# EvolDir

May 1, 2011

## Month in Review

## 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.

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

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# Conferences

## Adelaide Barcode

_Latest News on the Adelaide Conference_

* [1]Call for Abstracts and the online tool for submitting your abstracts are now available. Submission deadline is Sunday, 15 May 2011. * Interested in what will happen during the Barcode Conference in Adelaide? Take a look at the [2]agenda outline for the Conference to see the schedule for plenary, poster and technical sessions, and a half-day of free time to explore Adelaide! * Researchers and students from developing countries can now submit [3]Applications for Travel Bursaries through an online submission tool. The conference organizers hope to offer 30 bursaries, contingent on the availability of funds. Deadline for submission is Sunday, 22 May 2011. * The Conference organizers invite you to consider becoming a co-sponsor or exhibitor at the Adelaide conference. It's a great way to raise the visibility of your organization or project. The [4]Sponsorship Opportunities brochure will explain how you can benefit from being a sponsor or exhibitor.

Links: 1. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=df041b13b5&e=3ac5b5eacd 2. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=5d8e75ef16&e=3ac5b5eacd 3. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=6ae796a731&e=3ac5b5eacd 4. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=f367426f12&e=3ac5b5eacd Fourth Conference Organizers <jettk@si.edu>

## Belfast SystematicsAssociation Jul4-8

8TH SYSTEMATICS ASSOCIATION BIENNIAL QUEEN'S UNIVERSITY BELFAST 4-8 JULY 2011

Dear Colleagues,

We are pleased to announce that registration is open for the 8th biennial conference of the Systematics Association, held for the first time in Northern Ireland!

There is an exciting programme that includes both plenaries and thematic symposia, as well as a large number of contributed sessions. Currently scheduled symposia include:

- Next Generation Systematics - Studying Evolution and Diversity in an Era of Ubiquitous Genomics - Arthropod Systematics: are Morphology, Palaeontology and Molecules Coming Together? - Algal Systematics: Where Next? - Advances in Using Museum Specimens and Ancient DNA in Systematics Research

Symposia will include a mixture of talks from invited speakers and other contributions. The Biennial also presents excellent opportunities for contributed papers on any aspect of systematics and is a great forum for students and young researchers to present their work. For further details, please see http://www.systass.org/biennial2011/ . On behalf of the conference organisers, we hope to see you there!

Juliet Brodie, President James Cotton, Programme Officer Peter Olson, Treasurer Christine Maggs, Local Organiser

Sponsors: British Phycological Society, Cambridge University Press, Genetics Society, Linnean Society, Queen's University Belfast

– The Wellcome Trust Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

james.cotton@sanger.ac.uk

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## Berlin ConservationGenetics Sep14-17

Symposium: Conservation Genetics V From Genomics to Landscape Genetics Berlin, Germany, September 2011

We are pleased to announce a special symposium on Conservation Genetics V From Genomics to Landscape Genetics

as part of the 8th International Conference on Behaviour, Physiology and Genetics of Wildlife in Berlin, Germany (September 14th - 17th, 2011).

We are accepting oral presentations and posters covering all aspects of conservation genetics, with emphasis on studies that use innovative approaches for wildlife conservation research (e.g. genomic or landscape genetic approaches). Contributions from students are particularly encouraged. Our keynote speaker will be Prof. Dr. Lisette Waits from the University of Idaho, USA. Prof. Waits is a leading expert in non- invasive genetic sampling (using Next Generation Sequencing Technologies) and landscape genetics.

Registration is now open and the deadline for abstract submission is

June 1st, 2011.

Please go to https://www.bayceer.uni-bayreuth.de/izw8/ for online registration or download the conference flyer for more information (http://www.izw-berlin.de/de/veranstaltungen/8th-IZW-Conference/downloads/IZW_flyer_8thConference_Sept2011.pdf).

The conference is organized by the Leibniz-Institute for Zoo and Wildlife Research (IZW) and the European Association of Zoos and Aquaria (EAZA). Other symposia topics include non-invasive monitoring of hormones (post-conference workshop), ecophysiology, and behavioral rhythms of wildlife.

Berlin is the history-rich capital of Germany and offers abundant opportunities for cultural activities. Sites of interest include more than 170 museums, 150 performance stages, eight symphonic orchestras, three opera houses, 265 movie theatres, world famous architecture, two zoos and much more. Berlin also has a vibrant nightlife with thousands of restaurants, bars and clubs. At the same time, Berlin is also the cheapest capital of Europe, making it a very affordable destination.

Were looking forward to meeting you in Berlin!

Prof. Simone Sommer (sommer@izw-berlin.de), Niko Balkenhol (balkenhol@izw-berlin.de) Leibniz-Institute for Zoo and Wildlife Research (IZW) Evolutionary Genetics Postfach 601103 10252 Berlin Germany

"Sommer, Simone" <SOMMER@izw-berlin.de>

## BucknellU Evolution Jun13-14

Registration is now open for an international conference to be held at Bucknell University in Lewisburg, Pennsylvania, USA on Monday, June 13 and Tuesday, June 14, 2011, entitled "Evolutionary Ecology across Trophic Levels - A Symposium in Honor of Warren Abrahamson."

Registration is available from the conference website: http://www.bucknell.edu/x65430.xml Registration costs have been reduced to $15 for students and postdocs and $35 for others. Evening meals are no longer included in this price, and can be selected separately if desired. Registration fees will increase on May 1.

The conference will feature twenty scientific talks to be given by alumni, collaborators, and friends of the Abrahamson Lab. Confirmed speakers include:

-Doug Allchin, University of Minnesota Twin Cities -Catherine Blair, Bucknell University -Jackie Brown, Grinnell College -Timothy Craig, University of Minnesota-Duluth -Sarah Diamond, University of North Carolina -Netta Dorchin, Museum Koenig -Micky Eubanks, Texas A&M University -David Hartnett, Kansas State University -Christine Hawkes, University of Texas at Austin -John Horner, Texas Christian University -Jason Irwin, Central Washington University -Ann Johnson, Florida Natural Areas Inventory -Eric Menges, Archbold Biological Station -Patricia Peroni, Davidson College -Peter Price, Northern Arizona University -Otto Solbrig, Harvard University -John Stinchcombe, University of Toronto -Hilary Swain, Archbold Biological Station -Mizuki Takahashi, Bucknell University -Art Weis, University of Toronto -Michael Wise, Roanoke College

Tentative titles are available on the symposium website. Topics will address the diversity of subjects and approaches taken by Abe over his career, from the ecology and evolution of plant-insect interactions to community and ecosystem approaches to fire ecology, restoration, and conservation of natural landscapes.

A contributed poster session is also planned, and can be selected as part of the registration. Activities will include a banquet, picnic, and talent show, as well as regional natural history excursions. Events will be held in the Elaine Langone Center on the Bucknell University Campus.

Conference fees include daytime meals and snacks, but not lodging. Additional tickets to the picnic and banquet are available for attendees and guests. Lodging in Bucknell dormitories is available for $38/night single and $30/night double occupancy, with a one-time key charge of $10. There are many high-quality hotels, inns, and B&Bs in the region as well.

The Bucknell University campus provides easy access to the downtown shopping, dining, and entertainment district of Lewisburg, a town noted for its historical preservation and vibrant culture. The central Susquehanna valley offers many recreational opportunities. Details can be found at: http://www.lewisburgpa.com/ This conference will celebrate Warren Abrahamson's 38 years of service to Bucknell University and the scientific community in anticipation of his upcoming retirement in the summer of 2012. During his career, Abe has supervised approximately 200 undergraduate research students, 18 Master's recipients, and 21 postdoctoral fellows, many of whom have remained active in science. In 2009 he was named a AAAS fellow. His main research interests include 1) multitrophic plant-insect interactions using the goldenrod system and 2) fire ecology and plant demography in Florida's upland communities.

For more information on Warren Abrhamson and his work, please visit his lab website: http://www.facstaff.bucknell.edu/abrahmsn/ Questions and comments can be addressed to steve.jordan@bucknell.edu

Steve Jordan, Associate Professor Department of Biology Bucknell University Lewisburg, PA 17837 Office: 302 Bio. Bldg. +1 570-577-1254 Lab: 331 Bio. Bldg. +1 570-577-3816 Fax: +1 570-577-3537 http://www.facstaff.bucknell.edu/sdjordan/-jordan.html steve.jordan@bucknell.edu

## Galway Ireland RECOMB ComparativeGenomics Oct8-10

Dear colleagues: It is with great pleasure that I announce the 9th annual RECOMB satellite workshop on Comparative Genomics (RECOMB-CG), to be held in Galway, Ireland. Please see the Call For Papers attached below. Regards, Aaron Darling (Program Committee Chair) Cathal Seoighe (Conference & Program

Chair)

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RECOMB-CG, 2011 October 8-10, 2011 Galway, Ireland http://recombcg.org CONFIRMED KEYNOTE SPEAKERS

* Ed Green (UC Santa Cruz, USA) * Kateryna Makova (Penn State University, USA) * Julian Parkhill (Sanger Institute, UK) * Nikolaus Rajewsky (Max-Delbrück Center for Molecular Medicine, Germany) * Christopher Greenman (TGAC, UK) * Jerome Salse (INRA, France)

KEY DATES Paper submission deadline June 03, 2011 Notification of paper acceptance June 24, 2011 Poster submission deadline September 20, 2011 Workshop October 8-10, 2011 More details available at http://recombcg.org THEME AND SCOPE

The continuing advance of DNA sequencing technology has produced an avalanche of genome sequence and genome structural information across the evolutionary spectrum. Transforming that information into biological knowledge requires creative and innovative new computational and statistical methods for comparative genomics.

The RECOMB Satellite Workshop on Comparative Genomics aims to provide the premier forum for new computational developments applied to all aspects of comparative genomics. We solicit contributions on topics including comparison of genome structure and organization, genome function, and evolution. We particularly encourage contributions that use new computational methods to acquire new insight into biological processes. Advances in computational theory are welcome, though all submissions should include genome-scale analyses informed by comparative data.

New for 2011, all peer-reviewed and accepted RECOMB-CG manuscripts will be published in a supplement to BMC Bioinformatics as open access, author subsidized, articles.

Specific topics of interest include but are not limited to:

Gene and genome duplication Gene family evolution Genome structural variation Algorithms for comparative genomics Genome rearrangement Ancestral genome reconstruction Multiple genome alignment Genome sequence comparison Modeling genome evolution Comparative genomics for genome annotation Gene tree reconciliation Species and gene tree inference Comparative metagenomics Comparative genomics linked to proteomics, metabolomics, and other 'omic data Comparative genomics and gene expression and regulation Applications of comparative genomic methods

CALL FOR PAPERS

Papers should be submitted via the EasyChair system. Submissions must be received in electronic form by 11:59pm (Samoa time), June 3rd, 2011.

Submissions should be typeset as double-spaced A4 pages with 1-inch margins all around in a minimum of 10 point font. Submissions should be limited to 16 pages, everything included (title, authors, addresses, abstract, references, figures, tables). Exceptions to this limit may be granted by consultation with the Program Committee Chairs. Authors are encouraged to use the BMC document templates when preparing manuscripts. Templates are available in Microsoft and LaTeX formats. Submitted manuscripts must be rendered to PDF format prior to upload into EasyChair at the review stage. Submissions must include the corresponding author's email address. Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

At least one author per each successful submission is required to register and present the paper at the workshop. The paper will be included in the conference proceedings, which will be published in BMC Bioinformatics. Address any questions to the program committee chairs: Aaron E. Darling (aarondarling at ucdavis.edu) and Cathal Seoighe (cathal.seoighe at nuigalway.ie)

CONFERENCE CHAIR

Cathal Seoighe (National University of Ireland, Galway, Ireland)

PROGRAM COMMITTEE CHAIRS

Aaron E. Darling (University of California, Davis, USA) Cathal Seoighe (National University of Ireland, Galway, Ireland)

PROGRAM COMMITTEE

Aida Ouangraoua, INRIA Lille, France Anne Bergeron, UQAM, Canada Benedict Paten, University of California Santa Cruz, USA Bernard Moret, Ãcole Polytechnique FÃ©dÃ©rale de Lausanne, Switzerland Cedric Chauve, Simon Fraser University, Canada Craig Nelson, University of Connecticut, USA Daniel Falush, Max Planck Institute Leipzig, Germany Dannie Durand, Carnegie Mellon University, USA Des Higgins, University College Dublin, Ireland Elisabeth Tillier, University of Toronto, Canada

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## HarvardU InvertebrateMorphology Jun20-23

Please join us at the 2nd International Congress on Invertebrate Morphology (ICIM), the venue that interconnects researchers from the International Society for Invertebrate Morphology (http://zoologi.snm.ku.dk/english/Forskning/Invertebrates/isim/) and other societies interested in the morphology and evolution of invertebrate animals.

The 2nd ICIM will be hosted by the Museum of Comparative Zoology, the Department of Organismic and Evolutionary Biology, and the Harvard Museum of Natural History, at Harvard University, from June 20th to June 23rd 2011. The congress will include the following Symposia:

Neurophylogeny Meiofauna - comparative morphology and evolution Invertebrates as parasites Sponge morphology and evolution Controversies about the morphological evolution of arthropods Invertebrate morphology in 3D - non-invasive imaging, visualisation, and data storage Comparative developmental biology Round Table: Data and metadata standards in zoomorphology

Visit the congress website for details of speakers, special symposia, and submission of abstracts for poster and oral presentations:

http://icim.harvard.edu/ The deadline for abstract registration is April 30, 2011. Please click here to begin your registration:

http://icim.harvard.edu/registration-open We look forward to seeing you in June!

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

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extavour@oeb.harvard.edu

http://www.extavourlab.com Extavour Lab Administration: Barbara Hanrahan Tel. 1 617 496 2132 bhanrahan@oeb.harvard.edu

EDEN: Evo-Devo-Eco Network http://www.edenrcn.com edenrcn@fas.harvard.edu

EDEN Administration: Barbara Perlo perlo@fas.harvard.edu

extavour@oeb.harvard.edu

## Heraklion Crete Genomics Sep14-17

**Call for Abstracts**

The *G*enomics In Aquaculture symposium 2011, 14-17 September 2011 (_www.GIA2011.com_) organizing committee invites you to submit high-quality papers for oral/poster presentation on any topic related to genomics and proteomics research involving aquaculture species.

Areas of particular interest are:

- Nutrigenomics - Larval Quality - Selective Breeding - Toxicogenomics - Environmental Impact - Stress - Immunology - Growth - Development of Molecular Markers - Genomic Resources - Comparative Genomics - Bioinformatics - Phylogenomics - Epigenomics - Proteomics

Looking forward seeing you in Crete,

The organizing Committee

sarris@her.hcmr.gr

## Irapuato BiodiversityGenomics Jul23-26

Registration is now open for the annual symposium of the American Genetic Association. Go to:

http://www.theaga.org/2011/ The meeting will be held from July 23-26 in Irapuato and Guanajuato, Mexico and the theme is “Genomics and Biodiversity”. The first day will take place at LANGEBIO, the National Laboratory of Genomics for Biodiversity in Irapuato http://www.langebio.cinvestav.mx/. The 2nd and 3rd days will take place in the stunning Spanish colonial town of Guanajuato, at the Hotel Camino Real. A preliminary list of invited speakers is available on the web site, and includes leading researchers from the US, Mexico and beyond. Registration is $150 (USD) for faculty and postdocs and $75 for graduate students. Small travel grants will be available to student registrants through the web site. Regular attendees are encouraged to present posters and the web site allows submission of abstracts for the conference book. This meeting promises to be a landmark gathering of researchers using next-gen and other approaches to study the evolution of life, from bacteria to humans. We hope to see you there!

For more information, please email Scott Edwards, AGA President, at sedwards@fas.harvard.edu

Additional breaking news: we have just received funding from NSF for a pre-meeting bi-national workshop on next-gen sequencing and analysis in phylogeography and phylogenetics. This workshop will take place at Langebio from approximately July 19-22, and workshop participants are expected to also attend the AGA meeting. Further details on applying for the workshop will be forthcoming. Please contact Stacey Lance <lancestacey@gmail.com> for more information.

sedwards@fas.harvard.edu

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## Irapuato Mexico GenomicsBiodiversity Jul23-26

Registration starts next week for AGA 2011! We are keeping registration fees low to encourage participation from scientists and students throughout the Americas.

If you are planning to arrive from the US, book your flights to Leon, Guanajuato (airport code BJX). Transportation during the meeting will be by chartered bus.

This year's theme, Genomics and Biodiversity, recognizes the remarkable new Laboratoria Nacional Genomica para la Biodiversidad (LANGEBIO, http://www.langebio.cinvestav.mx/), the National Laboratory of Genomics for Biodiversity, located in Irapuato, Guanajuato, Mexico. The Laboratory's mission is "to bring together interdisciplinary groups to carry out cutting-edge research and to generate genetic knowledge about Mexican biodiversity." The meeting also recognizes that Mexico is ranked 5th in the world in terms of biodiversity, leading all other countries in, for example, the number of reptiles, pines and cacti. What better place to celebrate the role of genomics in generating knowledge of biodiversity than the National Laboratory of Genomics?

Invited Speakers include:

Gabriela Olmedo - Cinvestav Unidad Irapuato Andres Moreno - Stanford University Angelica Cibrian - American Museum of Natural History/ National Laboratory of Genomics for Biodiversity, Mexico Anne Bronikowski - University of Iowa Bill Murphy - Texas A & M University Bryan Carstens - Louisiana State University Carlos Bustamante - Stanford University Chris Amemiya - Benaroya Research Institute, Seattle Ed Green - University of California Santa Cruz Elena Alvarez-Buylla - Institute of Ecology, Universidad Nacional Autónoma de México Joshua Der - Penn State University Katie Piechel - Fred Hutchinson Cancer Research Center, Seattle Pablo Vinuesa - Center for Genomic Science, Mexico Patricia Escalante - Institute of Biodiversity, Universidad Nacional Autónoma de México Pina Aguilar - Autonomous University of Yucatan Rachel Mueller - Colorado State University Robert K. Wayne - University of California, Los Angeles Ruairidh Sawers - National Laboratory of Genomics for Biodiversity, Mexico Stacey Lance - Savannah River Ecology Lab, University of Georgia Valeria Souza - Institute of Ecology, Universidad Nacional Autónoma de México Therese Markow - University of California, San Diego

Our opening evening reception takes place July 23. On the 24th, we will have a day-long symposium at LANGEBIO where attendees can meet the scientists and see the remarkable research facility. The talks on July 25th and half-day July 26th will be held in the wondrous Spanish colonial town of Guanajuato (about 40 km from Irapuato), a World Heritage site with ample accommodation and restaurants. Attendees can fly into Leon (about three hours north of Mexico City by car) and stay in Guanajuato. The meeting will end with a banquet at the historic Mision Guanajuato on the evening of the 26th and a day-long field trip on the 27th to survey biodiversity in the area and the equally stunning city of San Miguel de Allende. We hope to see you there!

Watch the AGA website ( http://www.theaga.org/) – the conference link will be available in the next few days.

Scott V Edwards, President American Genetic Association

agajoh@oregonstate.edu

## KualaLumpur Bioinformatics Nov30-Dec2 CallParticipation

Announcing InCoB/ISCB-Asia Joint Conference 2011

10th International Conference in Bioinformatics (InCoB)/1st ISCB-Asia Conference Kuala Lumpur, 30 November â 2 December 2011

Key Submission Deadlines Paper Submission: 25 May 2011 Poster, Demo, and Tutorial Abstracts: 01 July 2011 Late Breaking Abstracts: 01 October 2011

CALL FOR PARTICIPATION

The Tenth International Conference on Bioinformatics (InCoB)/1st ISCB-Asia Joint Conference, InCoB/ISCB-Asia 2011 (http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid%8&l=-http–www.incob2011.org ) will be held at Renaissance Hotel, Kuala Lumpur, Malaysia on 30 November

â 2 December 2011.

InCoB/ISCB-Asia 2011 is jointly hosted by the Asia-Pacific Bioinformatics Network (APBioNet, http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid$3&l=--http–www.apbionet.org/) and the International Society for Computational Biology (ISCB, http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid%9&l=--http–www.iscb.org). In collaboration with the International Immunomics Society (IIMMS, http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid$5&l=--http–www.iimms.org/), we will also organize a joint session with the 4th Conference of Basic and Clinical Immunogenomics and Immunomics (BCII2011) on 2 Dec. 2011.

InCoB/ISCB-Asia 2011 aims to bring together scientists working in bioinformatics and computational biology, spanning a wide range of underpinning disciplines including computer science, biology, biotechnology, genomics, proteomics, transcriptomics, immunomics, mathematics and statistics.

Prof. Minoru Kanehisa (Kyoto University), Dr. Alex Bateman (Sanger Institute), Dr. Pascale Gaudet (Swiss Institute of Bioinformatics), Prof. Arthur Olson (Scripps Research Institute) and Dr. Jun Wang (Beijing Genomics Institute) have accepted to present Keynotes at InCoB/ISCB-Asia 2011. For the latest list of other invited speakers kindly check the conference website.

We invite you to participate in the following sessions:

1. Full papers for oral presentation and publication in one of the conference journals: BMC Genomics, BMC Bioinformatics, Immunome Research, Bioinformation or Journal of Integrative Computational Biology. 2. Abstracts for pre-conference tutorial presentations 3. Abstracts for (A) poster and (B) software/tool/resource/database/technology demo presentations. 4. Late-breaking abstracts for short oral or poster presentations 5. APBioNet Annual General Meeting 6. Collaboratively organized sessions such BCII2011 and others which will be announced on our website.

Submissions to InCoB/ISCB-Asia 2011 may cover any aspect of bioinformatics, computational biology, chembioinformatics, bioinformatics-related cloud computing, biocomputing, health care genomics, personalized medicine, environmental genomics, synthetic genomes and organisms, metagenomics, pharmacogenomics, and immunomics conveying a scientific result.

1. FULL PAPERS

SUBMISSION DEADLINE: 25 MAY 2011 ACCEPTANCE: 30 JULY 2011

InCoB/ISCB-Asia 2011 will feature oral presentations from full paper submissions of original research, with acceptance intended for potential publication in:

* BMC Genomics (IF 3.78; http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid$6&l=--http–www.biomedcentral.com/bmcgenomics)
* BMC Bioinformatics (IF 3.43; http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid$7&l=--http–www.biomedcentral.com/bioinformatics) * Immunome Research (preliminary IF 5.33); new URL http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid&0&l=--http–www.immunome-research.net, previously: http://iscb.12all.com/lt.php?c6&m1&nl=-4&s&4ed7a67b1287a670d4232b408022f0&lid&1&l=-http–www.immunome-research.com)

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## Kyoto SMBE2011 Jul26-30 Update

Dear Evoldir subscribers:

Followings are updates of SMBE2011 Kyoto Conference.

1) Deadline for "Graduate Student/Postdoctoral Fellow travel award" and "Undergraduate Student Mentoring Program award" is Monday, April 25. Because Japan standard time is ahead of many standard times, we will wait until ALL standard times on earth will become Tuesday, April 26. We hope many young people will apply for these two awards.

