an NIH- and NSF-funded research project to elucidate genetic mechanisms of physiological adaptation to high-altitude hypoxia in vertebrates. The research project involves a combined evolutionary and functional analysis of physiological adaptation, and spans multiple hierarchical levels of biological organization, from whole-animal physiological performance to protein biochemistry. The work also integrates a diverse range of approaches including pathway-level population genomics and proteomics, molecular population genetics, molecular evolution, biochemical physiology, and protein engineering. Much of the work revolves around functional studies of hemoglobin and other globin proteins in high-altitude mammals and birds.

For more information about research in the lab, see the following web-site: <http://www.biosci.unl.edu/labs/storz/index.html> The ideal candidate would have expertise in molecular evolution, bioinformatics, genomics, and/or proteomics, and an enthusiasm for integrative evolutionary biology.

If interested, please send a CV, cover letter, and contact information for three references. The position could start as early as summer 2010, but the start-date is flexible. Funding is potentially available for 3+ years. Salary will be determined by the NIH pay scale and will include full benefits. Please feel free to contact me (jstorz2@unl.edu) with any questions.

I will be attending the Evolution meeting in Portland, Oregon, so I would also be happy to meet with prospective candidates in person.

Jay Storz

Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 E-mail: jstorz2@unl.edu www.biosci.unl.edu/labs/storz/index.html Jay F Storz <jstorz2@unlnotes.unl.edu>

UNebraska PlantEvolutionaryComparativeGenomics

A postdoctoral position in evolutionary comparative genomics is available in the Mower lab at the University of Nebraska-Lincoln. The position is available for 2 years starting in January 2011, with the possibility of continuing support for up to 4 years.

The major goals of the project are to understand the causes and consequences of large increases in substitution rate in different lineages of plants by comparative phylogenomic analysis from multiple species and all three genomic compartments (nucleus, plastid, mitochondrion). For this project, complete mitochondrial genomes, plastid genomes and nuclear transcriptomes will be generated and analyzed from 5+ closely-related plant species with variable substitution rates.

A PhD in evolution, genetics, genomics, bioinformatics, computational biology or similar field is required. Applicants should have demonstrable experience in one or more of the following areas: 1) preparation of genomic DNA and/or RNA for next-generation sequencing technologies, 2) assembly and annotation of genomes and/or transcriptomes from next-gen data, and 3) evaluation of genomic and transcriptomic data using tools of molecular evolution, comparative genomics, and phylogenetics. The ideal applicant should have programming experience in a linux environment using perl or python (or similar language) and proficiency with relevant software packages for genome assembly, molecular evolution, and phylogenetics. Salary will be highly competitive and dependent upon candidate's background and experience.

Informal inquiries about the projects are encouraged. Applicants should submit a pdf document that includes: 1) cover letter describing previous experience and fit to the position, 2) full CV, and 3) contact information for 3 references. Applications and all queries may be sent to Jeff Mower at jmower2@unl.edu. Applications will begin to be reviewed Sept. 1 but will continue to be accepted until the position is filled.

Jeffrey P Mower Assistant Professor Center for Plant Science Innovation University of Nebraska Lincoln Lincoln NE 68588

jmower2@unlnotes.unl.edu

UNevada Reno Phylogenetics

Where: the University of Nevada, Reno, Department of Biology

When: start date is flexible, preferably Fall-Winter 2010, but Spring 2011 is also possible

Deadline: position is open until filled

We are seeking a qualified postdoctoral candidate to be a part of a diverse research program involving coevolutionary interactions, ecological speciation, tri-trophic interactions, and dispersal ecology. The successful candidate will have excellent molecular lab skills, and an understanding of technologies including Sanger and next-generation sequencing. One of the primary objectives will be the amplification of DNA from curated Lepidoptera. The position will be primarily in the Forister lab, but also working closely with the Dyer lab (see URLs below). Although our work involves butterflies and moths, previous experience with insects is not required.

The candidate must hold a Ph.D. in a relevant field, and be able to provide references testifying to the following skills: (1) lab and analytical skills in phylogenetics and populations genetics, (2) an ability to work with others, including mentoring of undergraduates, and (3) a commitment to productivity and communication of results in publications and contributed talks at national and international meetings.

We currently have 1 year of funding for this postdoctoral position (salary dependent on experience), but extension beyond 1 year is possible. The University of Nevada, Reno, affords a high quality of living for people interested in outdoor activities. Fishing and kayaking are possible in the Truckee river in downtown Reno, and camping/hiking/rockclimbing opportunities are abundant in the Sierra and Great Basin.

Please send the following: (1) a cover letter explaining your interest in the position and abilities with reference to the skills outlined above, and (2) an academic CV. If these materials are competitive, I will ask you to have letters of reference sent.

Send your cover letter and CV to: Matt Forister, forister@gmail.com.

websites:

the Forister lab <http://web.me.com/mforister/>-

GreatBasinBugLab/Home.html the Dyer lab <http://wolfweb.unr.edu/~ldyer/> the University of Nevada, Reno <http://www.unr.edu/> the Biology Department <http://www.unr.edu/biology/> forister@gmail.com

UParis HumanPopGenetic

Proposal for a PostDoctoral position Supervisors: Evelyne Heyer and Frédéric Austerlitz UMR 7206 Eco-anthropologie CNRS/MNHN/Université Paris 7 Equipe “génétique des populations humaines” Muséum National d’Histoire Naturelle, Paris, France

<http://www.ecoanthropologie.cnrs.fr/-spip.php?article300> http://www.ese.u-psud.fr/-pages_perso/spip.php?article18 Inferring the history of human populations using genetic data. Link with environmental changes.

DNA polymorphism data allow the inference of some aspects of the history of human populations. Various methods have been developed, in particular coalescent-based methods, which allow detecting demographic processes, such as migration or population growth and inferring their chronology, using genetic polymorphism within DNA sequences, SNPs and microsatellites. Other methods based on linkage disequilibrium can bring complementary knowledge on these events, allowing in particular the inference of more recent events. These methods include likelihood method and Bayesian methods, in particular the recently developed Approximate Bayesian Computation methods.

The aim of this PostDoctoral position will be to develop and apply these methods to human populations living under contrasting life styles: hunter-gatherers, pastoral nomads, sedentary farmers. The postdoctoral fellow may work in collaboration with a PhD student on this subject. The aim will be to assess whether these populations underwent demographic events, and also the timing of such events in order to assess if they are linked with environmental changes. The available data for this study will be DNA polymorphism data available in public databases, as well as data sets already available or under development within our laboratory. These data sets concern populations of pastoral nomads and farmers from Central Asia, as well as those from hunter-gatherer (pygmies) and farmers from Central Africa, two regions that went through strong climatic changes during the past millennia.

The candidate should have a strong background in population genetics, in particular on theoretical questions, and on data analysis. Some experience in bioinformatics is required. For any additional information, please contact Evelyne Heyer (hey@mnhn.fr) or Frédéric Austerlitz (frederic.austerlitz@u-psud.fr).

The Postdoctoral position is funded for one year by the French CNRS. The applicant should have defended his PhD thesis no more than two years before the beginning of this position. Net salary should be around 2038euro. Potential candidates should send us by email a CV, three references and a letter of motivation. The deadline for application is September 1st 2010. The successful candidate will start the position no later than December 1st 2010.

frederic.austerlitz@u-psud.fr

UParis Sud PopulationGenomics

POSTDOCTORAL POSITION ON AT THE UNIVERSITY PARIS-SUD (FRANCE) ON "POPULATION GENOMICS & METAGENOMICS"

A postdoctoral contract of 18 months starting from January 2011 (negotiable) and funded by the French National Research Agency is available in the "Microbial diversity and evolution" team headed by Purificación López-García at the University of Paris-Sud (<http://www.esu-psud.fr/spip.php?rubrique7>). The University of Paris-Sud is located at the pleasant botanical-garden campus of Orsay, 25 km south of Paris, 30 min by direct train (RER B line).

The scientific project aims at extracting population genomics data from prokaryotic genomes or genome fragments reconstructed from deep-sea metagenomic libraries. The targeted organisms are primarily marine archaea belonging to groups lacking cultivable members (Group I Crenarchaeota/Thaumarchaeota and Euryarchaeota), but might also involve selected abundant deep-sea bacteria from uncultured groups. Population genetics and genomics studies in these genomes/genome fragments will produce data about recombination levels and genome evolution. These will be correlated with metabolic predictions and environmental data to understand the population dynamics of these uncultivated organisms and the selective forces shaping their evolution. The candidate will join a team already working on the construction of archaeal genome scaffolds, their annotation and phylogeny.