2) Walter Fitch Student Prize speakers were selected by SMBE Council. You can see their list at "Speakers" (http://smbe2011.com/speakers.html).

3) Kyoto is safe, as well as most of Japan!

We provide following websites regarding radiation levels in Japan at Top page (http://smbe2011.com/):

IAEA: Fukushima Nuclear Accident Update Log Important Information from Japanese Government Radiation in Kyoto Prefecture Radiation map of Japan

For your information, Kyoto City is located more than 500km away from Fukushima Daiichi nuclear power plants. Please do not worry.

4) Many symposia and workshops now have confirmed speakers. Please see "Symposia and Workshops" (http://smbe2011.com/symposia.html) page, which is frequently updated.

5) Deadline for early registration and Deadline for application of oral presentation were postponed to May 31. You have enough time. Please visit "Important dates" (http://smbe2011.com/important_dates.html) page.

6) We opened web site for hotel reservation. Please visit "Accommodation" (http://smbe2011.com/accommodation.html) page.

If you have any question, please feel free to send your inquiry to: SMBE2011@lab.nig.ac.jp.

Yours,

Chair, SMBE2011 Domestic Organizing Committee Saitou Naruya National Institute of Genetics Mishima, Japan

nsaitou@genes.nig.ac.jp

## Kyoto SMBE Jul26-30 TravelAwards

SMBE 2011 Travel Awards for Postdoctoral Researchers and Graduate Students

As many of you are aware, the northeast part of Japan was hit by a series of earthquakes. Kyoto is located in western Japan, and thankfully was left unscathed. The schedule for the SMBE2011 Kyoto Conference is unaffected, namely, it will take place from July 26 to 30, this year. However, periodical electricity shutdowns sometimes take place, including Mishima City where conference headquarter is located. We therefore moved SMBE2011 website to a private server located outside Japan. The new URL is http://smbe2011.com/ Because of a series of national holidays in early May and because of earthquake, we decided to delay the deadlines. Please see http://smbe2011.com/important_dates.html How to apply for SMBE 2011 awards is now described athttp://smbe2011.com/awards.html. We are sorry for the short notice, but we hope many young people will apply these awards.

The Nei Lecture, four Plenary talks, and Walter Fitch Student Symposium will be held on July 29, 2011. Please visit http://smbe2011.com/lower_level/July_29_speakers.html For list of symposia and workshops, please visit http://smbe2011.com/symposia.html As of today, April 1, 85 persons registered to SMBW2011 at Kyoto. Maximum number of attendants is 1,200. First come, first served basis. We would appreciate your cooperation to register as early as possible.

Chair, SMBE2011 Global Organizing Committee Gojobori, Takashi Vice Director & Professor DNA Data Analysis Laboratory National Institute of Genetics, Mishima, 411-8540, Japan Email: tgojobor@genes.nig.ac.jp Phone/FAX: +81-55-981-6847/+81-55-981-6848 Lab Home Page: http://www.nig.ac.jp/labs/DnaData/ Chair, SMBE2011 Domestic Organizing Committee Saitou, Naruya Professor Saitou Laboratory National Institute of Genetics, Mishima, 411-8540, Japan Email: saitounr@lab.nig.ac.jp Phone/FAX: +81-55-981-6790/+81-55-981-6789 Lab Home Page: http://sayer.lab.nig.ac.jp dgraur@gmail.com

## Kyoto SMBE Jul26-30 updates

April 1, 2011

To evoldir people:

As many of you are aware, the northeast part of Japan was hit by a series of earthquakes. Kyoto is located in western Japan, and thankfully was left unscathed. The schedule for the SMBE2011 Kyoto Conference is unaffected, namely, from July 26 to 30, this year. However, periodical electricity shutdown sometimes take place, including Mishima City where conference headquarter is located. We therefore moved SMBE2011 website to private server located outside Japan. New URL is http://smbe2011.com/ Because of series of national holidays in Japan in early May and because of earthquakes, we decided to delay deadlines. Please see http://smbe2011.com/important_dates.html How to apply SMBE 2011 awards are now described in http://smbe2011.com/awards.html. We are sorry for short notice. But we hope many young people will apply these awards.

Nei Lecture, four Plenary talks, and Walter Fitch Student Symposium will be held on July 29, 2011. Please visit http://smbe2011.com/lower_level/July_29_speakers.html For list of symposia and workshops, please visit http://smbe2011.com/symposia.html As of today, April 1, 85 persons registered to SMBW2011 at Kyoto. Maximum number of attendants is 1,200. First come, first served basis. We would appreciate your cooperation to register as early as possible.

Chair, SMBE2011 Global Organizing Committee Gojobori, Takashi Vice Director & Professor DNA Data Analysis Laboratory National Institute of Genetics, Mishima, 411-8540, Japan Email: tgojobor@genes.nig.ac.jp Phone/FAX: +81-55-981-6847/+81-55-981-6848 Lab Home Page: http://www.nig.ac.jp/labs/DnaData/ Chair, SMBE2011 Domestic Organizing Committee Saitou, Naruya Professor Saitou Laboratory National Institute of Genetics, Mishima, 411-8540, Japan Email: saitounr@lab.nig.ac.jp Phone/FAX: +81-55-981-6790/+81-55-981-6789 Lab Home Page: http://sayer.lab.nig.ac.jp Saitou Naruya <nsaitou@genes.nig.ac.jp>

## Lunteren Netherlands GalaxyCommunity May25-26

Hello all,

This is a reminder that early registration for the 2011 Galaxy Community Conference ends in less than two weeks. You can save 20% if you register on or before 24 April. http://galaxy.psu.edu/gcc2011/Register.html We've also added a partial list of confirmed speakers. More will be added in the coming weeks as the schedule firms up. http://galaxy.psu.edu/gcc2011/Programme.html Dave C. clements@galaxyproject.org

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We are pleased to announce the 2011 Galaxy Community Conference, being held May 25-26 in Lunteren, The Netherlands. The meeting will feature two full days of presentations and discussion on extending Galaxy to use new tools and data sources, deploying Galaxy at your organization, and best practices for using Galaxy to further your own and your community's research. Seehttp://galaxy.psu.edu/gcc2011/ for complete details.

About Galaxy: Galaxy is an open, web-based platform for accessible,reproducible, and transparent computational biomedical research.

Accessibility: Galaxy enables users without programmingexperience to easily specify parameters and run tools and workflows. Reproducibility: Galaxy captures all information necessary sothat any user can repeat and understand a complete computational analysis. Transparency: Galaxy enables users to share and publishanalyses via the web and create Pages–interactive, web-based documents that describe a complete analysis.

Galaxy is open source forall organizations. The public Galaxy service (http://usegalaxy.org) makesanalysis tools, genomic data, tutorial demonstrations, persistent workspaces,and publication services available to any scientist that has access to theInternet. Local Galaxyservers can be set up by downloading the Galaxyapplication and customizing it to meet particular needs.

Conference Overview: This event aims to engage a broader community of developers, data producers, tool creators, and core facility and other research hub staff to become an active part of the Galaxy community.

We'll cover defining resources in the Galaxy framework, increasing their visibility and making them easier to use and integrate with other resources, how to extend Galaxy to use custom data sources and custom tools, and best practices for using Galaxy in your organization.

Additional topics include, but are not limited to: * Talks submitted by the Galaxy community * Integration of tools (including NGS analysis tools) and distributed job management * Deployment of Galaxy instances on local resources and on the Cloud * Management of large datasets with the Galaxy Library System * Using the Galaxy LIMS functionality at NGS sequencing facilities * Visualizing Data without leaving Galaxy * Performing reproducible research * Performing and sharing complex analyses with Workflows * An "Introduction to Galaxy" session, offered on May 24, for Galaxy newcomers. Registration: The conference fee is euro 100 on or before April 24, and euro 120 after that. The meeting is being held at the Conference Centre De Werelt in Lunteren, The Netherlands, which is also the conference hotel. You are encouraged to register early, as space at the hotel (and at the "Intro to Galaxy" session) is limited and is likely to fill up before the conference itself does. See http://galaxy.psu.edu/gcc2011/Register.html Abstract Submission: Abstracts are now being accepted for short oral presentations. Proposals on any topic of interest to the Galaxy community are welcome and encouraged. The abstract submission deadline is the end of February 28. See http://galaxy.psu.edu/gcc2011/Abstracts.html Sponsors The 2011 Galaxy Community Conference is co-sponsored by the US National Science Foundation (NSF, http://www.nsf.gov/), and the Netherlands Bioinformatics Centre (NBIC, http://www.nbic.nl/). NBIC is a collaborative institute of the bioinformatics groups in the Netherlands. Together, these groups perform cutting-edge research, develop novel tools and support platforms, create an e-science infrastructure and educate the next generations of bioinformaticians.

We are looking forward to a great conference and hope to see you in the Netherlands!

The Galaxy and NBIC Teams

– http://galaxy.psu.edu/gcc2011/ http://getgalaxy.org http://usegalaxy.org/ clementsgalaxy@gmail.com

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## Manchester GenomeEvolution May13

We are pleased to announce that the second annual Manchester Molecular and Genome Evolution Symposium will take place on Friday 13th May. The remit of the symposium is broad and includes all aspects of molecular and genome evolution, ranging from computational algorithm development to wet-lab experiments investigating the molecular basis of fitness.

The symposium will be a day long event consisting of two plenary lectures, a series of talks, and a poster session. Themed sessions will include Molecular Evolution and Adaptation, Molecular Evolution and Disease, and Experimental Evolution. Other topics will be covered in a general session.

Our plenary lectures are by Prof. Christian Schlötterer (Vienna) "The genomic architecture of adaptation to a novel environment" and Dr Mike Brockhurst (Liverpool) "The Red Queen accelerates molecular evolution". Other scheduled talks will cover the evolution of mosquitoes, the evolution of disease causing genes, and population genomics.

We encourage anyone interested to attend the symposium and, if they wish, to submit an abstract. We are particularly keen to give PhD students and post-docs a chance to present their work. The best abstracts will be selected to give talks with the remainder invited to present posters. All talks and posters will also be considered for a prize, presented at the drinks reception following the symposium.

There are limited places so please register for the symposium online at the URL http://tinyurl.com/ManMage (full URL: http://www.survey.ls.manchester.ac.uk/TakeSurvey.aspx?PageNumber=1&SurveyID=n242lm2). If you have any questions about the symposium please contact me (simon.whelan@manchester.ac.uk) or Caroline Aylott (caroline.aylott@manchester.ac.uk).

Regards,

Simon Whelan

– Simon Whelan | T: +44-(0)161-3068901 | F: +44-(0)161-2755586 Computational and Evolutionary Biology, University of Manchester Michael

Smith Building, Oxford Road, Manchester, M13 9PT, UK http://www.ls.manchester.ac.uk/people/profile/index.aspx?PersonID=1716 Simon Whelan <simon.whelan@manchester.ac.uk>

## Marseilles 15thEvolBiol Sep27-30 AcceptedAbstracts

Dear All,

We are pleased to inform you that the fist accepted abstracts of the 15th Evolutionary Biology Meeting at Marseilles, Marseilles, France, 27-30 September 2011, are now available on our web site: http://sites.univ-provence.fr/evol-cgr Best wishes,

Pierre Pontarotti

Universite EGEE <Egee@univ-provence.fr>

## Montpellier ModelsEvolutionaryEcol Jun8-10

Student seminar: "Models in Evolutionary Ecology". Montpellier (France), June 8-10, 2011 http://www.seminar-mee.org/ Application deadline: May 13th 2011

We are pleased to invite you to the second edition of the workshop "models in evolutionary ecology". This workshop is organized by PhD students and postdocs, is dedicated to students (PhD students, postdocs, undergrads) interested in theoretical approaches in evolutionary ecology and has three objectives:

- give a broad overview of modeling techniques used in evolutionary ecology and their relationship with experimental work - encourage dialogue between PhD students using different approaches - discuss on how to communicate on the models and their meaning to the general public

The workshop is intended to favour exchange as much as possible, and consists in a series of methodological sessions by invited researchers, talks by researchers and students, journal clubs, poster sessions and roundtables. The detailed program is here: http://www.seminar-mee.org/home/programme Registration to the workshop is free, but we require all participant to present their work in a talk or with a poster.

For organization purposes, it would be great if you could pre-register quickly (i.e., before the end of April). You can then take your time to complete your registration before May, 13th by submitting an abstract. http://www.seminar-mee.org/home/inscription Confirmed faculty:

Thomas Broquet Vincent Devictor Richard Gomulkiewicz Sébastien Lion Guillaume Martin Denis Roze

We look forward to seeing you in June!

The organizers, Ronan Becheler, François Blanquart, Etienne Loire and Timothée Poisot.

http://www.seminar-mee.org/ Francois BLANQUART <Francois.BLANQUART@cefe.cnrs.fr>

## Montreal TunicateEvolution Jul3-7 Registration

Subject line: Registration now open for the 6th International Tunicate Meeting, July 3-7 2011 in Montreal, Canada

Dear tunicate (and chordate/deuterostome) biologists:

The registration page of the 6th International Tunicate Meeting website http://apps.mni.mcgill.ca/tunicate/ is now open.

The ITM is the principal scientific gathering of tunicate researchers, and is an organic outgrowth of this wide-spread and diverse, but very collegial, scientific community. It is a regular biennial meeting of ~150-200 researchers from around the world, organized as a scientific conference with research presentations given in plenary sessions and poster sessions. The 6th International Tunicate Meeting (ITM) will be held July 3-7 2011 at McGill University, Montreal, Quebec, Canada. Previous meetings were in Okinawa, Japan (2009), Villefranche-sur-Mer, France, (2007) Santa Barbara, California (2005), Marseille, France, (2003) and, in 2000, the inaugural ITM was held on main-island Japan.

The ITMs cover all aspects of tunicate research including, but not limited to, (alphabetically listed) developmental biology (including embryogenesis, metamorphosis, budding and regeneration), ecology and population diversity, evolution (tunicates/chordates/deuterostomes), genomics/proteomics, immunity and allo-recognition, invasive species, neurobiology, physiology and systematics. These will all be featured in the 6th ITM in Montreal, including invasive species biology, reflecting the importance of tunicates as problematic invasive species in Canada and elsewhere. Plenary session talks are selected from submitted abstracts.

Abstracts may be submitted until April 30, a registration+lodging package will be available until May 31, and registration will be open until June 30.

The 6th ITM takes place in Montreal during its summer festival season and overlaps with the International Jazz Festival, Cirque du Soleil performances in the Old Port, and the Juste Pour Rire comedy festival.

We hope to see you in Montreal this summer!

On behalf of the 6th ITM Program Committee

Ken

Ken Hastings Organizing Host, 6th International Tunicate Meeting Montreal Neurological Institute McGill University 3801 University Street Montreal, Quebec Canada H3A 2B4 514-398-1852 (phone) 514-398-1509 (fax) ken.hastings@mcgill.ca

Cameron Christopher <c.cameron@umontreal.ca>

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## Norman Evolution2011 Jun17-21 DeadlineMay1

The DEADLINE for submitting talk/poster submissions for the Evolution 2011 Meeting in Norman, Oklahoma (17-21 June) is fast approaching. It is THIS Sunday - 1 May! Please log onto the meeting website for instructions on how to submit your presentations. http://www.evolution2011.ou.edu/-talk_poster_submission.html Looking forward to welcoming everyone to Evolution 2011 here in Norman in June!

Larry Weider, Rich Broughton, Ingo Schlupp Dept of Zoology, The University of Oklahoma Tri-chairs, Evolution 2011 Organizing Committee

“Weider, Lawrence J.” <ljweider@ou.edu>

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## Norman Evolution 2011 Jun17-21 MeetingDeadlines

Dear Friends:

The SSE and I cordially invite you, as one of our members, to join us in Norman, Oklahoma this summer (June 17-21, 2011) at EVOLUTION 2011.

With an estimated attendance of roughly 1500, EVOLUTION 2011 is the premier annual international meeting of evolutionary biologists on the planet. The talks and plenary sessions present cutting-edge research on topics ranging from molecular evolution to behavioral ecology, comparative genomics to computational analysis of biological data. And, of course, there are always a lot of exciting and productive conversations with our colleagues.

Early-bird registration for EVOLUTION 2011 will end on April 17. Visit www.evolutionsociety.org to learn more! The deadline for submitting talks and posters is May 1st.

As an SSE member, you’ll receive a significant discount on your registration.

I look forward to seeing you at the conference!

All the best,

Jerry Coyne President, Society for the Study of Evolution SSE- http://www.evolutionsociety.org Mission: The objectives of the Society for the Study of Evolution are the promotion of the study of organic evolution and the integration of the various fields of science concerned with evolution.

Bill Dahl for Jerry Coyne <wdahl@botany.org>

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## Norman Evolution2011 Jun17-21 RegistrationExtended

Early-bird registration for Evolution 2011 (17-21 June, Norman, OK) has been extended until 1 May 2011.

The talk/poster submission deadline also is the 1 May 2011.

Many thanks!

Larry Weider, Rich Broughton, Ingo Schlupp

Dept of Zoology, U. of Oklahoma

Tri-Chairs, Evolution 2011 Organizing Committee

"Weider, Lawrence J." <ljweider@ou.edu>

## Norman iEvoBio Metagenomics Jun21-22

Special Session on Metagenomics, Barcoding, and Biodiversity at iEvoBio (Informatics for Phyogenetics, Evolution, and Biodiversity)

This year, iEvoBio will have a special focus Session on Metagenomics, Barcoding, and Biodiversity and the challenges that these new approaches raise for evolutionary informatics. We now have over 6000 genomes and vast quantities of metagenomic sequences in the public domain, primarily from bacteria and archaea from many habitats. Various short sequences (e.g. barcodes) for quick identification of eukaryotes are emerging. The availability of this sequence data and ever-cheaper methods for producing it offer exciting opportunities for understanding molecular evolution and biodiversity. However, the data are growing faster than the infrastructure to support it. Moreover, the eukaryotic and microbial informatics communities have independent histories and approaches, so synergy is not easy. These challenges typify the intersection of fields that are the scope of iEvoBio. Invited speakers in this special session include Neil Davies (http://moorea.berkeley.edu/aboutus/people/-ndavies) from the Moorea Biocode project, Linda Amarral-Zettler (http://amarallab.mbl.edu/) from the Marine Biological Laboratory Wood's Hole, and Holly Bik, from the Hubbard Center for Genome Studies at the University of New Hampshire. After the talks, there will be an open panel with all the speakers, including keynote speaker Dawn Field (http:/-/ceh.academia.edu/DawnField) from the Center for Ecology and Hydrology at Oxford.

More details about the program and guidelines for contributing content are available at http://ievobio.org. You can also find continuous updates on the conference's Twitter feed at http://twitter.com/iEvoBio . iEvoBio is sponsored by the US National Evolutionary Synthesis Center (NESCent) in partnership with the Society for the Study of Ecolution (SSE) and the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2011 Organizing Committee: Rob Guralnick (University of Colorado at Boulder) (Co-chair) Cynthia Parr (Encyclopedia of Life) (Co-chair) Dawn Field (UK National Environmental Research Center) Mark Holder (University of Kansas) Hilmar Lapp (NESCent) Rod Page (University of Glasgow)

robgur@gmail.com

## PacificSymposiumBiocomputing MicrobiomeEvolution Jan3-7

Call for papers We invite you to submit manuscripts to be considered for presentation at this special session of PSB. Papers will be published in the peer-reviewed proceedings and indexed in Medline.

The objective of this Microbiome Studies special session is to expand our understanding of the composition, structure, and function of microbial ecosystems and their impact on human health and well-being. We particularly encourage studies that apply "next generation" sequencing technologies, and reports of tools that support the analysis and sharing of data from such studies. Problems of specific interest may include, but are not limited to:

Algorithm, statistical, software, and database development for analyzing data from shotgun metagenomics, 16S hypervariable region surveys, and microbial transcriptomics.

Association studies of microbial consortia with human health, agriculture, bioremediation, climate change, and engineering.

Theoretical and simulation studies of microbial ecology, function, and evolution.

The role of microbial consortia in natural ecosystems.

Interactions among different microbial systems and macrobiological systems

Other topics within the subject area are welcome. Note that all submitted papers should make clear their relevance for the study of Microbiome Studies. If unsure whether your paper fits the session theme, please contact one of the co-chairs.

For details, see the special session website: http://-psb.stanford.edu/cfp- ms

We invite you to submit your work to this year's special session!

Submission deadline is 11 July 2011

James A. Foster Professor, University of Idaho Init. for Bioinformatics & Evol. STudies

foster@uidaho.edu

## Palermo CrustaceanEvolution Sep27-29

Dear Colleagues and Friends,

we are pleased to announce and invite you to the forthcoming conference "NEW FRONTIERS FOR MONITORING EUROPEAN BIODIVERSITY: THE ROLE AND IMPORTANCE OF AMPHIPOD CRUSTACEANS", which will be held in September 27th-29th, 2011 in Palermo, Italy.

The meeting is supported by the AIT (Ateneo Italo-Tedesco / Deutsch-Itanienisches Hochschulzentrum) and the University of Palermo. It is organized by the Department of Environmental Biology and Biodiversity of the University of Palermo (Italy) and the Universität Potsdam (Germany). The aim of the congress is to promote cultural and scientific exchanges among scholars interested in all the aspects of amphipod research.

The themes of the meeting range from pure to applied topics, regarding both inland-water and marine taxa; six main sessions are scheduled:

Session 1 - New needs, Old tools: how taxonomy can help in monitoring the present-day biodiversity changes. Session 2 - How much diversity in Amphipoda (morphotypes, ecotypes, trophic categories). Session 3 - Novel interactive tools recently developed and based on morphological characters. Session 4 - Novel interactive tools recently developed and based on molecular characters. Session 5 - Examples of the use of the taxon Amphipoda in environmental monitoring. Session 6 - How decline in popularity of traditional taxonomy could impact on biology and society and which agencies support taxonomic research.

We are looking forward to meet you in Palermo!

All the kindest regards

Sabrina Lo Brutto

Valerio Ketmaier

For more information about this meeting, visit our web-site (http://www.meb-conference.com). You can also follow us on Facebook "Zoology in Sicily".