The net salary will be of at least 1800 euros including social security and medical assistance depending on the candidate experience.

We are seeking motivate candidates with good experience in population genetics/genomics, comparative genomics and/or metagenomics. Skills in modelling and database management will be appreciated.

Candidates should send a CV, a cover letter and the names of at least two referees before November 1st 2010 to:

Purificación LOPEZ-GARCIA, e-mail: puri.lopez@u-psud.fr

or David MOREIRA, e-mail: david.moreira@u-psud.fr

Unité d'Ecologie, Systématique et Evolution, UMR CNRS 8079

Université Paris-Sud. Bâtiment 360, 91405 Orsay cedex, FRANCE

<http://www.esu-psud.fr/spip.php?rubrique7>
"puri.lopez" <puri.lopez@u-psud.fr>

Vienna DrosophilaAging

Vienna, Austria: POSTDOCTORAL POSITION IN DROSOPHILA AGING

A postdoctoral research position in the genetics of Drosophila aging is available in the group of Thomas Flatt at the University of Veterinary Medicine (Department of Biomedical Research, Institute of Population Genetics), Vienna, Austria. The postdoc position is funded by a grant from the Austrian Science Foundation (FWF) and will be for three years.

This research project will focus on the identification of the molecular basis of the trade-off between reproduction and lifespan in the fruit fly, *Drosophila melanogaster*, a powerful genetic model system. In many organisms, from fruit flies to humans, reproduction shortens lifespan, but the underlying mechanisms remain unknown (see Flatt & Promislow 2007 in Science). Experiments in *C. elegans* suggest that hormonal signals from the gonad affect longevity (Hsin & Kenyon 1999 in Nature), and we have recently found that germline ablation extends lifespan and affects insulin signaling in *Drosophila* (Flatt et al. 2008 in PNAS). However, the details of this systemic regulation of lifespan by the reproductive system remain un-

clear. In our project we are interested in dissecting the hormonal and metabolic mechanisms that modulate the reproduction-longevity trade-off. By employing mutant and transgene analysis, genetic manipulation of the gonad, epistasis experiments, metabolic measurements, and hormonal manipulations we will examine the endocrine mechanisms whereby signals from the reproductive system modulate adult longevity and physiology.

We are seeking a talented, independent, hard-working and self-motivated young biologist with good social skills. The successful candidate will have a Ph.D. and a strong background in genetics and molecular biology using the *Drosophila* system. Some background in the biology of aging, evolutionary biology, and/or endocrinology would be ideal, but is not required. The working language in the laboratory is English, so the candidate should be proficient in spoken and written English. German skills, although helpful, are not essential. The initial appointment will be made for one year, with a possible extension to up to three years. The annual salary is 56,110 Euro (before tax). The position is available as of now, but the starting date is negotiable.

In a 2009 world-wide survey by the William M. Mercer Institute, Vienna ranked first world-wide in terms of standards of living. Vienna is a beautiful, historical yet modern city, located in the heart of Europe, close to the Alps and to major cities like Munich, Zurich, Prague, and Budapest. Being famous for its concert sites, opera houses, theaters, museums, and coffee shops, Vienna also provides great outdoor activities, such as sailing on the Neusiedler See, ice skating, biking and hiking in the Viennese woods and the nearby Alps. Moreover, the city has a wide range of great restaurants, bars, wineries, cinemas, clubs, libraries, galleries, and art collections. The Vienna area is also an exceptional and highly international research environment. Four major life science universities and three world-class research institutes (GMI, IMBA, IMP) provide a dynamic and interactive setting. Vienna hosts an active *Drosophila* community, and the onsite availability of the *Drosophila* RNAi center (VDRC) provides a great opportunity for functional *Drosophila* work. In population genetics and evolutionary biology, the Vienna research area also provides excellent prospects, due to a growing number of evolutionary research groups.

To apply, please send a single pdf file including: (1) a cover letter explaining why you would like to join our group, (2) your Curriculum Vitae (including a description of your skills), (3) your publication list, (4) a statement of research interests, and (5) contact details for 2-3 references who are willing to write a reference

letter on your behalf to the following e-mail address: thomas.flatt@vetmeduni.ac.at Informal inquiries are welcome and should be sent to the same e-mail address. For further information see (http://i122server.vu-wien.ac.at/pop/Flatt_website/flatt_home.html).

The deadline for submission is 15 August 2010.

Dr. Thomas Flatt Institute of Population Genetics Department of Biomedical Sciences University of Veterinary Medicine Vienna Veterinärplatz 1 A-1210 Wien Austria/Europe

VOX +43-1-25077-4334 FAX +43-1-25077-4390 E-mail: thomas.flatt@vetmeduni.ac.at

Lab Website: http://i122server.vu-wien.ac.at/pop/Flatt_website/flatt_home.html Vienna Graduate School of Population Genetics: <http://www.popgen-vienna.at> flatt.thomas@gmail.com

Vienna StatisticalGenetics

A postdoc position is available at the Institute of Population Genetics at the Vetmeduni Vienna (<http://i122server.vu-wien.ac.at/pop>) to work on the analysis of next generation sequencing data aiming to understand the genotype phenotype relationship in *Drosophila*. Available data will include experimental evolution, speed mapping and comparisons of natural populations. Candidates with a strong statistical background and experience with large data sets are particularly encouraged to apply.

The position is available from September 2010 for two years with a possibility of extension. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, and the names of three references with contact details. While search will continue until the position is filled, applications should be received by August, 15 to assure full consideration.

The Vetmeduni Vienna hosts several research groups covering a wide range of research areas including functional genetics, life history evolution, evodevo, population genetics, statistical genetics, and bioinformatics. The Vienna Graduate School of Population Genetics (<http://www.popgen-vienna.at/>) is based at the Vetmeduni Vienna and an Illumina sequencer is available with privileged access for members of the Institute of Population Genetics. Off campus, Vienna offers an excellent scientific environment for this

project. An active community in evolutionary research (<http://www.univie.ac.at/evolvienna/>) as well as a thriving *Drosophila* community (e.g.: VDRC, <http://stockcenter.vdrc.at/control/main>) provide ample opportunities for interaction.

Christian Schlötterer Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Bau-

mann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390
<http://i122server.vu-wien.ac.at/pop> Vienna Graduate School of Population Genetics <http://www.popgen-vienna.at> VetCore Illumina Sequencing Service <http://i122server.vu-wien.ac.at/pop/seq/VetCore2.htm>
 schlote@gmail.com

WorkshopsCourses

Bergen Norway ContemporaryEvolution Oct4-9 ...	76	Switzerland Speciation Aug29-Sep4 2	80
BodegaBay ConservationFilms Oct10-17	77	UCaliforniaLosAngeles MathComput Genomics	
ChapelHill NC StatisticalGenetics Aug16-20	77	Fall2011	80
NIMBioS HPC Phylogenetics Oct13-15	78	York EvolutionaryMorphometrics Oct11-14	81
Piacenza GenomicsSummerSchool Sept6-9	79		
Plon Germany EvolutionaryGenetics	79		

Bergen Norway ContemporaryEvolution Oct4-9

Nordic Marine Academy Course held in Bergen, Norway Oct. 4-9, 2010

Contemporary Evolution: Humans as Agents of Selection Credits: 3 ECT Course website: <http://www.bio.uib.no/evofish/pages/NMA2010/-NMA2010.php> Deadline for application: Aug. 20th

Lecturers: 10 invited lecturers from Norway, the Netherlands, the US, and Finland

Course Description: In medicine and agriculture, managing evolution is commonplace. Breeders of domesticated animals and plants have steered evolution for millennia, whereas during past decades, attempts to avoid resistance evolution has become a major issue in both human health and agriculture. In dealing with wild populations, awakening to contemporary evolution has just started. Yet there is little doubt that humans are the greatest evolutionary force of modern times. Whenever humans are present, pristine habitats are absent

or rare, and even the most remote places are influenced by climate change and pollutants. Humans transport animals and plants to novel environments. Populations that are resources to humans may have humans as their primary predator or herbivore. All these changes have evolutionary implications, and understanding them is an important task in managing and conserving the environment.

The course is an opportunity to bring together young and experienced scientists with various backgrounds in evolutionary ecology. The course aims to present theory and techniques, statistical and modeling, to measure human-induced evolution in marine, freshwater, and terrestrial environments, covering topics from the effects of environmental degradation and noise pollution through to selective removal of individuals (hunting). The course will suit both experienced postdocs and doctoral students curious in expanding their quantitative skills.