Sabrina Lo Brutto â Dipartimento di Biologia Ambientale e BiodiversitÃ â University of Palermo -Via Archirafi, 18 - 90123 Palermo â ITALY- Tel. 091.23891835 - Fax 091.23860855/60751 - sabrilob@unipa.it

Valerio Ketmaier - Universität Potsdam - Karl-Liebknecht-Str. 24-25, D-14476 Potsdam, Germany-Tel: +49-331-977-5604 ketmaier@uni-potsdam.de

Valerio Ketmaier <ketmaier@rz.uni-potsdam.de>

## Paris SexChromsomeEvol Jun9-10

international meeting "Genetics, Epigenetics and Evolution of Sex Chromosomes" - last call for abstract

The international meeting "Genetics, Epigenetics and Evolution of Sex Chromosomes", organized by the French Genetics Society (SFG) and the Jacques Monod Institute (University Paris-Diderot) will be held in Paris on 9-10 June 2011. The deadline for abstract submission (oral communication or poster) is May 1st 2011. All informations can be found on the web site : www.sfgenetique.org/meeting2011/ Catherine.Montchamp@legs.cnrs-gif.fr

## Paris Speciation Jul19-23 NewDeadlines

Dear colleagues

The deadline for abstract submissions for poster and oral contributions in the European Congress of Mammalogy has been changed to the:

20th of April.

please find above our invitation to participate to the symposium: Mechanisms of speciation in mammals

Best Wishes Guila Ganem & Carole Smadja

We invite abstract submissions for oral and poster contributions in the symposium "Mechanisms of Speciation in Mammals" to be held at the European Congress of Mammalogy (ECM 2011: http://www.alphavisa.com/-

ecm2011), Paris, France (July 19-23 2011).

This symposium will address the mechanisms of speciation in mammals, with the intention to providing an overview of theoretical background, recent advances and new challenges in this field of research. It will bring together researchers working in different disciplines and developing various approaches from genomics to behaviour, to explore the mechanisms favouring the evolution of reproductive barriers. Particular attention will be given to recent advances in understanding speciation in the context of ongoing gene flow and to studies providing new insights into the factors favouring adaptive speciation in mammals.

Deadline for submission: 1st April 2011. Instructions for preparing and submitting your abstract can be found on the ECM website. Organisers: Guila GANEM & Carole SMADJA Guila.ganem@univ-montp2.fr and carole.smadja@univ-montp2.fr

“guila.ganem” <guila.ganem@univ-montp2.fr>

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## RutgersU GenomeStructure Aug9-11

Conference on Effects of Genome Structure & Sequence on the Generation of Variation and Evolution DIMACS, Rutgers University, New Brunswick, NJ

August 9 â 11, 2011

CALL FOR POSTERS

A special invitation for Graduate Student & Postdocs

About the Topic:

The structure of DNA is not monotonous, but rather varies along its sequence, sometimes dramatically so. Such variation in structure leads to sequenceâdependent variations in the fidelity of DNA copying and repair.

That the probability of distinct classes of mutations varies along a DNA sequence has implications for evolutionary theory because selection acts on heritable variation when this variation affects fitness.

Highly mutable sequences have, in fact, evolved in genome regions such as those encoding pathogen coats where increased diversity in a population favors survival.

The goal of this conference is to inspire a dialogue among evolutionary biologists and broad interdisciplinary group of researchers to explore the impact of our increase understanding of DNA structure, repair, replication and organization on evolutionary theory.

Registration and call for posters:

Online registration and additional information can be found at http://dimacs.rutgers.edu/Workshops/-GenomeStructure If you would like to contribute a poster, please send title/abstract to Christine Spassione at spassion@dimacs.rutgers.edu no later than June 1, 2011. You will be notified of acceptance of your poster as soon as possible after you submit it. For questions or more information, see the website or contact Eugene Fiorini, Associate Director of DIMACS and Program Coordinator (gfiorini@dimacs.rutgers.edu).

Graduate Student and Postdoc Support Financial support is available to US graduate students and postdocs. Review of applications begins May 1, 2011.

The Workshop is organized by the Center for Discrete Mathematics and Theoretical Computer Science (DIMACS with funding provided by the US National Science Foundation and the International Union of Biological Sciences.

Lynn Caporale <caporale@usa.net>

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## UMunich MetazoanPhylogeny Oct11-14 Registration

Dear colleagues, this is just a friendly reminder that early-bird registration for the international conference âDeep Metazoan Phylogeny 2011 â new data, new challenges“, to be held from October 11-14, 2011 at the University of Munich (Germany) closes *May 1, 2011*!

The conference will bring together mathematicians, theoreticians, molecular systematists, and morphologists that aim at resolving deep branches in the animal tree of life for a better understanding of the evolution and diversification of multicellular life on Earth.

During the conference, new data, new analytical tools and new results will be discussed. Challenges and pitfalls in phylogeny reconstruction based on molecular and/or morphological data will be identified, aiming for a critical and constructive view of the state of the art of the metazoan tree of life.

The meeting will consist of sessions with several invited leaders in the field and open sessions with short presentations. In addition, there will be ample space and time to present posters.

The meeting focuses on three major themes: (1) Innovations in the analyses of molecular and morphological data (2) Molecular phylogeny: new markers and phylogenomic analyses (3) The evidence found in morphology

Full list of confirmed keynote speakers can be found at < www.palmuc.de/dmp2011 >

The conference is organised in collaboration with the Priority Program "Deep Metazoan Phylogeny" of the German Science Foundation (DFG). This program is a joint effort of more than 20 participating workgroups bringing together molecular, morphological and bioinformatic expertise with the goal to establish a (hopefully) robust backbone metazoan phylogeny. Details on the priority project "Deep Metazoan Phylogeny" can be found at < http://www.deep-phylogeny.org >.

More information is available on the conference website < www.palmuc.de/dmp2011 >, which will continuously be updated.

*Important Dates & Deadlines*: Early registration with reduced fees until 1st of May 2011 Regular registration fees then until 1st of July 2011 Latest abstract submission 1st of July 2011 Notification of oral presentations until 1st of August 2011

We look forward to welcoming you in Munich in October!

for the organizing team

Gert Wörheide

— Prof. Dr. Gert Wörheide Molecular Geo- & Palaeobiology Department of Earth and Environmental Sciences & GeoBio-CenterLMU Ludwig-Maximilians-Universitaet Muenchen Richard-Wagner-Straße 10 80333 Muenchen Germany

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Director, Bavarian State Collections of Palaeontology and Geology Spokesman of the Executive Board, GeoBio-CenterLMU

Lab publications: www.mol-palaeo-lit.de/papers.php www.researcherid.com/rid/C-1080-2008 woerheide@lmu.de

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## UNottingham Popgroup Jan4-7

Advance notice that the 45th Population Genetics Group (PGG or PopGroup) meeting will be held at the University of Nottingham, UK, from the evening of the 4th January to midday on 7th January 2012. This year, the event organisers are Dr Angus Davison, Prof John Brookfield, Dr Sara Goodacre, and Dr. Tamsin Majerus.

In case you are unaware - how could you be? - PopGroup is an informal international meeting which annually brings together ~200 scientists working in all areas of population genetics and evolutionary biology. Talks and posters from early career scientists are particularly encouraged. The conference is officially registered with the Genetics Society as a special interest group (see www.populationgeneticsgroup.org)

Registration will open in October, but we have had requests for earlier information this year, so you can now sign up to the mailing list from the website http://www.populationgeneticsgroup.org/contact/ (if you have attended any of the last 3 meetings, Cardiff, Liverpool or Hull, you will already be on the mailing list)

– Dr. Angus Davison School of Biology University Park University of Nottingham NG7 2RD

Angus.Davison@nottingham.ac.uk

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## Vienna ISCB Jul15 GenomeCanadaStdAwards

Dear colleagues,

It is my pleasure to inform you that Genome Canada is providing funds for 3 students from Canada to attend the 7th ISCB Student Council Symposium (SCS7).

The symposium, held in Vienna on Friday July 15 as a satellite meeting of ISMB/ECCB 2011, aims at bringing together young computational biologists from all research areas and regions of the world. Student presentations will be selected from the submitted abstracts, accepted abstracts will be published in BMC Bioinformatics journal, and awards will be given to best poster and presentation.

Preference will be given to Canadian applicants for the Genome Canada fellowships. This is a great opportunity!

Submission website: http://symposium.iscbsc.org/-content/submissions Travel Fellowship information: http://symposium.iscbsc.org/content/tfsubmission General information: http://symposium.iscbsc.org

Important dates April 29: Abstract submission closes May 6: Travel Fellowships submission closes May 23: Travel Fellowship winners and Abstract acceptance notification

We look forward to receiving your abstract,

On behalf of the organizing committee, Magali Michaut, University of Toronto

– Magali Michaut, PhD http://baderlab.org/-MagaliMichaut mlou@evol.biology.mcmaster.ca

# GradStudentPositions

## BangorU CatfishSpeciation

NERC funded PhD position: Mimicry, polyploidy and speciation in neotropical catfishes. Applications are invited for a fully funded NERC studentship for full time study in the School of Biological Sciences at Bangor University (start date Autumn 2011) supervised by Dr Martin Taylor, Prof. Gary Carvalho and Dr Si Creer. The Corydoradinae are a species rich group of neotropical catfishes distributed widely over South America comprising more than 170 described species. The group demonstrate multiple genome duplication events and also exhibit complex mimetic colour pattern relationships (http://www.nature.com/-nature/journal/v469/n7328/full/nature09660.html). This project will use a multidisciplinary approach (including next generation and Sanger sequencing, pigment cell analysis, genome size analysis and ecology) to investigate the evolution of polyploidy and mimicry and its broader implications for speciation within the group. The successful applicant will join the large, thriving team in the Molecular Ecology and Fisheries Genetics Group (http://mefgl.bangor.ac.uk/-), in purpose-built molecular laboratories and aquarium facilities in the Environment Centre, Wales. (http://mefgl.bangor.ac.uk/documents/-

BrambleFreshwaterTropicalaquarium.pdf). There will also be opportunities for fieldwork in South America. Informal enquiries should be addressed to Martin Taylor (m.taylor@bangor.ac.uk). The studentship is funded by NERC and potential applicants should refer to the NERC Studentship Handbook 2011-2012 for eligibility and residency requirements (http://www.nerc.ac.uk/funding/application/studentships/) Applications should include a full CV (with details of two academic referees), and a covering letter that includes a clear statement confirming eligibility for the studentship. These should be sent to Dr Martin Taylor, Molecular Ecology and Fisheries Genetics laboratory, ECW Building, School of Biological Sciences, Bangor University, Gwynedd, LL57 2UW either by post or email (m.taylor@bangor.ac.uk) by Friday 13th May 2011.

Dr Martin Taylor, Molecular Ecology and Fisheries Genetics laboratory, ECW Building, School of Biological Sciences, Bangor University, Gwynedd, LL57 2UW

nitram8@hotmail.com

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## FondazioneEMach Italy TickPopGenetics

A PhD Fellowship is available for the study of population genetics and dispersal of the wood tick, Ixodes ricinus

We are seeking an highly motivated student that, within the large collaborative FP7 project EDENext (WP Tick-borne disease), will study the population structure and dispersal of the wood tick using a landscape genetics approach.

This challenging project will include field and laboratory work based at the Department of Biodiversity and Molecular Ecology at the Research and Innovation Centre of the Fondazione E. Mach, in the stunning Province of Trento, Italy. The student will be part of a multidisciplinary team of researchers, and can also take advantage of the stimulating environment offered by the PhD network of EDENext (which includes more than 40 collaborating institutions from across Europe).

Please see this link: http://www.fmach.eu/sperimentazione_context2.jsp?ID_LINK=4019&area=6 where you will find details of the application process, application forms, and more information about the Fondazione.

Please contact us if you have any further questions. Heidi C. Hauffe Cristiano Vernesi Annapaola Rizzoli

– Heidi C. Hauffe Department of Biodiversity and Molecular Ecology, Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, 38010 S. Michele all'Adige (TN), Italy tel.: 0461-615558 cell.: 348-7263653 e-mails : heidi.hauffe@iasma.it annapaola.rizzoli@iasma.it cristiano.vernesi@iasma.it

heidi.c.hauffe@gmail.com

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## ImperialCollege London FishSpeciation

PhD Studentship

Ecological Genomics and Speciation in Annual Fish

Annual killifish (Cynolebiasines) have undergone an extraordinary evolutionary radiation in the ponds ('temporary islands') of South America. There are over 30 species in the genus Austrolebias alone, which vary tremendously in size, colour, diet and other ecological adaptations (e.g. small crustivores vs. large piscivores). These fish are a remarkably good system for ecological and evolutionary studies. They can be easily grown in the lab, grow very fast (about three months to maturity) and die soon (they are annuals). They have interesting embryonic diapauses, and their eggs can be stored dried for months. So, there is no other vertebrate that is even remotely as amenable to the study of life-history genetics as these fish.

The student will look at a few species pairs of killifish, chosen for their contrasting traits of interest, i.e. those potentially linked to speciation scenarios and ecological adaptation. Experiments, hybridization and next-generation genomic tools will be applied (e.g. genomic and transcriptomic scans, candidate loci, expression analyses) to identify potential loci underlying these traits. This will be the basis for disentangling the molecular basis of life-history variation and speciation.

The project will be based in Savolainen Lab at Imperial College at Silwood Park (savolainenlab.org), co-supervised by Prof. Armand Leroi (www3.imperial.ac.uk/people/a.leroi) and Dr Tom Van Dooren (Ecole Normale Superieure, Paris; tomvandooren.eu).

The PhD studentship is funded for three years by the UK NERC. Eligibility criteria apply, e.g. UK students with Masters Degree. Applicants should only apply if they meet all of NERCs eligibility requirements for fees and maintenance http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp .Start date: September 2011

To apply, please send a CV, letter of motivation, names of 2 referees as a single pdf file to v.savolainen@imperial.ac.uk no later than 25 April 2011.

Prof. Vincent Savolainen Imperial College London & Royal Botanic Gardens Kew Silwood Park Campus, Buckhurst Road SL5 7PY Ascot, Berks, UK Tel: +44 (0)20 7594 2374 Fax: +44 (0)20 7594 2339 v.savolainen@imperial.ac.uk www.savolainenlab.org www3.imperial.ac.uk/people/v.savolainen

"Savolainen, Vincent" <v.savolainen@imperial.ac.uk>

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## KansasStateU CricketSpeciation

Hello All,

I have a graduate research assistantship (GRA) available for a M.S. or Ph.D. student to work in my evolutionary genetics laboratory. Our specific interests lie in identifying the genes and proteins that underlie postmating, prezygotic reproductive isolation in a complex of crickets that are only isolated by such phenotypes. We use a wide range of proteomic, molecular, behavioral and physiological analyses to identify and functionally test candidate genes (see my lab website for more information www.k-state.edu/cricketlab).

If you are interested in applying, please contact me by e-mail (cricket@ksu.edu) and I will forward you the necessary materials. Also, I am happy to offer more information or answer any questions you may have.

Best, Jeremy

Jeremy L. Marshall, Ph.D. Associate Professor Department of Entomology Kansas State University Manhattan, KS 66506

Phone#: 785-532-5588 e-mail: cricket@ksu.edu lab website: www.k-state.edu/cricketlab

Jeremy Marshall <cricket@k-state.edu>

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## Leipzig VisualizingHumanGenomics

PhD position - Visualizing Human Ancestry using Genomic Data

The DNA sequencing revolution has led to the production of an unprecedented quantity of data on human ancestry and promises the advent of "personal genomics". We are looking for an individual with a strong quantitative training and perhaps a dash of visual flair to develop statistical tools that represent relationships between individuals and populations based on genetic data. The goal is to provide historically and demographically informative summaries that reflect the mosaic nature of human ancestry as well as differences amongst groups. Applications include medical genetics, studies of human population history, comparative demography and science communication.

The Max Planck Institute for Evolutionary Anthropology in Leipzig represents a unique environment for this research. As well as sequencing the genome of Neandertals and other ancient hominids, a variety of projects seek to characterize diversity in human and ape populations. See http://www.eva.mpg.de/genetics/. This project is part of an ongoing a collaboration between Daniel Falush and Simon Myers (University of Oxford

http://www.stats.ox.ac.uk/~myers/) to develop statistical genetic methods for ancestry reconstruction.

Talented and enthusiastic candidates with a degree in any strongly quantitative discipline (e.g. Maths, Physics,

Computer Science) will be considered. Particularly advantageous would be a knowledge of Markov chains, modern computationally intensive statistical methods, etc. Good programming ability is a major plus as is involvement in informatics projects with a visual component. Knowledge of evolutionary biology or population genetics would be advantageous but is not required. Please contact daniel_falush@eva.mpg.de to apply and for further information.

daniel_falush@eva.mpg.de

## MasseyU ComputationalBiology

PhD Scholarship in Computational Biology Dr Murray Cox Institute of Molecular BioSciences, Massey University, New Zealand

A PhD scholarship is now open for a highly motivated and productive student in the Computational Biology Research Group at Massey University, New Zealand. The successful candidate will study how human social arrangements, such as marriage practices, affect patterns of genetic diversity in small communities. Although there is scope to accommodate existing research interests, the successful candidate will develop, implement and test new methods in statistical genetics, and apply these methods to genetic and cultural anthropology datasets. This research will initially be directed toward determining whether human social practices have constrained or directed genetic evolution in the Pacific region, a major focus of my research group.

This PhD scholarship offers a rare opportunity to develop your skills as a researcher within an internationally recognized computational biology research group, while taking advantage of New Zealand's unique natural and cultural environment. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located close to the North Island's central mountains, and presents regular opportunities for hiking, skiing, surfing and adventure sports, as well as experiencing New Zealand's unique indigenous culture. Nevertheless, my research group maintains extensive international connections, especially with colleagues in Australia, Indonesia, France and the United States, and is linked firmly into the international scientific community.

MINIMUM QUALIFICATIONS: - A Masters or Honors degree (First Class or equivalent) in computational biology, bioinformatics, applied mathematics, computer science, population genetics, molecular evolution, or other relevant field. - Able to conduct independent cutting-edge research. - Solid analytical, quantitative and mathematical skills. - Experience with probabilistic modeling and statistical genetics. - Candidates should be comfortable working in a UNIX environment, and have a strong programming background.

PREFERRED QUALIFICATIONS: - Candidates with a background in interdisciplinary research, spanning both biological sciences and applied mathematics/computer science, are especially encouraged to apply. - Candidates should have proven research experience, preferably with evidence of scientific publications. - Candidates will ideally be conversant in a compiled programming language (e.g., C or C++), a scripting language (e.g., Perl), and a statistical environment (e.g., R). - Experience with parallel computing on large clusters and/or parallel programming would be highly advantageous.

APPLICATION DEADLINE: Sunday 15 May 2011

Funding is available for three years in the first instance, with a probation period of one year prior to full confirmation.

This position will remain open until filled, and informal inquiries are welcome. To apply formally, please send the following documents in PDF format to Murray Cox at <m.p.cox@massey.ac.nz>:

1. A brief statement of research interests, qualifications and experience. 2. A brief statement describing how your career goals are consistent with the research area described above. 3. A curriculum vitae, including (if relevant) a list of scientific publications. 4. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

Dr Murray P. Cox Institute of Molecular BioSciences Massey University Private Bag 11 222 Palmerston North 4442 NEW ZEALAND

http://massey.genomicus.com/ m.p.cox@massey.ac.nz

## MaxPlanck 10 EvolutionaryBiology

The International Max-Planck Research School for Evolutionary Biology is offering up to 10 PhD fellowships.

The graduate school is dedicated to highest level of research and training in all areas of contemporary Evolutionary Biology. It is a joint initiative of the Max-Planck Institute of Evolutionary Biology, the University of Kiel and the Leibniz Institute for Marine Sciences in Kiel (IFM Geomar). The graduate school offers an internationally competitive research environment with state of art facilities. The participating groups are working on a broad variety of research topics including molecular, behavioral, theoretical and organismal approaches.

The graduate program starts with a rotation period of three months followed by a PhD project of three years including seminars, courses and workshops. The language of the graduate school is English. Financial support is provided throughout the program.

To obtain further information about our PhD program and application details please visit our website athttp:/-/imprs.evolbio.mpg.de . Well-motivated and highly-qualified students from all countries are welcome to apply. A Master of Science degree or a Diploma as well as a strong interest in Evolutionary Biology are prerequisites for application. We are looking forward to your application for a PhD fellowship in the beautiful landscape of Northern Germany.

The deadline for applications is May 15, 2011. The start of the program will be September 19, 2011.

Contact: Dr. Kerstin Mehnert, August-Thienemann-Str. 2, 24306 Plön, Germany email: imprs@evolbio.mpg.de phone: +49(0)4522 763 233

The coordinator Kerstin Mehnert

The steering comittee Diethard Tautz, Hinrich Schulenburg, Manfred Milinski and Thorsten Reusch

Dr. Kerstin Mehnert Scientific Coordinator, Press and Public Relations

Max-Planck-Institute for Evolutionary Biology International Max Planck Research School (IMPRS) August-Thienemann-Str. 2 24306 Plön, Germany

phone: ++49 - (0)4522 - 763 - 233 fax: ++49 - (0)4522 â 763 - 351 e-mail: mehnert@evolbio.mpg.de

www.evolbio.mpg.de, imprs.evolbio.mpg.de

Kerstin Mehnert <mehnert@evolbio.mpg.de>

## Netherlands 5 Biodiversity

Starting August 2011, the Netherlands Centre for Biodiversity Naturalis offers:

Five PhD positions 36 hours per week

We seek to attract PhD students who will be working on one of the projects described in the appendix. You are an energetic and enthusiastic scientist with interest in systematics or geology in general and one of the projects specifically. You are eager to join our new institute and to study the natural history collections of NCB Naturalis.

General requirements You have a master degree in systematics, evolutionary biology, palaeontology or other relevant discipline. You have a scientific and critical attitude, excellent time management and organizational skills, the ability to work independently, good verbal and written communication skills. Fluency in English is required.

We offer A fulltime contract (36 hours per week) for a period of four years. A maximum salary of circa euro 35,000 gross per year. All our employees are incorporated into a pension fund. The successful candidates will be employed by NCB Naturalis in Leiden. The candidate will also be affiliated to either the Leiden University, the University of Amsterdam or Wageningen University. The appointment must lead to the completion of a PhD thesis. Supervisors are mentioned with the project proposals.

Procedure You are invited to submit your application including the project of interest, your curriculum vitae, a list of publications, up to five keywords describing your research interests, and the names and e-mail addresses of at least two persons who can be contacted for reference (and who have agreed to be contacted) before 15 May 2011 by e-mail to; sollicitaties@ncbnaturalis.nl, or by mail; NCB Naturalis, HR department, PO Box 9517, 2300 RA Leiden, the Netherlands.

Research projects Research staff of NCB Naturalis has identified exciting research projects as described in the summaries that can be found here: http://-www.ncbnaturalis.nl/nl/werken-bij-ons/vacatures/-five-phd-positions/research-projects-descriptions/ We invite you to indicate in your application your interest in one or more projects. Describe your motivation for each project selected separately.