Intended audience: The course will be of interest to those working on organisms spanning both terrestrial and aquatic systems in evolutionary ecology, fisheries, behavioral ecology, life history theory (including exploitation-induced and contemporary evolution), wildlife biology, and conservation biology.

For more information, contact: Jennifer Devine jennifer.devine@bio.uib.no <http://www.bio.uib.no/evofish>
Jennifer Devine <jennifer.devine@bio.uib.no>

BodegaBay ConservationFilms

Oct10-17

We'd like to pass this information along to anyone who may be interested in this exciting opportunity to gain valuable science communication skills and apply them to research, management, conservation or web-related projects. If you feel this is appropriate, please forward this announcement and attached flyer to any colleagues who may be interested:

Workshop Announcement: Science Filmmaking at Bodega Bay Marine Laboratory, October 2010

Note: Registration deadline for this workshop has been extended to Sept 1, 2010

Overview: This 7-day immersion workshop will teach participants to communicate scientific findings, natural history information, or conservation messages by creating compelling, professional-quality videos. Topics will include story selection, planning, writing, camera technique, voiceovers, technical aspects of video and audio production, basic video and audio editing, project output, and distribution. These technical elements will underpin the main focus of the workshop: effective storytelling through video. The "hands-on" approach will be emphasized, and participants will put concepts introduced in lecture into daily practice. Opportunities will exist for shooting in the field and studio and participants will also critique existing documentaries. By the end of the workshop, students will have the opportunity to produce a short film on a topic of their choosing.

Target audience: This workshop is intended for academic scientists at any level (undergraduate, graduate, postdoc, faculty, or emeritus) as well as professional biologists (government, NGO, industry, etc.). Interested individuals from the general public will also be considered. No prior film making experience is required. The workshop will run with a minimum of 10 participants, and a maximum of 20.

Instructors: Jeff Morales (National Geographic Film & Television, & VONIGO Films) and Dr. Colin Bates (Bamfield Marine Sciences Centre & Department of Botany, University of British Columbia).

Where: UC Davis Bodega Marine Laboratory, Bodega

Bay, CA

When: October 10 - 17, 2010

Cost: US\$1599 Includes workshop fees, supplies & some equipment, housing, food, and lab user fees. Discounts are available for those participants who do not require room and board. Registration deadline is September 1, 2010.

For further information and application materials, visit www.sciencefilm.org or contact Colin Bates (colinba@interchange.ubc.ca).

Thanks, and we hope to see you at BML in October. If you know of anyone else who might be interested, please pass this along.

Cheers, Colin Bates & Jeff Morales

– Jeff Morales Producer VONIGO FILMS RR1 H-42 273 David Road Bowen Island, BC V0N1G0 Canada +1 604-947-0667 h/o +1 604-375-0580 c jeffmorales1@gmail.com

Jeff Morales <jeffmorales1@gmail.com>

ChapelHill NC StatisticalGenetics

Aug16-20

There will be a five-day workshop in August 16-20, 2010 on statistical genetics, and featuring the Mendel Statistical Genetics Software package.

This short course will be taught by faculty from UCLA and UNC-Chapel Hill and is designed for researchers who will be doing statistical analysis of genetics projects.

More information is in the announcement below, and at <http://genomics.unc.edu/events/statgen/-index.html> Application deadline has been extended, but space is limited.

Thank you,

The Statistical Genetics Short Course Instructors.

Workshop Announcement:

STATISTICAL GENETICS SHORT COURSE August 16-20, 2010 At the Rizzo Conference Center Chapel Hill, North Carolina <http://genomics.unc.edu/events/-statgen/index.html> We will hold a five full-day intensive workshop on state-of-the-art statistical genetics methods for detection of genetic loci for complex traits, either qualitative or quantitative.

Each day will include hands-on computer exercises using statistical genetics computer programs, especially the Mendel software package, with its new graphical front-end.