We also offer the opportunity to propose your own personal research project. Before submitting such a proposal, you first need to contact one of the permanent researchers of NCB Naturalis to seek commitment as supervisor. Without a supervisor of NCB Naturalis, we cannot accept proposals for new projects. For NCB Naturalis, Zoology and Geology research staff, seehttp://www.science.naturalis.nl/research/people. For botany staff, seehttp://www.nhn.leidenuniv.nl/-index.php/nhn/institute/personnelleidenor http://-www.bis.wur.nl/UK/Staff/Marc+Sosef . For more information on current research and facilities, see the websites of the founding partners of the NCB Naturalis, onwww.ncbnaturalis.nl - www.nhn.leidenuniv.nl -www.science.uva.nl/zma - www.bis.wur.nl/UK/-Organisation/Herbarium Any additional information can be requested from: Prof. Dr. E. F. Smets, scientific director Netherlands Centre for Biodiversity Naturalis E-mail: erik.smets@ncbnaturalis.nl Phone:

+31 71 5687 675

merckx@nhn.leidenuniv.nl

## Netherlands 5 EvolutionaryBiol

Starting August 2011, the Netherlands Centre for Biodiversity Naturalis offers:

Five PhD positions

36 hours per week

We seek to attract PhD students who will be working on one of the projects described in the appendix. You are an energetic and enthusiastic scientist with interest in systematics or geology in general and one of the projects specifically. You are eager to join our new institute and to study the natural history collections of NCB Naturalis.

General requirements

You have a master degree in systematics, evolutionary biology, palaeontology or other relevant discipline. You have a scientific and critical attitude, excellent time management and organizational skills, the ability to work independently, good verbal and written communication skills. Fluency in English is required.

We offer

A fulltime contract (36 hours per week) for a period of four years. A maximum salary of circa ? 35,000 gross per year. All our employees are incorporated into a pension fund. The successful candidates will be employed by NCB Naturalis in Leiden. The candidate will also be affiliated to either the Leiden University, the University of Amsterdam or Wageningen University. The appointment must lead to the completion of a PhD thesis. Supervisors are mentioned with the project proposals.

Procedure You are invited to submit your application including the project of interest, your curriculum vitae, a list of publications, up to five keywords describing your research interests, and the names and e-mail addresses of at least two persons who can be contacted for reference (and who have agreed to be contacted) before 15 May 2011 by e-mail to; sollicitaties@ncbnaturalis.nl, or by mail; NCB Naturalis, HR department, PO Box 9517, 2300 RA Leiden, the Netherlands.

Research projects

Research staff of NCB Naturalis has identified exciting research projects as described in the summaries below. We invite you to indicate in your application your interest in one or more projects. Describe your motivation for each project selected separately.

We also offer the opportunity to propose your own personal research project. Before submitting such a proposal, you first need to contact one of the permanent researchers of NCB Naturalis to seek commitment as supervisor. Without a supervisor of NCB Naturalis, we cannot accept proposals for new projects.

For NCB Naturalis, Zoology and Geology research staff, see http://www.science.naturalis.nl/research/people . For botany staff, see http://www.nhn.leidenuniv.nl/-index.php/nhn/institute/personnelleiden or http://-www.bis.wur.nl/UK/Staff/Marc+Sosef . Research projects:

Project 1

Life history influences on range expansion and population connectivity in a widely distributed marine sponge

Supervisor: Nicole de Voogd (Nicole.devoogd@ncbnaturalis.nl)

Population connectivity is a topic of major interest in marine biology with implications for ecology, evolutionary biology, biogeography, conservation and the management of exploited resources. In general, species with a longer pelagic larval duration, will disperse greater distances. Realised dispersal, however, depends on a number of factors including larval life history traits, behaviour and oceanographic conditions, particularly current patterns. Vertical migration behavior can have an important impact on horizontal dispersal, by regulating the time spent by larvae within particular layers of vertically sheared flows. Temporal variation in current patterns is in turn strongly affected by winds, density stratification of the water column and instabilities caused by interaction of currents with bottom topography. The overall objective of the present research proposal will address (in part) this conceptual framework by examining questions related to species performance (reproductive output) population (genetic) structure, and larval dispersal over wide biogeographical scales by using a widely distributed and conspicuous coral reef giant barrel sponge (Xestospongia testudinaria) as a model. Giant barrel sponges are the largest and possibly longest living of sponges and are also important spatial competitors in reef environments and contribute to reef heterogeneity. This study will be one of the first detailed studies of connectivity in a tropical sponge. In particular we will:

1) Quantify reproductive output of X. testudinaria across wide latitudinal gradients from Indonesia to the central Great Barrier Reef.

2) Elucidate how populations are genetically connected over spatial scales that range from within reefs (metres) among reefs (kilometers) and between bio-regions (100-1000s of kms)

3) Establish the influence of larval dispersal and settlement on population maintenance and

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## StockholmU ancientDNA

STOCKHOLM UNIVERSITY announces a

PhD POSITION IN SYSTEMATICS AND EVOLUTION (ANCIENT DNA) at the Department of Zoology, Stockholm University (placed at the Molecular Systematics Laboratory, the Swedish Museum of Natural History).

Project title: Large carnivore population turnover and ecological change during the Late Quaternary

Final date for applications: May 2, 2011

Project description:

The aim of this PhD project is to investigate the extent and timing of large carnivore demographic and ecological change during the last Ice Age as well as more recent historical times. As a secondary objective, the project also aims to assess the relative contribution of humans and climate change on these demographic and ecological changes. The laboratory analyses will comprise ancient DNA technology, radiocarbon dating and analysis of stable isotopes on fossils up to 50 000 years old. Specific questions that will be addressed include i) the effect of climatic changes during the last glaciation, ii) the existence and contribution of cryptic and traditional refugia, iii) the impact of the arrival of anatomically modern humans in different regions, iv) the consequences of the rise of human societies and changes to agricultural landscapes during the Holocene, and v) the impact of anthropogenic hunting during the last two centuries. From a conservation perspective, the long-term goal of the project is to develop a better understanding of how climate change and anthropogenic pressure, and the interaction between them, will affect large carnivores in the future. The project will be done within the ancient DNA research group at the Department of Molecular Systematics, the Swedish Museum of Natural History. The PhD degree will be awarded in Systematics and Evolution at the Department of Zoology, Stockholm University. Dr. Love Dalén at the Swedish Museum of Natural History (Department of Molecular Systematics) will be the main supervisor.

Qualifications: To be qualified for research studies the applicant must have completed a research degree (e.g. Master's), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level ("examensarbete") within systematics and evolution, ecology, population genetics or a similar subject. Applicants who have in principle acquired the corresponding competence in Sweden or abroad, are also qualified.

Criteria for selection: Among qualified applicants, selection is made according to the ability to profit from the studies. The criteria to be used are the applicant's documented knowledge in subjects of relevance for the research area, ability to master language (including both spoken and written English), analytical ability, creativity, initiative, independence and ability to cooperate. The basis for judgement of how well the applicant fulfils these criteria is: the relevance of earlier studies for the research area, grades on courses at the university level, the quality of the independent project (master thesis or "examensarbete"), references, interviews and the applicant's letter of intent. Previous experience in practical genetic analyses is highly desirable, and knowledge in ecology, population genetics, stable isotope analysis, and computer programming are considered as additional qualifications.

To be included in the application: Maximum one A4-page of personal presentation and your reasons for applying (letter of intent). Curriculum vitae. Copy of independent project report (master thesis or "examensarbete"). Copy of degree certificates and transcripts of academic records (all attested). Also provide a list of two persons who may act as references (with phone numbers and e-mail addresses). Provide two copies of all documents and the thesis. To be considered, the application labelled "PhD ref. no. 2/11 LD" must have arrived at the address below by May 2, 2011.

Address to which the application should be sent: Stockholms universitet Prefekten Zoologiska institutionen 106 91 Stockholm Sweden

Terms of employment: The research education comprises 48 months at full time. The position is financed by a fellowship ("utbildningsbidrag") for the first years, and then continues with PhD-employment until the end of the PhD-program. Up to 20% of teaching may be included in the position. (If teaching is included, the position will be extended).

Union representatives: Bo Ekengren SACO, Lisbeth Häggberg ST, and Gunnar Stenberg SEKO. Phone: + 46 (0)8 16 20 00. PhD student representative e-mail: do@sus.su.se

For further information about the project, contact: Dr. Love Dalén, e-mail: love.dalen@nrm.se

Further information on the web: Stockholm University: http://www.su.se The Swedish Museum of Natural History: http://www.nrm.se The Department of Zoology: http://zoologi.su.se

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## StockholmU EvoDevo

PHD POSITION: “ADAPTIVE DEVELOPMENTAL PLASTICITY AND GENETIC POLYMORPHISM IN INSECTS IN VARIED ENVIRONMENTS”

The position is available in Ethology at the Department of Zoology, Stockholm University, with a May 2, 2011 application deadline.

The general research area of the project is theoretical evolutionary biology and evolutionary ecology. Specifically, the aim is to develop and test theoretical models of the evolution of phenotypic variation as a response to varied environments. Important phenotypes for insect adaptations to varied environments include habitat and host plant preference, dispersal capacity and tendency, and traits important for life-cycle regulation, such as diapause and voltinism. A major question for the project is whether phenotypic variation is expected to be a plastic response to environmental influences or, instead, a consequence of genetic variation. The methodology used will be adaptive dynamics modeling, combined with individual-based and population genetic computer simulations. The project can also include collaboration with empiricists examining variation in traits related to host plant choice and life-cycle regulation in butterflies, within the Strategic Research Program EkoKlim at Stockholm University.

The requirements are an MSc or similar degree in evolutionary biology, evolutionary ecology or related disciplines, including at least 80 weeks of biology studies, with a degree project, in a field related to the research area, of at least 20 weeks at advanced level. Applicants who have acquired corresponding competence in Sweden or abroad are also qualified. Applicants will be assessed based on their documented knowledge in fields relevant to the research area, their creativity, independence and social competence, the quality of their degree project thesis and other publications, and the cover letter. Applicants with documented experience of theoretical modeling in a field related to evolutionary biology will have an advantage in the selection process.

The application should include a one-page presentation (cover letter) of yourself and why you want to undertake a PhD within this project. The application should also include your CV, a copy of the thesis of your degree project, a copy of your diploma or degree certificate, and names and contact details (phone and e-mail) of two references. Please submit your application (stating the Ref Nr 2/11 OL 2) by 2 May 2011 to: Stockholm University, Head of Department, Department of Zoology, 106 91 Stockholm, Sweden.

For further information, contact Olof Leimar (e-mail: olof.leimar@zoologi.su.se), Department of Zoology, Stockholm University.

Olof Leimar, Professor Department of Zoology Stockholm University SE-106 91 Stockholm Sweden

olof.leimar@zoologi.su.se http://www.zoologi.su.se/research/leimar/ olof.leimar@zoologi.su.se

## UBern 2 PopulationGenomics

Two PhD positions: UBern Population Genomics of Adaptive Radiation

Two PhD positions are available at the University of Bern in the project “Population genomics of adaptive radiation”. This project, funded by the Swiss National Science Foundation, will investigate the genomic basis of population divergence during adaptive radiation at different timescales in the progression from invasion to speciation using two of the best vertebrate models available today to study this question: East African cichlids and threespined stickleback.

We will apply high-throughput next-generation sequencing techniques using the Illumina HiSeq platform. We will address questions related to the population genomic signatures of divergent selection and reproductive isolation, and the genomic architecture of divergent adaptation and speciation at different stages along the micro- to macroevolution continuum in adaptive radiation.

We are looking for candidates strongly motivated to address cutting-edge questions in evolutionary biology, who will analyse NGS data and apply bioinformatics in an evolutionary genetics context. Candidates should possess an aptitude to work with very large data sets, strong desire to develop new analytical methods, and ability to work in team. The ideal candidates will have a strong grounding in evolutionary biology with experience in programming and genetic data processing, or in bioinformatics or computer science.

Both students will be co-advised by Prof. Ole Seehausen, Dr. Arjun Sivasundar (University of Bern and EAWAG, the Swiss Federal Institute for Aquatic Research) and Prof. Laurent Excoffier (University of Bern). The students will also be part of the new doctoral program in Population Genomics (http://-www.unil.ch/pg/page75326.html) and benefit from its activities.

Both positions will be available starting immediately. Applications will be considered until the positions are filled.

Salary will be according to SNSF guidelines.

Please send an application letter, CV and contact information of two references to:

Susanne Maurer (Susanne.maurer@iee.unibe.ch)

For inquiries please write to Ole Seehausen (ole.seehausen@eawag.ch)

Ole.Seehausen@eawag.ch

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## UDublin EvolutionaryBiology

PhD Studentship in Evolutionary Biology Characterisation of lignin and cellulose formation genes in biomass and energy grasses (Poaceae)

Principal Investigator: Dr Trevor Hodkinson (University of Dublin, Trinity College, Ireland; Trevor.Hodkinson@tcd.ie). Collaborators: Susanne Barth (Teagasc), Nicolas Salamin (University of Lausanne), Elizabeth Kellogg (University of Missouri).

Grasses have received considerable attention as a source of woody biomass for bioenergy production to provide alternatives to fossil fuels. Potential bioenergy grasses include Miscanthus, maize, switchgrass and several woody bamboos. Most grasses are herbaceous but some subfamilies have evolved woodiness. Bamboos (subfamily Bambusoideae) have evolved a woody character via enhancement of the lignocellulosic component of vascular tissue, especially vessels. Reeds (e.g. Arundo, Phragmites, subfamily Arundinoideae) and Panicoideae (e.g. Saccharum, Miscanthus, Panicum) have also evolved this trait. It is not known if they have achieved this via alternative biosynthetic paths/genes. Grass cell walls differ from other angiosperms in their major structural polysaccharides, pectins, proteins and phenolic compounds. Recent advances in genomics have revealed cellulose synthase$B!>(Blike (Csl) gene families (unique to grasses) and the CslF gene (unique to Poales, the order to which the grass family belongs). An understanding of how these gene families and lignocellulosic biosynthesis evolved in grasses is key to improving the processing quality of grasses for bioenergy and the manipulation of the genes in future biotechnology and plant breeding. Objectives and methodology: 1) Investigate, via a candidate gene approach, the evolution of genes known to be of importance for woodiness in grasses (e.g. cellulose synthase genes, Cesl, a highly expressed gene family in developing vascular fibres, including CslF, and monolignol biosynthesis genes. 2) Investigate the effects of woodiness on grass evolution (e.g. investigate, using diversification statistics and molecular dating, whether woodiness was a significant key innovation for speciation in the groups that have evolved it).

Applications are sought from suitably qualified candidates to undertake doctoral research at the University of Dublin, Trinity College (www.tcd.ie), under this PRTLI-funded structured PhD programme. All applications must include the following documents in one email: 1) A completed Application Cover Form (download), 2) A complete Curriculum Vitae, 3) A Letter of Motivation outlining your interest in the specific project 4) Certified copies of academic transcripts and, where appropriate, 5) Evidence of proficiency in English. Application deadline is 13 May 2011 but the position will remain open until filled. All applications for this studentship must be made to Trevor.Hodkinson@tcd.ie AND http://www.ucd.ie/earth/graduatetraining/-phdprogrammeinearthandnaturalsciences/-applyingforaphdposition/ The 4 year studentship includes EU fees and an annual stipend of 16,000 Euro commencing from September 2011 (please note that non-EU applicants will be charged additional fees of c. 6,000 Euro per annum that are not covered by the funding programme).

Further details of the project, its programme, and application procedure: www.ucd.ie/earth/graduatetraining/-phdprogrammeinearthandnaturalsciences/-earthandnaturalsciencesphdprojects/- And http://www.ucd.ie/t4cms/-Strand%204%20Description%20Document%20v5.pdf Dr Trevor Hodkinson Senior Lecturer in Botany Botany Building School of Natural Sciences Trinity College Dublin Ireland

Phone 00353 1 8961128 Fax 00353 1 8961147 email Trevor.Hodkinson@tcd.ie http://people.tcd.ie/-hodkinst Trevor Hodkinson <HODKINST@tcd.ie>

## UGuelph EvolutionaryBiology

An MSc or PhD position is open in my lab. The research in my lab addresses questions in evolutionary biology, physiology and ecology using theoretical, computational biology and bioinformatic approaches. Please see my website for further information (http://-sites.google.com/site/griswoldlab/home ).

We are located in the Department of Integrative Biology at the University of Guelph in Guelph, Ontario Canada. The University of Guelph (www.uoguelph.ca) has a very strong tradition of research in the biological sciences. The city of Guelph is located in southwest Ontario, approximately one hour from Toronto.

The graduate position is open until filled. Please email me (cgriswol at uoguelph.ca) to inquire about the position.

Kind regards,

Cortland Griswold Assistant Professor Department of Integrative Biology University of Guelph

cgriswol@uoguelph.ca

## UGuelph MarineInvertBarcoding

University of Guelph (with West Coast DFO Research Placement)

We are seeking an enthusiastic Ph.D. student with an interest in applied evolutionary genetics and taxonomy to conduct a DNA barcoding study on marine invertebrates as part of a large multi-disciplinary network conducting studies on aquatic invasive species. This barcoding project is a collaborative one, involving researchers at the University of Guelph, Fisheries and Oceans Canada, and University of Windsor.

Many global invaders are marine invertebrates such as crustaceans, molluscs, and ascidians that often present taxonomic challenges, especially in early life history stages. DNA barcoding has been identified as a robust, widely applicable method that could serve as an international standard for the identification of aquatic invasive species on a global scale as it has practical advantages over classical taxonomic methods. However, its utility for this purpose needs to be validated-especially when invaders and co-occurring native species are very similar-and its usefulness is a function of the availability of validated DNA barcoding datasets.

The successful candidate will apply DNA barcoding methods to generate essential baseline data on invertebrate biodiversity in Canada's coastal waters and will then evaluate the utility of this approach for invasive species identification and detection. This project may also involve generating molecular phylogenies based on multiple nuclear markers where needed to resolve taxonomic uncertainties of important marine invaders. Species identifications will be obtained in collaboration with taxonomic experts, and the relationship between cryptic species diversity and body size will be explored using the resulting datasets.

We are looking for a highly motivated candidate who is interested in playing a substantial role in developing novel research directions for this project, using the sequence data to address exciting questions in ecology and/or evolution. Potential research topics include investigating the phylogenetic distribution of "invasiveness"; analyzing molecular evolutionary rates across different taxa; or comparing patterns of genetic diversity, species diversity, species complementarity, and invasive species prevalence among regions.

The student will be co-advised by Dr. Sarah Adamowicz (University of Guelph), Dr. Cathryn Abbott, and Dr. Thomas Therriault (both of the Department of Fisheries and Oceans Canada). The successful candidate will be based at the Pacific Biological Station in Nanaimo, B.C. for a portion of the studentship. This position provides the opportunity to conduct novel research in invasion biology, ecology, and evolution and will serve as an outstanding training ground for those interested in governmental, academic, or private-sector careers in biology and environmental science.

Stipend funding is available at NSERC network rates. Canadian citizens and permanent residents are preferred as there are no project funds for international student fees. The project start date is to be between May 2011 and January 2012. To be considered for this position please send your CV including a brief summary of your research interests and contact details of two references to cathryn.abbott@dfo-mpo.gc.ca.

“Abbott, Cathryn” <Cathryn.Abbott@dfo-mpo.gc.ca>

## UGuelph UNB 4 EnvironmentalGenomics

BIOMONITORING 2.0 A High-Throughput Genomics Approach for Comprehensive Biological Assessment of Environmental Change

Large-Scale Applied Research Competition seeks to apply an environmental genomics approach, based on next-generation sequencing technologies to develop a wholly novel approach for large-scale biomonitoring of different ecosystems. Focused on the boreal wetland habitats of Canada's largest national park, Wood Buffalo (WBNP), the project brings together genomics, bioinformatics and ecological researchers from across Canada to work with federal scientists and industrial partners in an exciting and challenging new project.

metal mining and hydro-power projects. The area also is home to many indigenous communities who rely on access to the land to make their living. The project will work in partnership with local stakeholders to mesh cutting edge genomics and bioinformatics technologies to provide rapid ecosystem assessment tools, which will facilitate rapid and accurate monitoring of ecosystem health, in partnership with Environment Canada's CABIN program and Parks Canada's Ecological Integrity program.

5. Graduate Student positions (MSc/PhD, 3 positions) based at University of Guelph, Department of Integrative Biology (2 positions) and Dalhousie University, Department of Biology (1 position). These positions involve the use of NGS data to address evolutionary and ecological questions in arthropod, plant and soil biodiversity. Graduate students will be supervised jointly by members of Biomonitoring 2.0 project and will gain insights in using NGS genomics approaches as well as bioinformatics tools to develop and explore their own hypotheses in ecology and evolutionary biology. Example projects include: investigating patterns of cryptic diversity in different taxa; comparative analysis of above and below ground plant diversity and its linkage to temporal variability in communities within locations, the short-to-medium term environmental changes that have occurred in the past and forecast future successional changes; reconstructing functional food webs through trophic guilds interactions for different sampling sites.

6. MSc Student position: This student will be focused on genomics-based biomonitoring as a solution for monitoring in communities in Canada's North. This project is jointly supervised by Donald Baird (University of New Brunswick, Fredericton, NB) & Sarah Rosolen (Aurora Research Institute, Fort Smith, NWT), and will focus on studying the implementation of genomics-based biological monitoring in local communities in Canada's north. The student will be registered at UNB-Fredericton campus, but will spend extended periods in Wood Buffalo National Park based at the Aurora Research Institute in Fort Smith. The position is available to start in July 2011. The student should have an undergraduate background in ecology or environmental sciences, with experience or formal training in aspects of genomics, social science / community or volunteer monitoring being an advantage, but not essential.

For each position, please submit your CV (including names and contact information of 3 references) and a cover letter to Dr. Mehrdad Hajibabaei (mhajibab@uoguelph.ca). Please indicate the title of the position you are applying for in the subject line of your email. We will start reviewing the applications on April 15, 2011.

Mehrdad Hajibabaei <mhajibab@uoguelph.ca>

## UHull Biodiversity

PhD position: 'Revealing the Routes to Biodiversity' Position available in the Department of Biological Sciences, University of Hull, UK.

This full-time UK/EU PhD Scholarship will include fees at the 'home/EU' student rate and maintenance (£13,490 in 2011/12) for three years, depending on satisfactory progress.

REVEALING THE ROUTES TO BIODIVERSITY

This studentship will aim to understand the origin and evolution of wide-scale patterns of diversity in animals. It is currently not clear how environmental factors interact with speciation, extinction, and genetic and morphological rates of change to produce diversity. It is often assumed that these different measures of diversity are closely tied; for example, where there are more species we would expect greater morphological diversity. There is a growing literature that suggests this is not the case: reproductive isolations can occur with little or no genetic change; genetically very closely related species can have wildly divergent morphologies; some large groups of species can be indistinguishable from gross morphology where as other, species-poor, groups are diverse. If this is the case how does diversity accumulate? The student will address this question using cutting-edge statistical phylogenetic comparative methods applied to multiple datasets encompassing a wide range of animal groups. The studentship has the potential to contribute to a real quantitative science of macroevolution and has implications for life history, ecology, evolutionary biology, conservation and population biology. Potential applicants are encouraged to contact Dr Chris Venditti (C.Venditti@hull.ac.uk) before submitting an application.

Closing date Friday 27 May 2011. Studentships will start in September 2011 (or soon after)

Visit http://www2.hull.ac.uk/student/-graduateschool/pdhscholarships.aspx to download a copy of the application form.

PhD students at the University of Hull follow modules for research and transferable skills development and gain a Masters level Certificate, or Diploma, in Research Training, in addition to their research degree.

Dr Chris Venditti Department of Biological Sciences University of Hull Hull HU6 7RX UK

Telephone: +44 (0) 1482 462077

Email: c.venditti@hull.ac.uk

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## UHull EvolutionaryBehaviour

PhD Position: 'Dealing with environmental change: Does early experience allow animals to adapt?' available in the Department of Biological Sciences, University of Hull, UK.

This full-time UK/EU PhD Scholarship will include fees at the 'UK/EU' student rate and maintenance (£13,490 in 2011/12) for three years, depending on satisfactory progress.

DEALING WITH ENVIRONMENTAL CHANGE: DOES EARLY EXPERIENCE ALLOW ANIMALS TO ADAPT? Supervisors: Dr Lesley Morrell (Hull), Dr Domino Joyce (Hull), Dr Ben Chapman (Lund)

One of the fundamental challenges in biology is to understand how animals respond to the unprecedented environmental changes caused by human activities. Animals adapt to environmental changes over evolutionary time, but we have only limited understanding of how individuals can adapt to human-induced change within their own lifespan. Fish are critical components of aquatic food webs and habitats, which are frequently subjected to significant adverse anthropogenic impacts. Fish are particularly vulnerable to changes affecting their sensory capabilities, such as increased turbidity and chemical pollution from agricultural and industrial sources. They rely on vision and olfaction in finding food, choosing mates and detecting predators, all of which are negatively impacted by loss of visual or olfactory information. Exposure to an altered environment during early life, however, may provide a mechanism by which animals can compensate for the effects of the change in adulthood, through plastic or learned responses. This project will investigate behavioural adaptations to environmental change within an individual[1]s own lifespan, using guppies as a model system.

We are looking for a highly motivated, dynamic and enthusiastic individual, who will join the thriving Evolutionary Biology group (www.hull.ac.uk/evolution). The project benefits from recent investment in extensive aquaria facilities at Hull and the successful candidate will be trained in experimental design and statistical analysis, behavioural observations and (depending on interests) simulation modelling and/or molecular techniques.PhD students at the University of Hull also follow modules for research and transferable skills development and gain a Masters level Certificate, or Diploma, in Research Training, in addition to their research degree.

For further information please contact Dr Lesley Morrell (L.Morrell@hull.ac.uk) by email, including a copy of your CV (preferably as a pdf).

To apply, visit www.hull.ac.uk/phd to download a copy of the application and reference forms, which should be returned to the admissions office by the closing date. In addition, email Dr Lesley Morrell with your CV and a covering letter outlining how your experience fits with the project, and why you are interested in this opportunity.

Closing date: Tuesday 31st May 2011. Studentships will start in September 2011

– Dr Lesley Morrell Lecturer in Evolutionary Biology Department of Biological Sciences University of Hull Kingston-upon-Hull HU6 7RX

+44 (0)1482 465874

www.hull.ac.uk/biosci L.Morrell@hull.ac.uk

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## ULouvain DispersalEvolution

PhD position: "Phenotypic plasticity and evolution of life history traits in Tetrahymena thermophila microcosms"

Biodiversity Research Centre Earth and Life Institute Université catholique de Louvain (UCL) Louvain-la-Neuve, Belgium www.uclouvain.be/en-bdiv A PhD position is available at our Biodiversity Research Centre. Focus will be on the evolution of life styles by means of artificial selection performed in lab-controlled microcosms of the unicellular eukaryotic ciliate Tetrahymena thermophila. The PhD-project is organized within the framework of a larger collaborative 5-year research program by a local consortium of three collaborating research groups, including faculty (Profs. Hans Van Dyck, Nicolas Schtickzelle and Caroline Nieberding), postdocs and PhD students. That program is entitled: "Integrating Evolution into Ecological Responses: Changing Life Styles of Organisms in Changing Environments". The overall aim is a better understanding of the role and mechanisms of plasticity for present and future adaptation and survival in changing environments in a series of model organisms (Pararge aegeria & Bicyclus anynana butterflies, Tetranychus urticae mite, and Tetrahymena thermophila ciliate). Different fields will be combined in this program including behaviour, life history, thermal ecology, genetics and genomics. Also the relevance for conservation biology will be explored.

Within this program, this particular PhD project will focus on experimental work with Tetrahymena thermophila microcosms as a model system to study the ecological consequences of changing environment in an experimental ecology and conservation biology framework. We maintain a series of clonal strains, each showing distinctive life styles, i.e. sets of life history traits (e.g. dispersal, kin cooperation, demography). The work will use GxE experiments to quantify the slope and range of variation of plasticity of these strains for various life history traits under different environments (temperature, habitat quality, O2 availability...). Then we will study the functional significance of plasticity in terms of adaptation and adaptability through a set of experimental evolution experiments. The PhD candidate will have the opportunity to develop her/his own PhD research programme within the global project, in close relation with postdocs and other PhD students, and under full supervision of Nicolas Schtickzelle (+ possible co-supervision of Hans Van Dyck or Caroline Nieberding according to the subject). She/he will also benefit from collaborations with the team of Drs Jean Clobert and Alexis Chaine (CNRS Moulis, France), working on Tetrahymena microcosms in a close collaboration.

We are looking for a strongly motivated PhD candidate with a background in the broad field of Evolutionary Biology and Ecology. We offer now one year of funding to start the PhD project, but the successful applicant is expected to apply, with our full support, for a PhD grant to extend funding for her/his position to 4 years, the average time to complete a PhD dissertation in Belgium. Previous history showed that our students had a very high success rate in obtaining this extended grant; however no formal 100% warranty can be given. Please do not apply to this position if this does not fit your expectations.

Salary ranges between 1500-1700 euros netto per month plus benefits (health insurance,.) which are included in the Belgian system. 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 www.uclouvain.be . Application should be sent to Nicolas Schtickzelle (nicolas.schtickzelle@uclouvain.be) and should 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. Informal enquires are welcome. Applications will be reviewed directly until the position is filled. Start date will be as soon as possible.

nicolas.schtickzelle@uclouvain.be

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## UOttawa FungalEvolution

One graduate student position in Fungal Evolutionary Genomics - University of Ottawa (CANADA)

One graduate research project is currently available in the field of fungal comparative genomics for a highly motivated graduate student. The research will be carried out in a newly established, CIFAR (Canadian Institute for Advanced Research) affiliated laboratory led by Dr. Nicolas Corradi in the Department of Biology of the University of Ottawa, Canada. The project will focus on the genomics of an ecologically relevant and evolutionary intriguing group of fungi: the Arbuscular Mycorrhizal Fungi (AMF). The graduate thesis will involve the study of several AMF transcriptomes, in order to shed light on the ecological success of this fungal lineage. Applicants for the PhD position on AMF genomics should have some experience in general molecular biology (PCR, cloning, DNA sequencing), and bioinformatics. Previous experience with either "in vitro" culturing of AMF, population genetics, bioinformatics, programming (BioPerl), Real-Time PCR, or with the analysis of high-throughput DNA sequencing technologies will represent strong assets for the selection of the candidate. Enquiries about specific projects currently performed in the lab can be sent to Dr. Nicolas Corradi (ncorradi@uottawa.ca). Complete application packages, including a CV and the names and e-mail addresses of 2 referees should be sent to ncorradi@uottawa.ca. Evaluation of applications will start now and continue until a suitable candidate is found. Lab Website: http://mysite.science.uottawa.ca/ncorradi/index.html Nicolas Corradi Professeur adjoint / Assistant Professor Chercheur de l'Institut canadien en recherches avancées / Scholar of the Canadian Institute for Advanced Research Université d'Ottawa / University of Ottawa Département de biologie / Department of Biology Pavillon Gendron / Gendron Hall Bureau 257 / Room 257 30 Marie Curie Priv. Ottawa ON Canada K1N 6N5 Tel. +1 (613) 5625800 # 6563 Website: http://mysite.science.uottawa.ca/ncorradi/index.html Nicolas Corradi <ncorradi@uottawa.ca>

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## UPorto Speciation

GradStudentPosition:

UniversityPorto.EcologicalSpeciation

We are seeking a highly motivated student interested in conducting a PhD within a research project entitled The paths of parallel evolution and their genetic crossroads. This project focuses on the study of ecological speciation in the flat periwinkle, Littorina fabalis, a common intertidal gastropod distributed along the NE Atlantic coast for which several ecotypes in different parts of the intertidal zone have been described.

This multidisciplinary project, led by Rui Faria, will be conducted at CIBIO, the Research Center in Biodiversity and Genetic Resources (http://cibio.up.pt/) - University of Porto, Portugal; and at IBE, Institute of Evolutionary Biology (http://www.ibe.upf-csic.es/) - Universitat Pompeu Fabra, Barcelona, Spain. It seeks to clarify the nature of the genetic variation responsible for repeated evolution of locally adapted ecotypes and ecological speciation in the intertidal realm; and integrates ecology, morphology, genomics, transcriptomics and modeling. The project is a part of an international collaboration between labs with long experience in Littorina evolution involving scientists from Portugal, Spain, England and Sweden.

The student would be primarily responsible for experimental design and for producing and analyzing genetic data obtained by high throughput sequencing (RAD sequencing and Rna-seq). The student is also expected to take part in fieldwork (sampling and ecological characterization of local habitats) and morphological analysis.

Essential qualifications are: motivation and ability to carry out research in an independent manner and a strong interest in the genetics of speciation. Some training and/or strong interest in bioinformatic analyzing tools are also highly meriting. Candidates should send an e-mail addressed to Rui Faria (rui.faria@upf.edu), attaching a motivation letter and the CV by April the 30th of 2011.

The selected candidate will have to apply for a PhD fellowship to the Portuguese Science Foundation (FCT) by June 2011. More information concerning FCT fellowship conditions can be found here: http://alfa.fct.mctes.pt/apoios/bolsas/regulamento2010 . For additional information send an e-mail to Rui Faria (rui.faria@upf.edu).

Rui Faria

Rui Faria <rui.faria@upf.edu>

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## UQueensland ReefFish

Maybe the Best Biology PhD in the world The function of reef fish colour patterns: how did the coral trout get its spots?

Ok, you didn¹t get the OBest Job In The World¹ (www.islandreefjob.com), which involved snorkeling on the Great Barrier Reef, living for weeks on remote tropical islands, and spending hours watching brightly coloured reef fish.

So, why not come to The University of Queensland and do all that, and get a PhD?

We are looking for 1-2 outstanding PhD candidates to work on a project investigating the evolution and function of reef fish colour patterns.

Students will be based at The University of Queensland, Brisbane, Australia, in the Queensland Brain Institute and work in collaboration with researchers in the School of Biological Sciences, UQ and at the University of Bristol, UK. Supervisors will be Prof. Justin Marshall, Dr. Karen Cheney, Dr. Shelby Temple and/or Prof. Tom Cribb.

Applicants should have interests and preferably experience in neuroethology, neurobiology, sensory biology, fish behaviour, evolution of visual signals, phylogenetics and/or animal communication mechanisms. The PhD will include behavioural experiments, field observations, field spectrophotometry, retinal anatomy and/or microspectrophotometry.

The ideal candidate would be a qualified SCUBA diver, have experience in the field, and be prepared to spend time at field stations, such as Lizard Island (http://australianmuseum.net.au/-Lizard-Island-Research-Station ) and Heron Island (http://www.science.uq.edu.au/facilities/heron-island ).

Prospective students will be expected to secure either an: Australian Postgraduate Award (APA; for Australian citizens) OR an International Postgraduate Research Scholarship (IPRS; International students). N.B. to be competitive for an IPRS at least one publication, preferably as first author, may be required. For information on these awards go to: http://www.uq.edu.au/grad-school/ This PhD will provide excellent scope for integrative research, for unique skill acquisition, as well as for personal development. For further information please contact Karen Cheney (k.cheney@uq.edu.au) or Shelby Temple (Shelby.Temple@bristol.ac.uk)

To apply, please send a C.V. and covering letter outlining past research experience to Karen Cheney: k.cheney@uq.edu.au. Deadline is 15th April, 2011.

k.cheney@uq.edu.au

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## URegensburg PlantSystematics

Open Ph.D. position in plant systematics and evolution at the Institute of Botany of the University of Regensburg (Germany)

Position description: A 3-years Ph.D. position is presently available in the area of plant systematics and evolution at the Institute of Botany of the University of Regensburg, under the supervision of Prof. Dr. Christoph Oberprieler (http://www.biologie.uni-regensburg.de/Botanik/Oberprieler/index.html) and in co-operation with Dr. Robert Vogt (Botanic Garden & Botanical Museum Berlin-Dahlem). The salary will be according the TV-L E13/2. The Ph.D. project will focus on the evolution of polyploidy in the genus Leucanthemum (Compositae, Anthemideae) and will use this genus of around 40 species distributed in southern and central Europe as a model to investigate the genetic, genomic, biogeographical and ecological consequences of polyploidy. Work packages envisaged will comprise (a) expression studies of genes in diploid and polyploid members, (b) the phylogeography of species and species groups of this genus, and (c) the taxonomical treatment of the genus in S France and Italy based on morphological, cytological, and molecular evidence. The project will complement a presently ongoing Ph.D. project dealing with the phylogeny of the genus throughout its whole geographical range. The project will include travelling throughout S Europe to collect plant material in natural populations.

Deadline for application: May 15, 2011. If needed, the position will remain open until a suitable candidate is found.

Starting date: July 1, 2011

Requirements: Applicants are expected to have their Masters/Diploma degree by the start of the Ph.D. project. Good knowledge of English and German are highly desirable. The ideal candidate will have documented experience in one or more of the following areas: molecular biology, expression techniques, phylogeny reconstruction, population genetics, and botanical field work (including the possession of a driver s licence). The selected candidate will be a member of the Regensburg International Graduate School of Biological Sciences (RIGeL; http://www.biologie.uni-regensburg.de/RIGeL/index.html).

How to apply: Please send you application including (a) an application letter addressing your motives for application and your career goals, (b) a detailed CV including a detailed list of molecular, analytical, linguistic, and field work skills, presentations at scientific meetings, and publications (if applicable), and (c) addresses of two academic advisors who could comment on your skills, your dedication to science, and your ability to work cooperatively in a team. Please, send applications by email to:

Prof. Dr. Christoph Oberprieler Institut für Botanik Universität Regensburg Universitätsstr. 31 D-93053 Regensburg Germany phone +49-(0)941-9433129 fax +49-(0)941-9433106 christoph.oberprieler@biologie.uni-regensburg.de

Christoph Oberprieler <Christoph.Oberprieler@biologie.uni-regensburg.de>

## USherbrooke AvianEvolution

I am a seeking a motivated PhD student to join my research group in the Department of Biology at the University of Sherbrooke (http://pages.usherbrooke.ca/dgarant/). The Department has an outstanding group of researchers in ecology and evolution and provides a dynamic and stimulating environment for graduate students.

The proposed project will investigate phenotypic and genetic correlations between reproductive traits and fitness in a long term studied population of tree swallows (Tachycineta bicolor) in southern Québec, Canada. The project will benefits from a genetic pedigree gathered over 8 years, which includes data collected over 10 000 individuals, to unravel the possible genetic constraints on population' evolutionary potential, and to assess links among traits and fitness in contrasted environments.

The fieldwork in southern Quebec will take place 2-3 months each summer. Ideally, the candidate will have previous research and fieldwork experiences and skills in handling birds would also be an advantage. A good background in evolutionary ecology and/or quantitative genetics is also desirable.

The position is open and funded for three years, starting as soon as September 2011. Please apply by sending your CV, including the email addresses of two referees, and a letter of motivation by 5 August 2011 to Dany.Garant@Usherbrooke.ca

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Je recherche un étudiant au PhD pour se joindre à mon groupe de recherche au département de biologie de l'Université de Sherbrooke ( < http://pages.usherbrooke.ca/dgarant/ > http://pages.usherbrooke.ca/dgarant/). Le département possède un groupe de recherche de haut niveau en écologie et évolution et procure un environnement stimulant pour les études gradués.

Le projet proposé portera sur l'analyse des corrélations phénotypiques et génotypiques entre traits reproducteurs et fitness dans un système d'étude à long terme de l'Hirondelle bicolore (Tachycineta bicolor) dans le Sud du Québec, Canada. Le projet bénéficiera d'un pedigree génétique couvrant une période de 8 ans et de données récoltées sur plus de 10 000 individus, pour établir le potentiel évolutif de la population, les contraintes génétiques possibles et les liens entre traits et fitness sous des conditions environnementales variables.

Les travaux de terrain se dérouleront pendant 2-3 mois à chaque été. Idéalement, le candidat aura de l'expérience avec les travaux de terrain, avec la manipulation d'oiseaux et de bonnes connaissances en écologie évolutive et/ou génétique quantitative.

Le poste est financé pour 3 ans à compter de septembre 2011 au plus tôt. Veuillez envoyer un CV, une lettre de motivation et les coordonnées de deux références avant le 5 août 2011 à Dany.Garant@Usherbrooke.ca

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Dany Garant Associate Professor Department of Biology University of Sherbrooke Sherbrooke QC J1K 2R1 Canada

Tel: (819) 821-8000 ext.63198 Fax: (819) 821-8049 Courriel: Dany.Garant@USherbrooke.ca

http://pages.usherbrooke.ca/dgarant/

## UTasmania 2 ConservationGenetics

Scholarships (x2) for PhD conservation genetics studies of Tasmanian fauna at the School of Zoology, University of Tasmania

Project1: Conservation genetics of Tasmanian mammals This project will focus on species of marsupials, such as the Tasmanian bettong and eastern quoll, which are now restricted to Tasmania, having gone extinct on mainland Australia, and which may be threatened by the recent invasion of the red fox. The project will assess current genetic structure and gene flow in these species across Tasmania. These data will be linked to dynamic species distribution models to identify high-priority populations that should be targeted for long-term protection against potential fox impact. The project would also use genetic methods to reconstruct the demographic history of the Tasmanian populations of these species, and this could include comparisons with lost genetic diversity from mainland populations based on DNA extracted from museum specimens. This project has the potential to make a major contribution to the conservation of Australia's biodiversity. Supervisors: Prof Chris Johnson and Dr Chris Burridge (University of Tasmania).

Project2: Population genetics of related montane butterfly species This project will focus on two closely related Tasmanian butterfly species that occupy high elevations: Oreixenica ptunarra (threatened species) and O. lathoniella. These species differ in abundance, range, and flight capabilities. Populations of O. ptunarra are often sympatric with the more abundant and widespread O. lathionella, and hence this study will contrast spatial genetic variation in the two species using phylogeographic and population genetic (microsatellite) analyses. The study will test hypotheses that relate differences in patterns of spatial genetic variation between the two species to differences in flight capabilities and habitat requirements. The threatened species (O. ptunarra) is of particular concern with respect to vegetation management (fire and grazing regimes), and this study will also investigate the species' ability to move between regions of suitable habitat as their location changes through time. Supervisors: Dr Chris Burridge, Dr Peter McQuillan (University of Tasmania) and Dr Phil Bell and Dr Clare Hawkins (DPIPWE, Tasmania). Both projects are based at the University of Tasmania (http://www.utas.edu.au ), one of Australia's oldest universities, with great opportunities for intellectual development and also outdoor recreation. The Central Science Laboratory contains a large, well-equipped molecular genetics facility.

Applicants minimally require a BSc with a substantial research component to part of their study (the latter may have been achieved by different means depending on the country of study; within Australia this typically represents a BSc Honours degree; externally, a MSc degree would be the most common means of entry). Demonstrated expertise with molecular laboratory procedures is desirable (DNA extraction, PCR, DNA sequencing, microsatellite genotyping) but not essential, as are interests and experience in conservation biology and GIS.

Scholarship comprises $AUS 22,500 per year (3 years, with a possible 6 month extension). Student fees will be required if the you are not an Australian or New Zealand citizen, or an Australian permanent resident ($AUS 19,376 per year, to be paid upfront each year), unless you are able to attract your own scholarship, in which case the fees will be waived. Please note that the scholarship cannot be used to pay the fees (the scholarship is provided in weekly instalments, not upfront), and applicants seeking to meet living costs or fee payments through additional employment simultaneously with their studies are unlikely to be successful. Students from a non-English speaking background will require proof of English-language ability (e.g. an IELTS of 6.5).

To apply: Please send a cover letter expressing your interest (in the form of an e-mail), contact details of at least two referees, and an curriculum vitae including details of undergraduate and any (post)graduate performance to Dr. Chris Burridge (chris.burridge@utas.edu.au ). Applications remain open until the positions are filled.

Please note, I am away from my office until April 26th, and may not be able to respond until after this date.

Chris Burridge School of Zoology University of Tasmania Private Bag 5 Hobart, Tasmania 7001 Australia

e-mail: chris.burridge@utas.edu.au phone: +61 3 6226 7653 fax: +61 3 6226 2745 web: http://fcms.its.utas.edu.au/scieng/zoo/pagedetails.asp?lpersonId=3D5232

Chris.Burridge@utas.edu.au

## UWindsor 3 EnvironmentalGenomics

University of Windsor; Environmental Genomics

Three Ph.D. positions beginning September 2011 or January 2012 are available at the Great Lakes Institute for Environmental Research (GLIER), University of Windsor. Research in our laboratories combines evolutionary biology with molecular genetics and genomics to address broad environmental and evolutionary questions. We study multiple stressors in aquatic environments with special emphasis on the metal-induced mutation process from genomes to populations. We also use lab experiments, field studies and computational analyses of large scale sequence data to test speciation patterns, the genetics of habitat transitions and local adaptation in aquatic crustaceans. Students train in our program will gain broad interdisciplinary perspective on the synergistic effect of micro-pollutants in aquatic environment.

We are looking for highly motivated graduate students. Candidates should have a strong background in biology or bio-geo-chemistry. Successful applicants must have obtained a research-based M.S. degree in a discipline of relevance to the project, and demonstrate interest and/or experience in team-based and interdisciplinary projects. International students with strong credentials and publication record are also considered.

Interested student should send their CV, a brief statement of research interest, and a list of 3 references to Dr. Melania Cristescu at Email: mcris@uwindsor.ca.