We will cover the general theory behind the methods as well as emphasize the practical aspects needed to give the best chances of success. The Course is designed to assist people who are actively studying the genetics of complex traits. Topics will include:

* Statistical Reviews * Genetic Study Design * Quality Control and other data issues * Haplotyping * Analysis of Qualitative and Quantitative Traits including: - Parametric and Non-Parametric Linkage (NPL) analysis - Methods for Large Pedigrees - Association Testing: + Case/Control + Genome-Wide Studies (GWAS) + Family-based * Copy Number Variation (CNV) * Ethnic Admixture Analysis * Other Recent Advances * Expert Panel Discussion on Next Generation Sequencing Data Analysis Methods and Challenges

Participants in the Course need no prior experience with these methods or programs. Participants will be required to bring a laptop computer to run the analysis exercises.

The Course features instructors from the Statistical Genetics Group of the UCLA Department of Human Genetics as well as Statistical Genetics instructors from UNC-Chapel Hill and NCS:

- Kenneth Lange - Jeanette Papp - Janet Sinsheimer - Eric Sobel - Hua Zhou

The cost of the course, which includes lunch and snacks every day and a group dinner on Thursday, is:

US \$900 for students and postdocs from non-profit institutions US \$1000 for staff and faculty from non-profit institutions US \$1200 for individuals from for-profit institutions

Transportation and lodging are not included

Application deadline has been extended, but space is limited. The course will be held 16-20 August 2010 in Chapel Hill, North Carolina. Lectures will be at the Rizzo Conference Center. Accommodations are available at the Rizzo Center or other nearby hotels.

For more information, including the simple application process, please visit <http://genomics.unc.edu/events/-statgen/index.html> Thank you!

“Sinsheimer, Janet” <Janet@mednet.ucla.edu>

NIMBioS HPC Phylogenetics Oct13-15

The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its “Fast, Free Phylogenies: HPC for Phylogenetics Tutorial” to be held Oct. 13-15, 2010, at NIMBioS.

Objectives: This tutorial focuses on how to use Tera-Grid, the CIPRES Portal, the iPlant Discovery environment, university clusters, and other typically free HPC resources for phylogenetic analysis. The tutorial is geared primarily toward biologists (including students, postdocs and faculty) who are at least moderately experienced with phylogenetic analysis and who have datasets to run but who are typically running analyses on their own desktops, though other researchers, such as statisticians or mathematicians working in phylogenetics, are encouraged to apply. Learning can be enhanced for people applying as a team (such as a pairing of a biologist and a statistician who collaborate in their work). Accepted students will have the option of receiving instruction in basic unix usage via webinar and self-paced online resources before the actual workshop, so lack of experience in this area should not be a barrier. Instructors and/or organizers include Eric Carr (NIMBioS); Jim Ferguson (National Institute for Computational Sciences, Univ. of Tennessee/Oak Ridge National Laboratory); Susan Holmes (Stanford Univ.); Brian O’Meara (Univ. Tennessee); Alexis Stamakatis (Technical Univ. of Munich); Dan Stanzione (Texas Advanced Computing Center/iPlant); and Bob Thomson (Univ. California Davis). Tuition is covered by NIMBioS and applicants may also request travel and lodging support.

Location: NIMBioS at the University of Tennessee, Knoxville

Co-sponsors: NIMBioS, iPlant, Oak Ridge National Laboratory

For more information about the tutorial and a link to the online application form, go to http://nimbios.org/-tutorials/TT_hpc2010 Participation is limited, and those selected to attend will be notified within two weeks of the application deadline. Application deadline: August 27, 2010

The National Institute for Mathematical and Biological Synthesis (NIMBioS) brings together researchers

from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, the U.S. Department of Homeland Security, and the U.S. Department of Agriculture with additional support from The University of Tennessee, Knoxville.

Brian O'Meara <http://www.brianomeara.info> Assistant Prof. Dept. Ecology & Evolutionary Biology U. of Tennessee, Knoxville

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You are also invited to spread the information to potential candidate in your institution.

Best regards.

Licia Colli

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Colli Licia <licia.colli@unicatt.it>

Piacenza Genomics Summer School Sept 6-9

Dear Colleagues,

I am pleased to inform you that the applications for the 3rd GLOBALDIV Summer school, to be held in Piacenza, Italy (6-9 September 2010) within the EU Project GLOBALDIV, are OPEN and some grants are available:

- 9 grants for accommodation (hotel and lunches paid directly by the organization) are available for students from Asia, Africa, Latin America and Eastern Europe;
- 4 grants with a lump sum of 350 euro in total are available from the European Science Foundation for students from UE (27 countries), Switzerland, Norway and UK.