Melania Cristescu <mcris@uwindsor.ca>

## UZurich 2 SystematicBotany

Two PhD. positions in Systematic Botany / Phylogenetics at the University of Zurich

Project description: The selected Ph.D. students will work with Dr. Colin Hughes http://www.systbot.uzh.ch/Personen/-ProfessorenundDozenten/ColinHughes.html on a research project entitled âThe Biogeography and Evolutionary Dynamics of Legume Diversificationâ, funded by a grant from the Swiss National Science Foundation (SNF) in the Institute of Systematic Botany at the University of Zürich. http://www.systbot.uzh.ch/-index=5Fen.html The uneven distribution of species richness across evolutionary lineages is one of the most pervasive and fundamental features of biodiversity across all organismal groups. The reasons why some lineages diversify and others do not, why some clades are species-rich and others are not, and the underlying factors determining these differences, are crucial to understanding how diversity evolves. One approach to address these questions involves estimating rates of species diversification, assessing among-lineage variation in diversification rates, localising rate shifts to particular branches on phylogenetic trees, and examining potential ecological, geographical and adaptive life history correlates of diversification. The Biogeography and Evolutionary Dynamics of Legume Diversification Project aims to address these questions using one of the largest and most evolutionarily successful families of flowering plants, the legumes. New empirical data for two contrasting legume lineages, the genus Lupinus and the subfamily Mimosoideae, will be used to gain insights into diversification patterns across broad geographical and ecological spans, and time frames. Key gaps in documentation of taxonomic diversity in each group will be plugged to determine the species richness of clades. Both study groups include multiple continental-scale radiations offering novel opportunities to compare the diversification trajectories of multiple lineages simultaneously across time and space. Research will involve field, herbarium collections based, and laboratory work to assemble relevant data, as well as large-scale phylogenetic and diversification analyses.

Position characteristics: The Institute of Systematic Botany in Zurich offers excellent research facilities and a stimulating working environment for graduate students in systematic botany. The project will also involve collaboration with leading researchers in legume systematics elsewhere. Salary is according to the Swiss National Science Foundation (SNF) guidelines. Funding, including for laboratory and field costs, is available for 3 years.

Requirements: Applicants should hold a Masters degree, ideally in taxonomy and biodiversity or related biological disciplines. Experience in molecular techniques, phylogenetic analysis, and fieldwork are highly desirable. Excellent knowledge of English, written and oral, is essential.

How to apply: Send the following documents by email AS A SINGLE PDF FILE to Dr. Colin Hughes, colin.hughes@systbot.uzh.ch: i) a two-page application letter describing your research interests, clearly stating why are you interested in a Ph.D. position in systematic botany, and your career goals; ii) your CV, including a list of publications (if applicable); iii) a copy of your undergraduate and graduate academic record; iv) names and contact details of at least two referees selected from your academic advisors (and who have agreed to be contacted).

Deadline for application: Applications will be screened from June 10th, 2011 onwards until the positions are filled.

Starting date: September/October 2011.

colin.hughes@systbot.uzh.ch

# Jobs

## Charleston LabManager MolEvol

Position Opening for Lab Manager in Molecular Evolution and Comparative Genomics

Gavin Naylor's research group based at the College of Charleston and the Hollings Marine Lab has an opening for a full time Laboratory Technician/Manager.

Required: Experience with molecular genetic methods including DNA isolation, PCR, automated sequencing, and database management, M.S. in biology/biochemistry/forensic science or equivalent.

Desired: Familiarity with Next generation sequencing. Computer programming/scripting in Perl/Python.

The position centers around research on comparative genomics and molecular evolution of chondrichthyan fishes (Sharks Skates, Rays and Chimaeras). Responsibilities include maintenance of laboratory equipment, curation of frozen tissue collection, sample preparation of genomic libraries for Illumina sequencing, purchasing of supplies and training students. The successful candidate will work closely with postdocs and graduate students in the lab, have strong organizational skills and show careful attention to detail while having an appreciation of the overarching goals of the different projects in the lab. Position available June 1, 2011 or soon thereafter. Interested parties should send a cover letter and CV with contact information for 2 references to Gavin Naylor at the following e-mail address: naylorg@cofc.edu

gnaylor@fsu.edu

## DukeU DirectorFossilPrimates

The Duke Lemur Center is seeking to fill the position of Director, Division of Fossil Primates. The position is that of Research Scientist and is not tenure track. Salary range is within $65 - $75K, depending upon skills and experience. The full job description can be found at the link below.

> http://lemur.duke.edu/about-the-duke-lemur-center/employment/ Interested applicants should submit a full CV and a list of three references to DLC-Job@duke.edu. Please include the words “Fossil Director” in the Subject Line. Review of applications will begin on May 16, 2011, with the hope that the successful candidate will begin on or shortly after September 1, 2011.

Anne Yoder <anne.yoder@duke.edu>

## EasternKentuckyU EvolutionaryBotany

Visiting Assistant Professor Botanist

The Department of Biological Sciences at Eastern Kentucky University, in Richmond, Kentucky, is accepting applications for a Visiting Assistant Professor, 9-month appointment, to begin August 15, 2011. There is a strong possibility that a tenure track position in botany will be advertised in 2012. Teaching assignment each semester (Fall and Spring) will include General Botany (lecture and lab) and introductory biology (lecture and/or lab). The teaching load is 12 hours per semester. Service on committees and mentoring of undergraduate researchers are also duties. Preference will be given to candidates who have a broad background in the botanical sciences, and who can provide evidence of excellent teaching and communication skills. Requirements include a Ph.D. (or ABD) from a regionally accredited or internationally recognized institution. Review of applications will begin on April 15, 2011, and will continue until the position is filled. Offers of employment are contingent upon satisfactory background check. Eastern Kentucky University is an EEO/AA institution that values diversity in its faculty, staff, and student body. In keeping with this commitment, the University welcomes applications from diverse candidates and candidates who support diversity. For more information contact: Dr. Pat Calie, Pat.Calie@eku.edu. Candidates must apply online at: http://jobs.eku.edu, search requisition 0609275. Quick link to apply is: http://jobs.eku.edu/applicants/Central?quickFind=3D66339 Jennifer Koslow, PhD Assistant Professor of Plant Ecology Department of Biological Sciences Eastern Kentucky University 521 Lancaster Avenue Richmond, KY 40475 office: Beckham 227 phone: 859-622-6258

Jennifer.Koslow@EKU.EDU

## GeorgiaTech ResScientist MicrobialGenomics

Research Scientist in Marine Microbial Genomics

A Research Scientist I position is available in Frank Stewart’s lab in the School of Biology at Georgia Tech. Our lab explores the ecology, physiology, and evolution of marine microorganisms using the tools of genomics. Primary topics include metagenomic and metatranscriptomic analysis of microbial metabolism and taxonomy, and molecular analysis of bacteria-eukaryote symbioses. The Research Scientist will work collaboratively with Dr. Stewart and other lab members to manage the lab, perform field and bench-top research, and synthesize results for publication.

Responsibilities include:

* Conducting experiments to support multiple research projects. Specific duties will likely include: field-based sample collection, DNA/RNA extraction and purification, PCR and RT-PCR, genetic manipulation of bacterial genomes, in situ hybridization, fluorescence microscopy, pulsed field gel electrophoresis, and preparation of DNA libraries for high throughput sequencing analysis. * Troubleshooting/optimizing protocols and developing new methods. * Managing data and running scripts via a command-line interface. * Assisting in drafting research papers and grant proposals. * Performing or overseeing routine lab management tasks, including cleaning/autoclaving, preparing media, ordering supplies and interacting with vendors, maintaining instrumentation, implementing laboratory safety standards. * Supervising and training lower-level technical and research personnel, including graduate and undergraduate students.

Qualifications:

Master-’s Degree, or higher, is preferred. Minimum qualifications include a Bachelor’s Degree in Biology, Molecular Biology, Biochemistry or a related discipline AND four years of relevant research experience; OR, Any equivalent combination of experience, training and/or education.

Additional Qualifications:

* Proven expertise in molecular biology and microbio-

logical techniques. * Superior oral and written communication skills and excellent organizational skills. * Ability to work both independently and collaboratively. * Experience in bioinformatics or programming is highly preferred. * Experience with high throughput DNA sequencing is highly preferred.

The successful applicant will be enthusiastic, motivated by experimental and analytical challenges, and skilled in a diverse range of laboratory techniques. The position is available for two years with the possibility of extension. Salary will be commensurate with experience and will include fringe benefits. Additional information about the lab can be found at www.fjstewart.org. Application materials should be emailed to Frank Stewart (frank.stewart@biology.gatech.edu) and should include a cover letter (describing your interest in the position, work experience, and availability), CV, and contact information (name, email, phone number) for at least three references. Please include the words "Research Scientist" in the subject line. Thank you for your interest -" we look forward to hearing from you.

Georgia Tech is a unit of the University System of Georgia and an Affirmative Action/Equal Opportunity Employer and requires compliance with the Immigration Control Reform Act of 1986.

– Frank J. Stewart, Ph.D. Assistant Professor School of Biology Georgia Institute of Technology ES&T building, office #1242 311 Ferst Drive Atlanta, GA 30332-0230 office: 404-894-5819 www.fjstewart.org frank.stewart@biology.gatech.edu

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## LandcareResearch NZ ResTech Biodiversity

This appointment is within the Ecological Genetics group and includes the Sustaining and Restoring Biodiversity Research programme, Reduced extinction risk by sustaining genetic diversity (http://www.landcareresearch.co.nz/research/-obi.asp?Proj_Collab_ID=24). The successful candidate will assist of projects ranging from the reproduction and population viability of rare plants to understanding the evolutionary dynamics of newly introduced species.

Advert:

Research Technician - Molecular Biology

Exciting opportunity to work in this cutting edge area of science and make a difference to New Zealand's biodiversity!

Landcare Research is New Zealand's leading provider of solutions and advice for sustainable development and the management of land-based natural resources. We passionately believe that excellent science and its effective application can contribute significantly to the economic transformation necessary to provide a higher quality of life for New Zealanders, while also ensuring our land environments are protected and respected.

We are seeking an experienced laboratory technician to support our research in plant conservation biology and weed biology for the Biodiversity and Conservation Team. The successful applicant will have experience in routine molecular laboratory techniques, such as DNA extraction, PCR, molecular cloning, RFLP, sequencing and flow cytometry.

Other key duties include: * Undertaking appropriate data handling and reporting, maintaining clearly documented records. * Maintaining a clean tidy and safe laboratory, including dealing with hazardous waste (ethidium bromide, new organisms). * Assisting with the inventory, requisitioning and maintenance of laboratory supplies and consumables, including hazard substances. * Willingness to work in the field under a range of weather conditions

The successful applicant will hold a postgraduate qualification in molecular biology or genetics, and must be able to work accurately and to deadlines. Experience in PCR (including quantitative), microsatellite DNA analysis, DNA sequencing and cloning is highly desirable.

We are specifically looking for someone who has an interest in conservation and being involved in research that makes a difference to New Zealand's biodiversity.

The position is full-time, permanent, and is based at our Lincoln site near Christchurch, New Zealand.

To find out more about this role or Landcare Research and to apply, please visit our website www.landcareresearch.co.nz/jobs Applications close 17th April 2011.

Judy Lamberts Human Resources

Judy Lamberts <LambertsJ@landcareresearch.co.nz>

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## NewMexicoStateU LabDirector

Job: Laboratory Coordinator, Genome Sequencing

Laboratory

New Mexico State University, Department of Biology

Qualifications: BS in Biology, Molecular Biology or related field, plus one year of experience; MS in Biology preferred. Strong background in molecular biology techniques including Roche 454 shotgun, amplicon, and transcriptome pyrosequencing, qPCR, construction of normalized cDNA libraries, Sanger sequencing and capillary electrophoresis are preferred. Ability to communicate clearly, both verbally and in writing, with researchers, clientele, and students regarding molecular biology protocols and experimental design relating to ecology and evolution; previous scholarly products (e.g., papers, presentations) and teaching or academic supervisory experience is preferred.

Examples of Duties: Preparation, management, and expansion of NMSU's core Genome Sequencing Laboratory. Daily operation and routine maintenance of a Roche 454 GS FLX emPCR pyrosequencer (training is not available). Successful operation of the instrument requires meticulous adherence to protocols. Additional laboratory duties include the preparation of a wide variety of samples for genomic sequencing, and training/supervising graduate student laboratory assistants. Other duties include project management, record-keeping, accounting, and purchasing reagents/expendables. Must keep abreast of technical advances in genomics in order to advise research clientele in experimental design and seek new applications of genomics technology. Must work collaboratively with team of faculty researchers, bioinformatics specialists, graduate students, and facilities staff.

Benefits Offered: Group medical and hospital insurance, group life insurance, long-term disability insurance, state educational retirement, worker's compensation, sick leave, annual leave and unemployment compensation. Opportunity fort educational advancement.

Conditions: Offer of employment is contingent on funding.

All offers of employment, oral and written, are contingent on the University's verification of credentials and other information required by Federal Law, State Law, and NMSU policies/procedures, and may include the completion of a criminal history check.

Reply to/Deadline for Applications: Submit a formal letter of interest, current resume, and three professional references with names, titles, addresses, daytime phone numbers, and email addresses preferably as email and attachments to:

phoude@nmsu.edu

or hard copy by snail mail to:

Peter Houde New Mexico State University Box 30001 MSC 3AF Las Cruces NM 88003

Review of applications will begin April 19 2011 and applications received after this date may be considered. Incomplete application packets will not be considered.

phoude@nmsu.edu

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## Nuffield MalariaStatistician

*Statistician - WWARN*

*NUFFIELD DEPARTMENT OF CLINICAL MEDICINE, Centre for Tropical Medicine*

*Grade 7: Salary £29,099 - £35,788 p.a.*

More than 500 million become severely ill with malaria every year and more than 1 million die from the effects of the disease. The Worldwide Antimalarial Resistance Network (WWARN), working with the World Health Organisation (WHO) and funded by the Bill and Melinda Gates Foundation, will set up a global drug resistance information resource so that more of the right drugs can get to the right people at the right time, and the drugs will last longer. Details can be found on the website at http://www.wwarn.org/ . This exciting post will support the Clinical Module of WWARN, ensuring that the clinical database i) meets the requirement of the clinical team and other stakeholders, ii) works with the database architecture (designed in collaboration with the informatics team), and iii) allows cross-referencing between the Clinical, In Vitro, Molecular and Pharmacological Modules of WWARN. The successful candidate will develop a wide variety of research and analytical tools including but not limited to: clinical trial, meta-analysis and time-series analyses.

You will have a postgraduate qualification in data analysis or statistics (or equivalent work experience), and experience working with database developers. Experience of working with data from countries in Africa, Asia or Latin America is highly desirable.

The post is available up to 31 December 2012 in the first instance.

Applicants for this vacancy are to be made online. To apply for this role and for further details, including a job description and person specification, please click on the link below:

https://www.recruit.ox.ac.uk/pls/hrisliverecruit/erq_jobspec_version_4.jobspec?p_id=100187 Only applicants received before 12.00 midday BST on *Tuesday 26 April 2011*will be considered.

Sam Smith <sam.smith@wwarn.org>

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## Purdue Bioinformatics

Bioinformatics Scientist/Core Manager - West Lafayette - The Cyber Center Job Number: 1100580

Description

The Bioinformatics Core at Purdue is a new organization designed to support and catalyze significant biological research efforts across the university. The Bioinformatics Scientist/Core Manager is responsible for providing the leadership to establish the core and manage day-to-day operations. The Core Manager will be part of the leadership team that implements the Bioinformatics Core vision and works to achieve its long term success for faculty researchers. Expectations of the Core Manager include: to interface directly with faculty and other personnel to provide timely, accurate, and beneficial bioinformatics services; to deliver the services personally or through the staff and students associated with the Core; to select, integrate, develop, and apply appropriate bioinformatics tools through a close working relationship with the resources of the Purdue Cyber Center; to work closely with other groups, including the Purdue Genomic, Proteomic, and Biostatistics groups to provide additive services for the university; and to stay current with relevant methodologies.

Qualifications

Required:

* PhD in the biological or computational sciences. * Minimum of five years of biological experience, including expertise in genomics, computational biology, bioinformatics, and genetics. * Experience and desire to focus on providing bioinformatics support to a scientific research community. * Substantive experience in the use and application of bioinformatics software and tools to address biological research needs. * Expertise in large, complex, and multidimensional data sets (with particular emphasis on 454, Illumina Solexa, SOLiD, and/or Affymetrix) and associated bioinformatics techniques. * Other relevant skills may include SNP identification and detection, RNAseq, genome and transcriptome assembly, and gene annotation. * Demonstrated leadership qualities through successful project, personnel, and resource management as well as through providing guidance and support to other staff members. * Demonstrated ability to interact with and guide programmers and computer scientists in implementing solutions to biological problems. * Ability to stay current on new biological and bioinformatics methodologies. * Ability to work independently and as part of a multi- disciplinary team. * Ability to work with and effectively communicate with statisticians, biologists, and programmers. * Ability to interface directly with faculty, understand their research, and provide useful and relevant services. * Highly motivated, team oriented, and able to reach across artificial and perceived boundaries. * Able to coordinate the daily activities of the bioinformatics core to provide valuable services to Purdue faculty. * Proficient with scripting languages, statistical analysis software, and relational databases. * Strong communication and excellent time management and organizational skills. * Strong sense of initiative and resourcefulness. * Ability to lift and carry 10 pounds frequently and 20 pounds occasionally.

Preferred:

* Experience with non-model organisms. * Experience with developing and participating in collaborative grant proposals.

Additional Information:

* FLSA: Exempt (Not Eligible For Overtime) * Retirement Eligibility: Fidelity Contributions Immediately. * Purdue University is an equal opportunity/equal access/affirmative action employer.

J. Andrew DeWoody Professor, Purdue University West Lafayette, IN 47907-1159 765-496-6109 http://web.ics.purdue.edu/~dewoody/index.php

dewoody@purdue.edu dewoody@purdue.edu

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## QueenMaryU Bioinformatics

Two permanent positions at

QUEEN MARY UNIVERSITY OF LONDON School of Biological and Chemical Sciences

1) Lecturer (= Assistant Professor)/ Senior Lecturer/ Reader BIO-INFORMATICS/PHYLOGENETICS

This appointment is part of a strategic investment programme in computational biology involving departments of Mathematics, Computer Science, Engineering, Physics and Medical Sciences.

We encourage applicants that complement and enhance the existing research strengths of the School of Biological and Chemical Sciences. (http://www.sbcs.qmul.ac.uk/research/index.html)

These include: - behavioural and - evolutionary biology

Expertise and interests in the following areas would also be an advantage: - computational phylogenetics and/or - comparative genomics - and a track record in evolutionary biology

Informal enquiries r.a.nichols@qmul.ac.uk Formal details from http://www.sbcs.qmul.ac.uk/ 2) Professor BEHAVIOURAL NEUROSCIENCE with interests complementing our existing strengths including - neuroethology - brain evolution - comparative cognition

Informal enquiries m.r.elphick@qmul.ac.uk Formal details from http://www.sbcs.qmul.ac.uk/ Richard Nichols Professor of Genetics http://webspace.qmul.ac.uk/ranichols/research.htm richard.alan.nichols@googlemail.com

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## StanfordU ResAssist DrosophilaGenetics

An evolutionary genetics laboratory at Stanford University is seeking a highly motivated Life Science Research Assistant (LSRA) interested in participating in research on Drosophila and yeast genetics and evolution. The LSRA will be responsible for maintaining and organizing a Drosophila facility in the lab and for facilitating the daily research activity related to all Drosophila and some yeast experiments. The LSRA will manage the lab Drosophila strains through breeding, DNA extractions, PCR-based genotyping and general maintenance of multiple lines. The maintenance of the stocks will include making basic food for the flies as well as more specialized food for specific experiments, taking care of the cultures by changing stocks on a regular basis, collecting embryos, and managing population cages. Some of the work is likely to involve basic molecular biology such as PCR and running of agarose gels. Some incidental glassware washing and preparation of solutions will be part of the work duties.

In addition, the LSRA will be involved in defined research projects and will be responsible for independently conducting and analyzing experiments. The LSRA is expected to interpret and analyze the results and suggest modifications to procedures as appropriate. Some projects might involve mentoring of undergraduates and graduate students in the techniques of fly work and instructing them on the fly room policies and procedures.

A successful candidate should: 1) have a Bachelor's degree in Biology or related scientific discipline; 2) be comfortable with handling Drosophila and yeast; 3) have basic lab skills; 4) be highly organized, detail-oriented, responsible, and able to work independently; 5) possess good communication skills; 6) want to contribute to fundamental research in genetics and evolution (some background knowledge is a big plus). Experience working with Drosophila and/or yeast is highly desired but not absolutely required.

Please send the queries to Dmitri Petrov at dpetrov@stanford.edu

Dmitri A. Petrov Professor Department of Biology Stanford University 371 Serra Street Stanford, CA 94305-5020

http://petrovlabblog.blogspot.com/ http://petrov.stanford.edu (650) 736 1169 (office) (650) 736 2249 (lab)

dpetrov@stanford.edu

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## Stockholm Bioinformatics

Open positions in Bioinformatics at Science for Life Laboratory Stockholm

Science for Life Laboratory (SciLifeLab) is a resource center dedicated to large scale research in molecular biosciences and medicine. The major funding for SciLifeLab comes from strategic grants from the Swedish government. The organisation is divided in two parts, SciLifeLab Stockholm and SciLifeLab Uppsala. SciLifeLab Stockholm is a joint collaboration between three universities, The Royal Institute of Technology (KTH), Karolinska Institute (KI) and Stockholm University (SU). SciLifeLab Uppsala is organised by Uppsala University (UU).

We are looking for new members to the Bioinformatics teams at SciLifeLab Stockholm. Their duties will include establishment of an informatics infrastructure for analysis of high-throughput data (for example from next-generation sequencing (NGS) instruments), development of data analysis pipelines, as well as working in project groups on data analysis in various bioscience contexts. Good collaborative and communicative skills (including ïEnglish) are required for all positions.

Deadline for applications is April 30.

For more information see: http://www.scilifelab.se/-en/scilifelab-stockholm/positions-at-scilifelab Yours Björn

Bjorn Nystedt, PhD Bioinformatics scientist SciLifeLab, Stockholm www.scilifelab.se Visting address: Karolinska Institutet Science Park Tomtebodavägen 23 A 171 65 Solna

Postal address: Box 1031 171 21 Solna

E-mail: bjorn.nystedt@scilifelab.se Phone: +46 (0)8 5248 1477 Mobile phone: +46 (0)73 625 1477

bjorn.nystedt@scilifelab.se

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## StonyBrookU EnvironmentalMedicine

A position in Environmental Medicine at Stony Brook University described formally below is a cross-university search coordinated by the Consortium for Inter-Disciplinary Environmental Research (CIDER). It is appropriate for individuals in the fields of evolution and ecology who fit in the categories: genetic toxicology and toxicogenomics; ecology and evolution of infectious diseases; and environmental or molecular epidemiology. An example of a good fit would be a theoretical population geneticist whose research involves human populations and epidemiology. Empirical evolutionists would also fit, so long as there is a dimension in medicine. Such successful candidates whose research provides an interface with medicine would nevertheless be located in Stony Brook Universitys Department of Ecology and Evolution. This department already houses two individuals who have been selected in previous cross-disciplinary searches by CIDER.

Tenure-track Position in Environmental Medicine

Consortium for Inter-Disciplinary Environmental Research

Stony Brook University invites applications for a new tenure-track position in the broad area of Environmental Medicine. We define environmental medicine broadly toinclude training in toxicology, environmental health, epidemiology, medicine, or environmental sciences as they relate to human health. This position is open at the Assistant or Associate Professor level and is part of a continuing recruitment effort associated with the Consortium for Inter-Disciplinary Environmental Research (CIDER). CIDER brings together Stony Brook faculty from the natural sciences, medical sciences, engineering, social sciences and humanities. Individuals that would complement existing strengths in any of the following areas are encouraged to apply: (a) environmental or molecular epidemiology; (b) genetic toxicology/toxicogenomics; (c) radiation biology; (d) ecology and population biology of infectious disease, and (e) health impacts of air or water pollution or microbial toxins. The successful candidate will hold a tenure-track appointment in an academic department that best suits his/her expertise; affiliation with nearby Brookhaven National Laboratory and collaboration with Cold Spring Harbor Laboratory is also possible. Faculty are expected to teach at the undergraduate and/orgraduate level, generate external funding to support their research and participate in interdisciplinary activities to support CIDER's mission. For more information, visit the Consortium for Inter-Disciplinary Environmental Research Web site at www.stonybrook.edu/CIDER . Required Qualifications: Ph.D. or M.D. in appropriate discipline, with active research program in environmental medicine. Preferred Qualifications: A record of achievement to include published papers; research awards;external funding. Proposed future lines of research consistent withmission of the Consortium for Inter-Disciplinary Environmental Research.

The review of applications will begin May 30, 2011 and will continue until the position is filled. Application Procedure: Those interested in this position should upload a CV, statement of research goals, the proposed Stony Brook University departmental affiliation(s), names and email addresses of at least three individuals whom we could contact as references, and a State employment application, in one PDF document to http://www.stonybrook.edu/jobs, category A, REF# F-6776-11-04 (electronic submission is strongly preferred).

Alternatively those interested in this position should submit a CV, statement of research goals, the proposed Stony Brook University departmental affiliation(s), names and email addresses of at least three individuals whom we could contact as references, and a State employment application to: Karen Warren CIDER Environmental Medicine Faculty (6776) Search 165 Dana Hall Stony Brook University Stony Brook, NY 11794-5000 Equal Opportunity/Affirmative Action Employer. Women, people of color individuals with disabilities, and veterans are encouraged to apply.

– Jeffrey Levinton Distinguished Professor Department of Ecology and Evolution Stony Brook University Stony Brook NY 11794-5245

tel (631) 632 8602 fax (631) 632 7626 Marine Biology Web Page http://life.bio.sunysb.edu/-marinebio/mbweb.html Research Web Site http://-life.bio.sunysb.edu/marinebio/levinton.main.html Jeffrey Levinton <jeffreylevinton@gmail.com>

## TexasAM ChairLifeSciences

Dear Evol Dir Members,

Please distribute the ad below widely. Evolutionary biologists , especially those working on marine biology related questions, are welcome!

Deb Overath

Chair, Department of Life Sciences

The College of Science and Technology invites applications for Chair of the Department of Life Sciences. As leader of the life sciences faculty, the chair will provide leadership, advocacy, oversight, and management for one of the most diverse and productive academic units at Texas A&M University-Corpus Christi. Since the university is rapidly expanding and is becoming more research intensive, we seek strong leadership in a Chair to help our department achieve national and international recognition for teaching and research. Specifically, the chair will play a vital role in insuring the success of a new Ph.D. program in Marine Biology, as well as the continued success of existing BS and MS programs within the department. Administrative duties include course scheduling, staffing, budgets, program assessments, and faculty evaluations. The candidate will be expected to maintain an externally funded research program and mentor graduate and undergraduate researchers.

The successful applicant will hold a PhD in one of the Life Sciences program areas (biological sciences or related fields), have an established record of peer-reviewed publications, federal funding as principal investigator, teaching, and administrative experience; the applicant will be hired at the rank of tenured full professor and should have sufficient experience to warrant this appointment. Research specialization is open, but should align with one of the Department's program areas.

The Department of Life Sciences (http://-lsci.tamucc.edu/) consists of 29 faculty, 4 staff, and over 1000 students. The Department offers six degrees in four program areas: Biology (BS, MS), Biomedical Sciences (BS), Fisheries and Mariculture (MS), and Marine Biology (MS, PhD).

Texas A&M University-Corpus Christi, a Hispanic serving institution, is located on the Gulf of Mexico with a modern campus overlooking Corpus Christi Bay. With more than 10,000 students, the university offers a wide array of academic programs with 18% of the students enrolled in graduate programs.

Applicants for this position should apply on line at https://islanderjobs.tamucc.edu. Applicants should upload their letter of interest, CV, and a position statement describing their leadership style, philosophy of teaching, research, and particularly, administration. Please provide the names and contact information for three references. References will be contacted and asked to provide letters for finalists for the position. Letters will be submitted to the Search Committee Chair Dr. Wes Tunnell, who can also be contacted for inquiries about the position at wes.tunnell@tamucc.edu or at (361) 825-2055. We seek to fill the position quickly so review of applications will begin on 6 June 2011 and continue until the position is filled. The desired start date for this position is 1 September 2011, but a start date of 3 January 2012 is also possible.

Texas A&M University-Corpus Christi is an Equal Opportunity/Affirmative Action Employer committed to diversity.

R. Deborah Overath, Ph.D. Assistant Professor of Biology Local Program Director Hispanic Leaders in Agriculture and the Environment Department of Life Sciences (ST 312) 6300 Ocean Drive, Unit 5800 Texas A&M - Corpus Christi Corpus Christi, TX 78412

Phone: (361) 825-2467 Cell: (361) 876-4542 Fax: (361) 825-2742

"Overath, Deborah" <Deborah.Overath@tamucc.edu>

## Tromso FishPopGenetics

Vacancy for a PhD Position in population genetics/ecology

The Institute of Marine Research (IMR) has a three-year PhD studentship (code 1017) to work on the project SNPFISK: “Use of Single Nucleotide Polymorphisms to improve fisheries management”. The position is in the Research Group on Population Genetic and Ecology, and the work place is Tromsø.

The aim of the SNPFISK project is to develop a method for the rapid identification of single nucleotide polymorphism (SNP) for fish species. SNPs will be developed for three target taxa: Greenland halibut, North Atlantic Redfish and Saithe. The three taxa span a wide geographical range in the North Atlantic, but the connections between possible sub-populations are still unresolved. In addition, species identification for redfish remains an acute problem for small individuals. The SNPs developed will be used to elucidate species identification (redfish) and population structure (all selected species). By resolving species identification and population structure the results are anticipated to support fisheries management advice for these key species in the North Atlantic. The successful candidate will carry out some laboratory work, conduct the statistical analyses and contribute to the implementation of the method in fisheries management in an ecological perspective.

As a part of the project, a stay at the University of Washington, Seattle USA, is planned.

We wish to appoint a highly motivated person with a master degree education in population genetic or ecology. Good knowledge of statistical inference and practical experience of statistical softwares is essential. Documented experience with SNP’s and populations genetic theory is desirable.

Personal qualities such as good communication and cooperation skills, the ability to work independently, efficiently and purposefully, as well the ability to generate, implement and report project activities will be emphasised.

Candidates must meet the admission requirements at the University of Tromsø.

We offer:

* a positive, challenging and creative work environment * the opportunity to work in a national institute with a high level of international contact * flexible hours, a good pension scheme and a wide range of welfare services.

The Institute offers governmental regulated salaries as PhD student (code 1017).

For more information, please contact Project leader Torild Johansen, email: Torild.Johansen@imr.no, tel: +47 77 60 97 10, Senior Scientist Benjamin Planque, email: Benjamin.Planque@imr.no, tel: +47 77 60 97 21, or Research Group Leader Terje Svaasand,

email: Terje.Svaasand@imr.no, tel: +47 55236891 or visit our web-site at www.imr.no .

The Institute of Marine Research is an “inclusive worklife” employer that encourages diversity, and we encourage all qualified candidates to apply for this position. Women are particularly encouraged to apply.

Please apply in writing, enclosing a CV, copies of relevant recommendations and academic transcripts together with a set of publications, to: Institute of Marine Research, Personnel Division, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway.

Application number: “09-11”. Closing date for applications: 31.04.11.

Lorenz Hauser <lhauser@uw.edu>

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## UAberdeen Genomics Atlanticsalmon

Institute of Biological and Environmental Sciences, University of Aberdeen, UK

Research Fellow The physiological and genomic basis to the timing of life history transitions in the Atlantic salmon

A 3 year position is available for an independent and highly motivated individual to work as a Research Fellow in the Institute of Biological & Environmental Sciences at the University of Aberdeen. The project aims to understand the molecular genetics underlying the seasonal control of the metamorphic transition of salmon from a juvenile freshwater form (parr) to a migratory form (smolt), which returns to the sea. This is a collaborative project involving specialists in biological timing (Prof. David Hazlerigg), and salmonid physiology (Dr. Sam Martin), and collaborators with expertise in molecular genetics and genomic biology at the Institute of Zoology, London, and the University of Edinburgh. This interdisciplinary project will suit a researcher with a strong interest in the evolution of physiological timing mechanisms in vertebrates.

A PhD in an appropriate area of biological science and good molecular biology skills are essential, with expertise in fish physiology, endocrinology or neuroscience all highly desirable. We encourage applications from candidates with a strong background in evolutionary genetics or genomic biology. Training will be provided to enable the candidate to extend and complement their existing skills. Informal enquiries may be made by email to Professor David Hazlerigg (d.hazlerigg@abdn.ac.uk), or Dr Sam Martin (sam.martin@abdn.ac.uk).

Application forms and further particulars can be found online at http://www.abdn.ac.uk/jobs/index.php Closing Date: - 30th April 2011 Informal enquiries may be made by email to Professor David Hazlerigg (d.hazlerigg@abdn.ac.uk), or Dr Sam Martin (sam.martin@abdn.ac.uk).

http://www.abdn.ac.uk/biologicalsci/staff/details/-sam.martin http://www.abdn.ac.uk/biologicalsci/-staff/details/d.hazlerigg The Zoological Society of London is incorporated by Royal Charter Principal Office England. Company Number RC000749 Registered address: Regent's Park, London, England NW1 4RY Registered Charity in England and Wales no. 208728

Kate.Ciborowski@ioz.ac.uk

## UAlabama LabManager Systematics

The Department of Biological Sciences at The University of Alabama seeks a Laboratory Research Specialist to manage the Steven Johnson Molecular Systematics Laboratory (SJMSL). Responsibilities of the Laboratory Research Specialist include management and supervision of SJMSL, which includes billing for lab and/or equipment use, ensuring maintenance of laboratory equipment and lab environment; ordering laboratory supplies and equipment; maintains inventories of reagents, buffers, and laboratory consumables; providing technical guidance training of personnel in techniques used in molecular systematics and population genetics.

Required minimum qualifications: a Masters degree in Biological Sciences or a relevant field and at least 3 years experience with molecular genetics research methods including DNA extraction, PCR, DNA sequencing, and DNA fragment analysis, OR a Ph.D. in Biological Sciences or a relevant field. Ability to effectively communicate and interact with faculty and students required.

Preferred Qualifications: experience with high-throughput molecular data collection and data management and analyses is essential. Applicants must have demonstrated proficiency with up-to-date molecular biology approaches, including standard and alternative methods of DNA extraction, standard laboratory skills for PCR and cloning, gel electrophoresis, DNA sequencing and DNA fragment (microsatellite, AFLP, RFLP) optimization and analysis. Knowledge of automated DNA sequencer usage and troubleshooting is preferred. Must demonstrate familiarity with analyses of DNA sequence and/or microsatellite data. Mac and PC platform proficiency required. Good organizational, time management, and problem solving skills are needed. The ability to perform tasks in an independent, organized, methodical and analytical manner is essential.

For more information see www.bsc.ua.edu/site/ and bsc.ua.edu/site/scf/index.html. For further information, please contact Dr. Phillip Harris at pharris@bama.ua.edu. Closing date is 6 May 2011.

Visit Employment Opportunities at http://jobs.ua.edu for more information and to apply. Select "Search Staff Postings", then "Laboratory Research Specialist" under Classification Title. The University of Alabama is an Equal Opportunity Educational Institution/Employer or EOE/AA.

Phillip M. Harris, Ph.D. Assistant Professor and Curator of Fishes Dept. of Biological Sciences Box 870345 The University of Alabama Tuscaloosa, AL 35487-0345

Phone: 205-348-1831 FAX: 205-348-6460

pharris@bama.ua.edu

http://bama.ua.edu/ ˜ pharris/lab Phillip Harris <pharris@bama.ua.edu>

## UAlaska Fairbanks BioinformaticsManager

University of Alaska Fairbanks seeks a Unit Manager for the Life Science Informatics/ Epidemiology Biostatistics cores. These cores provide technical computing services, such as database development and management, data dissemination services, optimization of technical software, custom data analysis pipelining, maintenance of computational clusters, and user training workshops to facilitate the growth and maintenance of a diverse user group. This position is jointly supported by campus-wide research groups, including the Center for Alaska Native Health Research (CANHR), the IDeA Network of Biomedical Research Excellence (INBRE), the IAB Spatial Ecology Laboratory, and grants to individual researchers.

The position requires significant attention to both substance and detail and a commitment to working collaboratively with faculty and staff involved in the Institute of Arctic Biology, as well as at other UA campuses. The Manager will interact with up to 150 researchers on a regular basis, and oversee the work of programmers and system analysts with an operational budget of approximately $750,000/yr. Experience with computer hardware including networks, clusters and servers, as well as an understanding of programming and scripting are also required. Capability in Red Hat or any Linux is required, while familiarity with SQL, PHP and/or Perl are strong pluses. Additionally, experiences in any field of bioinformatics are pluses.

Also desired are strong communication skills; human resource skills for management of the work flow for a small highly skilled and professional team, including direct supervision, budget authority and planning responsibilities. Typical education should include a graduate degree in bioinformatics, biology, medical science or a related field with strong computational aspects, or information technology/mathematics/statistics or related field with demonstrated biology underpinnings.

To apply, go to UAKJOBS.COM. < https://www.uakjobs.com/applicants/jsp/shared/frameset/Frameset.jsp?time=1301720728087 >

More information about the supporting programs can be found here:

CANHR < http://canhr.uaf.edu/ > INBRE < http://www.alaska.edu/inbre/ > Life Science Informatics < http://biotech.inbre.alaska.edu/ >

University of Alaska Fairbanks < www.uaf.edu > is the flagship university of Alaska with more than 10,000 students. There are active research programs in Biology < http://www.iab.uaf.edu/ > as well as in Chemistry and Biochemistry < http://www.uaf.edu/chem/ >. LSI also provides the support to researchers in UA Anchorage < http://www.uaa.alaska.edu/biology/ >.

Additional information about Fairbanks, Alaska: Fairbanks, Alaska is an exciting place for many people. This job offers a life-time opportunity for you to experience vibrant, diverse, and adventurous life with the comfort of medium-sized city. It is conveniently located and the direct flight from Seattle WA takes only 3.5 hours. It takes about 2 hours of driving to the magnificent Denali National Park, which offers unparalleled wilderness experience. < http://www.nps.gov/dena/index.htm > For more adventurous, Arctic National Wildlife Refuge < http://en.wikipedia.org/wiki/ANWR > or Wrangell-St. Elias National Park < http://en.wikipedia.org/wiki/Wrangell%E2%80%93St._Elias_National_Park_and_Preserve > can be easily accessed. You can enjoy the midnight sun during the summer. Even in the winter, we have a lot of fun things to do. The shortest day is about 4 hours, but there are plenty of light before the sun rise and after the sun set. We generally do not have wind, so it does not feel as cold as Chicago in the winter. We have lots of cultural activities such as active music community and arts, film and music festivals, too (e.g., < http://www.fsaf.org/ >).

A lot of us did not know how high the quality of life is in Fairbanks until we moved here, and most of us fell in love with the "Last Frontier" State. I hope you'll take up this opportunity and join us.

If you have any questions, feel free to contact me.

Naoki Takebayashi <ntakebayashi@alaska.edu> Search committee chair for LSI/EB core manager.

– Naoki Takebayashi <ntakebayashi@alaska.edu> Institute of Arctic Biology & Department of Biology and Wildlife

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

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## UGloucestershire MammalianEvolution

UofGlosUKSeniorLecturer

Text

The University of Gloucestershire intends to appoint a Senior Lecturer / Lecturer in Biology.

We are seeking an all round ecologist with a mammalian or non-animal specialism (for example, a strong background in plant, fungal or lichen ecology, or with an interest in specific ecosystems especially aquatic/marine) to teach across all levels of Biology and Animal Biology undergraduate degree programmes in a strongly teaching-focussed institution. A knowledge of GIS and/or ecological modelling would be desirable, as would capacity to contribute to postgraduate provision in sustainability science.

The successful applicant will be joining a small and dedicated team and will be expected to play a prominent role from the start in a diverse teaching environment that includes lectures, practicals and seminars. Applicants must have a flexible attitude towards teaching and be willing and able to contribute to modules outside of their immediate subject expertise. Applicants would be expected to teach on at least one residential field course each summer, and must be able to tailor field teaching to changing circumstances and requirements.

The successful applicant will also be expected to contribute towards the group's ongoing research programme, developing their own research interests and collaborating with existing research projects. Supervising postgraduate research students and developing postgraduate courses would be an expectation of the appointment in due course, although experience in this area is not required.

Further Details

For further information relating to the post, informal enquiries may be made to:

Dr Adam Hart, Reader in Science Communication

ahart@glos.ac.uk

+44(0)1242 714670

Further details and application form are available from: www.glos.ac.uk/jobs

Please quote reference number: A606 Email: hr@glos.ac.uk Telephone number: (01242) 715062 Closing date: 17th May 2011 Interview date: 27th May 2011

"HART, Adam" <ahart@glos.ac.uk>

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## UGuelph UNB Dalhousie Manager Postdoc EnvironmentalGenomics

BIOMONITORING 2.0 A High-Throughput Genomics Approach for Comprehensive Biological Assessment of Environmental Change

Large-Scale Applied Research Competition seeks to apply an environmental genomics approach, based on next-generation sequencing technologies to develop a wholly novel approach for large-scale biomonitoring of different ecosystems. Focused on the boreal wetland habitats of Canada's largest national park, Wood Buffalo (WBNP), the project brings together genomics, bioinformatics and ecological researchers from across Canada to work with federal scientists and industrial partners in an exciting and challenging new project.

metal mining and hydro-power projects. The area also is home to many indigenous communities who rely on access to the land to make their living. The project will work in partnership with local stakeholders to mesh cutting edge genomics and bioinformatics technologies to provide rapid ecosystem assessment tools, which will facilitate rapid and accurate monitoring of ecosystem health, in partnership with Environment Canada's CABIN program and Parks Canada's Ecological Integrity program.

1. Project Manager

Host institution: University of Guelph, Guelph, Canada (Hajibabaei Lab, Biodiversity Institute of Ontario & Department of Integrative Biology). Starting date: June 2011. Qualifications: MSc or PhD in Biological/Environmental or Computer Science (or related fields), minimum 2 years of experience in large- scale project management and budgeting (accounting), articulate, well- organized and excellent oral and written communication skills. Being computer/web savvy is an asset as the project manager will be in charge of updating the project website. We would also consider exceptional candidates who would like to pursue an alternative career path in science management after their PhD/postdoc. Duration: 3 years (initial contract for one year; renewal based on performance). Job Description: The Project Manager will be positioned at Guelph and report to the project leader but will also work closely with all project teams. Additionally, the Project Manager will visit WBNP to coordinate sampling efforts and build and strengthen linkages to local community and other stakeholders. The Project Manager will be responsible for the day-to-day management, the administrative and financial aspects. The Project Manager will make sure that report mechanisms are followed, and that links with the different research institutions and the government organizations and communities are in place. The Project Manager will also monitor to ensure that information flows via these linkages. The Project Manager will be responsible for content management and updating Biomonitoring2.0 web site.

2. Data Analysis Postdoctoral Fellow

Host institution: University of Guelph, Guelph, Canada (Hajibabaei Lab, Biodiversity Institute of Ontario & Department of Integrative Biology). Starting date: July-September 2011. Qualifications: PhD in molecular evolution, phylogenetics, molecular ecology, population genetics, bioinformatics or related fields. Excellent theoretical knowledge and experience in comparative sequence data analysis for biodiversity, evolutionary or ecological investigations, preferably using Next Generation Sequence (especially 454) data. Experience in using Linux and Python (or similar scripting languages) and knowledge of R would be essential. Duration: 3 years (initial contract for one year; renewed based on performance). Job Description: This postdoctoral fellow will be responsible for bioinformatics analysis of data generated in the genomics pipeline. Working closely with other bioinformatics team members (Golding and Beiko groups) the postdoc will amalgamate sequence assignment and GIS based software tools with molecular evolutionary and ecological analysis to develop a baseline as well as a comparative framework for genomics based characterization of sites and sampling events. In addition, the postdoc will aid in developing and optimizing analysis and visualization tools for NGS and collateral data and for channeling them to web portal for use by different stakeholders.

3. GIS Software Developer

Host institution: Dalhousie University, Halifax, Canada (Beiko Lab, Faculty of Computer Science) Starting date: June 2011. Qualifications: BSc or MSc in Computer Science, Bioinformatics or a related field. The scope of the project would also permit an applicant with a PhD to carry out research in the context of a postdoctoral position. Must be proficient in Python and C++, and ideally experienced in OpenGL and graphical software development. Experience with previous development projects is essential. Duration: 3 years (initial contract for one year; renewed based on performance). Job Description: seeking a talented software developer to assist with the development of bioinformatics tools, particularly enhancements to our

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## UKansas ResTech PlantEvolution

The Hileman lab in the Department of Ecology and Evolutionary Biology at the University of Kansas is seeking a research technician in the field of plant evolution and development beginning 1 May, 2011 (start date flexible). The successful candidate will work closely with a postdoctoral researcher in the lab to pursue both independent and supervised research. The scope of the research is to characterize genes controlling flowering time and branching architecture in snapdragon and close relatives. To learn more about research in the Hileman lab, please visit our website at: http://www.people.ku.edu/~lhileman/HilemanLab/Home.html To learn more about this position, including responsibilities, required and preferred qualifications, salary range, and information about applying, please see the online add at: http://jobs.ku.edu (position #00206357). Review of applications will begin 22 April, 2011. Questions about this position may be directed to Dr. Lena Hileman, lhileman@ku.edu. KU is an EO/AA Employer.

lhileman@ku.edu

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## ULausanne ComputationalBiology

The Faculty of Biology and Medicine of the University of Lausanne, Switzerland invites applications for the position of

Assistant Professor tenure-track for an Associate or Full Professorship in Computational Biology and Phylogenetics at the Department of Ecology and Evolution

The Department of Ecology and Evolution (http://www.unil.ch/dee) has a long track record of excellence in research. A start-up package, a state-of-the-art research infrastructure as well as a yearly research allowance for positions and consumables will be available within an environment favoring collaborations.

The successful candidate is expected to develop an internationally recognized research programme in computational biology and phylogenetics, funded by external sources. Teaching duties include a programming class for biology students. Pre-existing knowledge of French is not required but the candidate is expected to be able to teach in French within 2 years. The appointee will also supervise Master and PhD students and participate to other training activities (http://www.unil.ch/bec & http://www.unil.ch/ee).