Application is restricted to PhD students and junior researchers.

The deadlines for the application are the following:

- Students requesting the grant and needing VISA should apply within 25th July 2010;
- Students that DO not need VISA should apply within 15th August 2010.

The 2010 School focuses on the use of genomics for the characterization of genetic resources and on methods and software for large molecular data-set management and analysis. In addition, an update will be given on conservation strategy applied to wildlife that may be of interest for livestock management.

More information are available on the web at: www.globaldiv.eu/Summer_School_2010 or please consult the GlobalDiv Secretariat by contacting Dr. Elena Murelli at: elena@globaldiv.eu

Plön Germany Evolutionary Genetics

PhD STUDENT WORKSHOP ON 'EVOLUTIONARY GENETICS' IN PLÖN, GERMANY

The newly established working group (GEN-AG) 'Evolutionary Genetics' of the German Society of Genetics organizes its first workshop from 28 September to 1 October in Plön, Germany. The workshop will take place at the Kappelsberg Youth Hostel in Plön, Northern Germany. The venue is located very beautifully and is in close vicinity to the Max-Planck-Institute of Evolutionary Biology.

The workshop aims to establish a network of young scientists who work in the German-speaking countries and use theoretical or empirical approaches to study evolutionary genetic questions ranging from genes to ecosystems. Each participant will have the opportunity to present his or her work in 20 min talks or in a poster session. Three invited speakers will provide an overview of different fields of evolutionary genetics. In addition to the classical program, the workshop will include two so-called 'unconference' sessions, which are self-organized sessions by the participants.

Further information on the workshop, the program and the registration can be found at the following website:

<http://web.evolbio.mpg.de/~harr/home.html> The workshop fee be EUR 170.- for a single room and EUR 150.- (per person) in a double room. These costs include all meals. Student members of the GFG (Gesellschaft für Genetik) will be reimbursed for the accommodation, but not for the food (which costs EUR 60.-), when registering with the GFG BEFORE registering for the meeting. A membership form can be downloaded from the website above.

The closing date for registration is 15 August 2010.

The organizing team are Karl Schmid (University of Hohenheim, Stuttgart) as well as Bettina Harr and Emilie Hardouin (both at MPI of Evolutionary Biology, Plön). Please send any further questions regarding the workshop to karl.schmid@uni-hohenheim.de

Prof. Dr. Karl Schmid F.W. Schnell Endowed Professorship of Crop Biodiversity and Breeding Informatics Institute of Plant Breeding, Seed Science and Population Genetics (350) University of Hohenheim Fruwirthstrasse 21 D-70599 Stuttgart Germany Phone: +49 711 459 23487 Fax: +49 711 459 22343 Email: karl.schmid@uni-hohenheim.de <http://www.evoplant.uni-hohenheim.de> Karl Schmid <karl.schmid@uni-hohenheim.de>

Switzerland Speciation Aug29-Sep4

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We are still considering applications for our Speciation Summer School until next Sunday, 4 July.

This is an ESF-funded summer school “Methods in Speciation Research”, taking place August 29 to September 4, 2010 in Switzerland.

The program can be found at <http://www.eawag.ch/lehre/phd/schools/frospects/-practical/course.scheme.gif> The school is part of the European Science Foundation Networking Program Frontiers in Speciation Research (FROspects) and is open for PhD students, early stage Postdocs and exceptionally well qualified MSc students. Venue is the EAWAG Center of Ecology, Evolution & Biogeochemistry (CEEB) in Kastanienbaum on the shores of Alpine fjord Lake Lucerne.

Speciation research is currently one of the most vibrant fields in evolutionary research. Its success became possible because of advances in empirical methods, concepts and theory building in population genetics and evolutionary ecology. We are now in the early stage of yet another wave of advance, associated with the genomics era. Studying speciation is a deeply interdisciplinary endeavor that often requires good understanding of very many different concepts and methods in ecology, genetics and evolution. This makes speciation research sometimes more difficult to access for young scientists than more disciplinary research questions in ecology and evolution. In this summer school we want to introduce graduate students to the ways experienced and successful speciation researchers inte-

grate concepts and methods from ecology, genetics, genomics and behavioural biology in an attempt to elucidate causes, mechanisms and consequences of, and constraints to speciation.

The course, taught by an international team of established speciation researchers, will provide state of the art overviews of major topics, as well as first hand insights into specific issues. In four mornings Roger Butlin (U Sheffield), Scott Hodges (UC Santa Barbara), Catherine Peichel (Fred Hutchinson Cancer Research Centre) and Glenn-Peter Saetre (CEES Oslo) will teach empirical lecture modules. Latest developments in speciation theory will be taught in a fifth lecture module by Sander van Doorn (U Bern). In the afternoons we will offer workshops and excursions to speciation study sites. These and a series of evening spotlight-on-research lectures will be taught by Elena Conti (U Zürich), Martine Maan (U Bern, Eawag), Walter Salzburger (U Basel), Ole Seehausen (U Bern, Eawag), Arjun Sivasundar (U Bern), Piet Spaak (Eawag) and Alex Widmer (ETHZ). The class size will not exceed 25 students and students will have ample opportunity to interact with teachers and staff throughout the week. We provide students with travel grants up to Euro 300,-, free on-site accommodation and meals.

For more information see http://www.eawag.ch/lehre/phd/schools/frospects/index_EN If you are interested, email a letter of application and a CV to Nadja Pepe at nadja.pepe@eawag.ch before July 5th. Later applications will no longer be considered.

http://www.eawag.ch/organisation/abteilungen/-fishec/index_EN ole.seehausen@iee.unibe.ch

UCaliforniaLosAngeles MathComput Genomics Fall2011

Mathematical and Computational Approaches in High Throughput Genomics, September 12-December 16, 2011.

We would greatly appreciate your help in advertising this program. Feel free to print the attached poster and hang it in your department.

At this time, we are especially interested in receiving applications to participate for the entire fall semester and would in particular welcome an application from you. To get more information and/or apply please visit

*<http://www.ipam.ucla.edu/gen2011> All applicants should fill out the online application form and submit a curriculum vitae. It is important to include the desired dates of participation and possible references. Postdoctoral Scholars and Graduate Students should have two letters of recommendation sent on their behalf. Assistant Professors and Junior Faculty are advised to have one letter of recommendation sent on their behalf. Note that letters do not necessarily need to be as formal as those provided for a job application. They can be a couple of paragraphs by email, but should comment on how the person would contribute to and/or benefit from the program. IPAM is generally able to offer a housing and travel allowance to accepted participants coming from outside of the UCLA area. On the application, there is a place to indicate the support requested.

Please send any additional questions to [*gen2011@ipam.ucla.edu*](mailto:gen2011@ipam.ucla.edu). We look forward to hearing from you.

Sincerely, Amber Puha

Amber Puha, Associate Director Institute for Pure and Applied Mathematics 406 Portola Plaza, Suite 1158 Box 957121 MC: 712105 Los Angeles, CA 90095-7121 1(310)206-2831 1(310)825-4756 Fax Email: apuha@ipam.ucla.edu www.ipam.ucla.edu Amber Puha <apuha@ipam.ucla.edu>

York EvolutionaryMorphometrics Oct11-14

The Hull York Medical School Centre for Anatomical

and Human Sciences (CAHS) will host a four day workshop in York 11-14 October 2010

The statistical study of morphological evolution went through a revolution during the last decades with the introduction of geometric methods for shape analysis. Geometric morphometrics (GMM) has now become an essential tool for the quantification of biological shape, being widely used in many areas of evolutionary biology, including quantitative genetics, evo-devo and phylogenetic comparative studies of shape and function.

The course is aimed at postgraduates who already have some insight into GMM but may not have yet used these methods. During the four days of the course the basics of geometric morphometrics will be covered and key multivariate morphometric methods reviewed. Frequent examples will be presented using available GMM software and students will gain experience in using different software tools during the course of each afternoon's practical sessions using datasets we will provide.

Faculty

Paul O'Higgins CAHS, Hull York Medical School

Andrea Cardini Dipartimento di Biologia, Università di Modena e Reggio Emilia and CAHS, Hull York Medical School

Leandro Monteiro Department of Biology, University of Hull and CAHS, Hull York Medical School

Registration

The fee for the workshop is £175 for the four days to include tea, coffee, soft drink breaks, lunch each day and dinner on the nights of 11 and 14 October.

To book on the course please visit www.york.ac.uk/res/fme leandro <l.monteiro@hull.ac.uk>

Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as \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 formatted) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

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