The job description is available on the Web at the address www.unil.ch/fbm/page64812.html. For further information, please contact Prof. H. Kaessmann (henrik.kaessmann@unil.ch), chairman of the search committee.

Applications, including a curriculum vitae with a complete list of publications in which the five most significant ones are identified, a brief statement of research programme and teaching philosophy, and the names of three referees, should be sent by June 30th, 2011 to Prof. P. Francioli, Dean of the Faculty of Biology and Medicine, rue du Bugnon 21, 1011 Lausanne, Switzerland.

The University of Lausanne wishes to promote the access of women to academic careers and encourages applications from women.

With my thanks and best regards,

Maryline Primus

Unité de la relève académique - sciences fondamentales Décanat de la Faculté de biologie et de médecine Rue du Bugnon 21 - CH-1011 Lausanne Tél. +41 (0)21 692 50 32 Fax +41 (0)21 692 50 05

Maryline Primus <Maryline.Primus@unil.ch>

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## UManitoba EvoDevo

Assistant Professor, Department of Biological Sciences, Faculty of Science University of Manitoba, Position # 12858

The Department of Biological Sciences at the University of Manitoba invites applications for a full-time probationary (tenure-track) appointment at the rank of Assistant Professor to begin January 1, 2012. This position includes responsibilities for teaching, research and service. Applicants with expertise in developmental biology using established or emerging developmental systems, preferably with emphasis on mechanisms of development are encouraged to apply. The successful applicant must hold a PhD and preferably, have post-doctoral experience in a relevant discipline. Applicants should have a publication record indicative of their ability to establish an active, independent research program. Teaching experience is a strong asset. The successful candidate will be expected to establish a vigorous, externally funded research program and to promote research synergies within the department, the Faculty of Science and across campus, and contribute to undergraduate and graduate teaching. The position entails department-based instruction in developmental biology and areas appropriate to the candidate?s expertise.

This is an exciting opportunity to join a newly integrated Department of Biological Sciences and to define your own niche in science! The department has 36 faculty including 2 CRC Tier 2s, 70 graduate students and over 200 Major and Honours students with research strengths across the spectrum of biology and its sub-disciplines (www.umanitoba.ca/-science/biologicalsciences).

The department is located on the Fort Garry campus of the University of Manitoba in Winnipeg, a city with a rich cultural environment and abundant outdoor recreational venues (learn more about Winnipeg at http://-www.winnipeg.ca). The Faculty of Science offers excellent opportunities for research and teaching in a broad range of biological systems, collaborations across departments with biologically related interests and supportive infrastructure including a range of microscopy and imaging equipment, spectrometers and other chemical analysis instruments, molecular and cell biology facilities, and animal and plant-rearing facilities (aquatic and terrestrial).

Applications (ideally in pdf format) should include: a covering letter outlining interest in the position, CV, research plan with short and long term goals, statement of teaching experience and philosophy, and the name and contact information of 3 academic referees. Applications must be sent by June 15, 2011 to:

Dr. Judy Anderson Head, Department of Biological Sciences Faculty of Science University of Manitoba

Email: janders@cc.umanitoba.ca. Please refer to position # 12858.

The University of Manitoba encourages applications from qualified women and men, including members of visible minorities, Aboriginal peoples and persons with disabilities. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

Application materials, including letters of reference, will be handled in accordance with the protection of privacy provisions of "The Freedom of Information and Protection of Privacy Act" (Manitoba). Please note that curriculum vitaes may be provided to participating members of the search process.

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## UNebraska SeniorResAssoc Bioinformatics

SENIOR RESEARCH ASSOCIATE in Bioinformatics University of Nebraska Lincoln

The Nebraska Center for Virology is searching for a highly motivated and enthusiastic computational biologist with a proven track record in the area of Bioinformatics. The candidate will provide assistance to Dr. Charles Wood, Director of the Nebraska Center of Virology and faculty member of the School of Biological Sciences and other NCV faculty in the area of Computational Bioinformatics. Duties include the management of sequence data using statistical analysis and programming. Responsibilities include interactions with faculty, post-doctoral and lab personnel regarding methods, testing and analysis of conducted research using Next Generation Sequencing, Phylogenetic Analysis, Modulated Clustering, Microarray Analysis, Sequence Analysis, and other computational tests as needed by researchers.

The candidate will work with groups working on microbial genomics from a number of human, animal and plant viruses including HIV, herpesviruses, influenza, pox and algal viruses. PhD/Masters in Bioinformatics preferred. Experience in conducting sequence analysis by using various software applications including PERL, Java, R, UNIX environment. Virology background is desirable.

Informal inquiries about the projects are encouraged. For more information about the Center please go to www.unl.edu/virologycenter <goog_1791382225> Applicants should submit a resume, cover letter and contact information for three references in MS Word or PDF format. Applications and all queries should be sent to Dr Charles Wood at cwood1@unl.edu

Charles Wood PhD Director, Nebraska Center for Virology Lewis Lehr/3M University Professor School of Biological Science University of Nebraska Rm 102C, Morrison Center, 420 Fair St Lincoln, NE 68583-0900

Damien Tully <damientully@gmail.com>

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## UTurku EcologicalGenetics

Non-tenurable research fellowship in ecological genetics (1.8.2011 - 31.12.2015), Department of Biology, University of Turku, Finland.

The specific field of the fellowship is genetics and evolutionary biology, especially ecological genetics. Duties associated with the position include: actively conducting high quality research on topics related to ecological and evolutionary genetics/genomics; development and teaching of undergraduate courses for students specializing in genetics or evolutionary biology; supervision and examination of undergraduate thesis work; supervision of post-graduate students; participation in administrative duties within the department and the university.

Research merits of applicants that will be taken into consideration during the selection procedure include their publication record in the field of the position, success in gaining external research funding and experience in managing research projects in ecological and evolutionary genetics/genomics. Teaching merits considered as advantageous include experience in the development and teaching of undergraduate courses related to ecological and evolutionary genomics and genetics more broadly and well as student supervision experience. The demonstrated success with which applicants combine genetics and ecology/evolution in their research and teaching will play an important role in the selection procedure.

University research fellows require a PhD degree in the field of the position, as well as the ability to give high quality research-based teaching and to supervise academic theses.

The salary level is defined based on the university salary system and will be in the range of level 6-7 for teaching and research staff. When a performance component is included, the monthly salary is normally within the range of 3463 - 4200 EUR.

Applications should include an Academic protfolio (see http://www.utu.fi/opiskelu/oppaat/portfolio/ for details), a CV and publication list as well as any additional documents relevant for the position selection process. Applications must reach the office of the Department of Biology, University of Turku by 15:45 on 26.04.2011. The postal address is Department of Biology, Luonnontieteiden talo 1, 20014 UNIVERSITY OF TURKU, FINLAND (visiting address: Luonnontieteiden talo 1, 2nd floor, room 212). Applications may be sent by email (pdf files only, as few separate files as possible) : maiair@utu.fi . Application documents are not returned.

The Department of Biology hosts three ISI Highly cited scientists and a national Center of Excellence. Research in the genetics laboratory currently focuses on ecological and evolutionary genetics, molecular systematics as well as recombination mechanisms.

(see http://www.sci.utu.fi/biologia/en/research/-research_projects/ for more details)

These areas fall under two of the six research fields of emphasis in the University of Turku.

Turku, Finlandâs 5th largest city (176 000 people), is located in the South-Western part of Finland. It has a rich cultural history and is the gateway to a beautiful archipelago. The University of Turku is one of the major multidisciplinary universities in Finland and the City of Turku was ranked third in the most recent classification of medium-sized âSmart Citiesâ (http://www.smart-cities.eu)

For more information contact Academy prof. Craig Primmer, tel. +358 2 333 5571, craig.primmer@utu.fi , Prof. Harri Savilahti, tel. +358 2 333 5586, harri.savilahti@utu.fi or Prof. Pekka Niemelä, tel. +358 2 333 5777, pekka.niemela@utu.fi

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Craig Primmer

Academy Professor Division of Genetics and Physiology Department of Biology (Vesilinnantie 5) 20014 University of Turku FINLAND

Office +358 2 333 5571 Mobile +358 40 1560 365 Fax. +358 2 333 6680 craig.primmer@utu.fi http://users.utu.fi/primmer Craig Primmer <craig.primmer@utu.fi>

## UTurku MolecularSystematics

Non-tenurable research fellowship in molecular systematics (1.8.2011 â 31.12.2015), Department of Biology, University of Turku, Finland.

The specific field of the fellowship is genetics and evolutionary biology, especially molecular systematics. Duties associated with the position include: actively conducting high quality research on topics related to molecular systematics; development and teaching of undergraduate courses suitable for students specializing in evolutionary biology, biodiversity or genetics; supervision and examination of undergraduate thesis work; supervision of post-graduate students; participation in administrative duties within the department and the university.

Research merits that will be taken into consideration during the selection procedure include applicantâs publication record in the field of the position, success in gaining external research funding and experience in managing research projects within the field of molecular systematics. Teaching merits considered as advantageous include experience in the development and teaching of undergraduate courses related to molecular systematics and evolutionary biology more broadly as well as student supervision experience. Earlier co-operation with biological museums is also advantageous.

University research fellows require a PhD degree in the field of the position, as well as the ability to give high quality research-based teaching and to supervise academic theses.

The salary level is defined based on the university salary system and will be in the range of level 6-7 for teaching and research staff. When a performance component is included, the monthly salary is normally within the range of 3463 - 4200 EUR.

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For more information contact Academy prof. Craig Primmer, tel. +358 2 333 5571, craig.primmer@utu.fi , Prof. Harri Savilahti, tel. +358 2 333 5586, harri.savilahti@utu.fi or Prof. Pekka Niemelä, tel. +358 2 333 5777, pekka.niemela@utu.fi

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Craig Primmer

Academy Professor Division of Genetics and Physiology Department of Biology (Vesilinnantie 5) 20014 University of Turku FINLAND

Office +358 2 333 5571 Mobile +358 40 1560 365 Fax. +358 2 333 6680 craig.primmer@utu.fi http://users.utu.fi/primmer Craig Primmer <craig.primmer@utu.fi>

## UVienna SystematicEvolutionaryBotany

Job Announcement

As stated in its development plan (http://www.univie.ac.at/rektorenteam/ug2002/entwicklungsplan.html) the University of Vienna aims at strengthening its position as a major research-oriented university. Key elements of this strategy include the provision of an attractive range of research-based study programmes, support for furthering the work of junior academic colleagues, and high-calibre professorial appointments.

The Faculty of Life Sciences of the University of Vienna announces the position of a

Full Professor of Systematic and Evolutionary Botany

(full time permanent position under private law). The University of Vienna intends to increase the number of women on its faculty, particularly in high-level positions, and therefore specifically invites applications by women. Among equally qualified applicants women will receive preferential consideration.

The Faculty of Life Sciences, University of Vienna, invites applications for a full professorship in Systematic and Evolutionary Botany. Applicants should have an excellent international track record in modern integrative research topics such as molecular systematics, phylogenetic analysis, biogeography, speciation or any other related field. International perspectives and collaborations are expected.

Candidates should be interested in building bridges between Systematic and Evolutionary Botany and the main branches of organismic biology within the Faculty of Life Sciences. The professorship is part of the thematic cluster 'Patterns and Processes in Plant Evolution and Ecology' at the Faculty Center of Biodiversity. Current research at the Faculty Center includes molecular phylogenetics, biogeography, population genetics, cytogenetics, mycology, phytochemistry, plant morphology, vegetation science, alpine ecology, landscape ecology, conservation biology, plant-animal interactions, and tropical ecology.

The Faculty Center offers excellent research and teaching conditions including a well equipped set of molecular, cytogenetic, and morphological laboratories; IT facilities; an extensive botanical library; a herbarium (1.4 million sheets); a Botanical Garden (Core Facility of the Faculty; 8ha, with more than 11000 species); and access to a tropical research station (La Gamba, Costa Rica).

The candidate will be required to teach at all academic levels including current M.Sc. curricula such as “Plant Sciences” and “Evolutionary Biology”. Excellent teaching and mentoring skills are necessary and should be documented in the application. Although teaching is largely in German, the University of Vienna is committed to expand teaching in English.

Successful candidates will have the following qualifications:

< PhD and post-doctoral experience at a university or other research institution. (Austrian or equivalent international academic degree in the relevant field)

< Outstanding research and publication record, with an excellent reputation as an active member in the international academic community -(Habilitation (venia docendi) or equivalent international qualification in the relevant field is desirable)

< Experience in designing, procuring and directing major research projects, and willingness and ability to assume the responsibility of team leadership

< Experience in university teaching, and willingness and ability to teach at all curricular levels, to supervise theses, and to further the work of junior academic colleagues

The University of Vienna offers

< Attractive terms and conditions of employment with a negotiable and performance-related salary, associated with a retirement fund

< A “start-up package” for the initiation of research projects

< An attractive and dynamic research location in a city with a high quality of life and in a country with excellent research funding provision

< Support for relocation to Vienna, where appropriate

Candidates should send an application containing at least the following documents:

< Academic curriculum vitae

< Brief description of current research interests and research plans for the immediate future

< List of publications together with

a) specification of five key publications judged by the applicant to be particularly relevant to the advertised professorship together with an explanation of their relevance

< PDF versions of these five publications provided either as email attachments or through URLs of downloadable copies

< List of talks given, including detailed information about invited plenaries at international conferences

< List of projects supported by third-party funds

< Short survey of previous academic teaching and list of supervised PhD theses

Applications, written in English and in electronic form (preferably as a pdf file), should be sent to the Dean of the Faculty of Life Sciences of the

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## UVirginia GenomicsBioinformatics 2

Research Scientist

The Department of Biology at the University of Virginia invites applications for a Research Scientist position. The research will focus primarily on the genomic and bioinformatic resources to be used in the identification of sodium channel genes in reptiles. The position also involves analyzing and preparing materials for publication, data management and dissemination, and mentoring graduate and undergraduate students.

A Ph.D. degree in Biology or a related discipline and at least three years post-doctoral experience is required. Candidates must be proficient with maximum likelihood and mixed-model multivariate statistical analyses of quantitative genetic data. Candidates with a background in evolutionary biology and experience in the development of analytical mathematical models are preferred. Candidates must have effective oral and written communication skills.

To apply, please submit a candidate profile on-line and attach a cover letter, curriculum vitae, and the contact information for three references through Jobs@UVA (https://jobs.virginia.edu); search on posting number 0607414.

Review of applications will begin April 15, 2011; however, the position will remain open until filled.

Questions regarding this position should be directed to:

Dr. Edmund Brodie III bbrodie@virginia.edu

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to:

Shawna Edinger 434-982-5615 se5k@virginia.edu

Women and members of underrepresented groups are encouraged to apply. The University of Virginia is an Equal Opportunity/Affirmative Action Employer.

"Edinger, Shawna (se5k)" <se5k@eservices.virginia.edu>

## UVirginia LabManager Sequencing

Operations Manager, Sequencing Facility University of Virginia, Biology Department

The Biology Department at the University of Virginia is seeking an Operations Manager for its Genomics Core Sequencing Facility. The manager is responsible for all operations and facility management aspects required to run the sequencing facility. These duties include purchasing and maintenance of laboratory supplies and equipment, creation and implementation of facility operating policies and procedures, oversight of facility operating budget, and the marketing of facility services to prospective customers. The manager is also responsible for all technical laboratory duties required to run diverse samples on a 454-FLX high-throughput automated genome sequencer. Duties include, preparing DNA samples, creating DNA libraries, and running the sequencer and assembler. A Bachelor's degree in Biology or a related field and at least four years experience working in a laboratory setting is required. A strong background in molecular biology laboratory methods and techniques is required. Applicants with Genomics, DNA sequencing, or statistical experience are preferred.

Please apply on-line at: https://jobs.virginia.edu< https://jobs.virginia.edu/ > ; search posting number 0607557

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

Shawna Edinger UVA Biology Department Phone: (434) 982-5615 Fax: (434) 982-5626

"Edinger, Shawna (se5k)" <se5k@eservices.virginia.edu>

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## UYork EvolutionaryBiology

Lecturer / Senior Lecturer in Evolutionary Biology

Job reference UoY01214

Location York, UK

Based at University of York - Heslington Campus

Grade 7 or 8

Department Biology

Closing date 9 May 2011

Salary range is £35,788 to £44,016 p.a. for a Lecturer or £45,336 to £52,556 p.a. for Senior Lecturer.

The Role

The Department of Biology at York is an expanding Department that represents a thriving research community of the highest international calibre. We ranked first-equal among UK broad-spectrum biology departments for research judged "world-leading" by the 2008 UK RAE. The Department covers the spectrum of contemporary biological sciences with no internal barriers and encourages collaborations and external links.

As part of major developments in the department, we are seeking an outstanding and dynamic scientist with a proven track record of high quality research who is keen to develop a research programme of international standing, and teaching in the same field. Your research will cover any area of evolutionary biology, including adaptation, phylogenetics, population genetics and environmental genomics. You should be using advanced data acquisition and/or analytical approaches (e.g., high-throughput sequencing or other "omics", Bayesian statistics, bioinformatics).

We will consider applicants at either level. Applicants for Senior Lecturer will be expected to show a developed research programme so are likely to have extensive experience as Lecturer or Independent Fellow.

Informal enquiries may be made to Professor Peter Young (peter.young@york.ac.uk; +44 1904 328630) or the Head of Department (Professor Deborah Smith, biohod@york.ac.uk; +44 1904 328555)

For more information, download the job description and person specification from http://www.york.ac.uk/jobs/ The University of York

Times Higher Education University of the Year 2010

jpy1@york.ac.uk

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## WheatonCollege Evolution

VISITING ASSISTANT PROFESSOR(s)/INSTRUCTOR(s)/sabbatical replacements (Fall 2011 & Spring 2012) - Wheaton College Department of Biology is seeking applicants to teach an upper division undergraduate course in EVOLUTION in Fall 2011 (3 hrs lecture and 3 hrs lab/wk) and a course in either DEVELOPMENTAL BIOLOGY or MARINE BIOLOGY in Spring 2012 (3 hrs lecture and 3 hrs lab/wk). Completion or near completion of Ph.D. required. Candidates may apply for either or both semesters' positions. Send CV and cover letter detailing teaching experience to Dr. Robert Morris, Chair, Dept. of Biology, Wheaton College, Norton, MA 02766 or rmorris@wheatonma.edu. Deadline May 1 or until positions are filled.

Wheaton College is an independent selective liberal arts college with 1,600 undergraduates. Wheaton College seeks educational excellence through diversity and strongly encourages applications from women and men from minority groups. Wheaton College is an affirmative action / equal opportunity employer.

Information about the department may be found at http://wheatoncollege.edu/biology/ . smccaffe@wheatonma.edu

# Other

## AFLP and dfdist

Dear Evoldir members,

I am having trouble working out the infile required for the program dfdist to identify outlier loci, for use with AFLP markers. If anyone has used the program for this purpose with AFLP's then I would be grateful for an example infile (used by the datacal program distributed with dfdist).

Many thanks, Jo Bluemel

***** Joanna Bluemel OnE - Organisms and Environment, PhD student Cardiff School of Biosciences, Biomedical Sciences Building, Cardiff University, Museum Avenue, Cardiff, CF10 3AX, UK +44(0) 29 20875073 *****

BluemelJK1@cardiff.ac.uk

## CenterGenomicsBioinfor Nasonia

Dear Colleagues,

The Center for Genomics and Bioinformatics (CGB) at Indiana University, in collaboration with participating research communities and Roche NimbleGen Inc., offers an evolving series of complete transcriptome and high-throughput genotyping microarrays, hybridization and data analysis service to various research communities.

Here download a 2-page flyer/datasheet introducing the Nasonia vitripennis Gene Expression Microarray.

https://wiki.cgb.indiana.edu/download/attachments/36372862/Nasonia_GSF_expression_datasheet_2011.v1.pdf

Also download a separate 2-page flyer introducing the Nasonia vitripennis Comparative Genotyping Microarray.

https://wiki.cgb.indiana.edu/download/attachments/36372862/

Nasonia_GSF_genotyping_datasheet_2011.v1.pdf

These Nasonia microarrays and not-for-profit data services are supported in part by NIH grant 1R24GM084917 (PI: John Werren) and by the META-Cyt Initiative of Indiana University, funded in part through a major grant from the Lilly Endowment, Inc.

These custom microarrays – including CGB's automated analysis pipeline – are the most cost effective means of conducting replicated and large-sample functional genomics and fine-coverage genotyping experiments. Our research communities also benefit from amassing functional genomics data on shared and regularly updated open-source platform designs.

For more information, please contact: CGB Genomics Service Facility By email: gsf@cgb.indiana.edu http://cgb.indiana.edu John Colbourne, The Center for Genomics and Bioinformatics 915 East Third Street, Bloomington, Indiana USA 47405-7107

John Colbourne <jcolbour@cgb.indiana.edu> John Colbourne <jcolbour@cgb.indiana.edu>

## Corophium volutator samples

Hello All,

I am requesting assistance in obtaining samples of *Corophium volutator* for a phylogeographic study throughout this species' range. I am part of a collaborative research group at the University of New Brunswick studying mudflat evolution and ecology, with most of our work based in the Bay of Fundy, Canada. I am hoping to expand my existing sequence database to include populations from Europe, the Mediterranean, Japan, and the Ponto-Caspian (Black, Azov, and Caspian Seas).

Ideally, I would like to receive ~20-50 individuals shipped in one or two sealed tubes (<50mL total) of 95% ethanol to our laboratory in Fredericton, New Brunswick, Canada for analysis. This collection would require minimal time investment if researchers are already conducting field work in *C. volutator *habitat. However, I would also be grateful for any contact information for researchers who might encounter *C. volutator *during their field studies, or to resources that might mention specific areas that are known *C. volutator *habitat outside of North American and European waters. All shipping charges will be covered by our research group. Please do not hesitate to contact me (tony.einfeldt@gmail.com) should you be able to provide any information regarding this project.

Myriam Barbeau - principle investigator for the mudflat research group: http://www.unb.ca/fredericton/science/biology/Faculty/Barbeau.html Jason Addison - my direct supervisor: http://www.unb.ca/fredericton/science/biology/Faculty/addison/addison.html Thank you for your time,

Tony Einfeldt

Email: tony.einfeldt@gmail.com

– Tony Einfeldt, M.Sc. Candidate University of New Brunswick Department of Biology PO Box 4400 Fredericton, NB, Canada, E3B 5A3 506-262-3456

Tony Einfeldt <tony.einfeldt@gmail.com>

## Drosophila shipments to Canada

Hi everyone,

Shipments from the Bloomington Drosophila stock center to Canada are becoming increasingly more difficult. Several of our recent shipments have arrived dead. Bloomington used to ship via FedEx and DHL but both couriers have now refused to ship live insects (not just on Canadian shipments) leaving us with a 2-3 week shipment time via AirMail as the only current option.

Does anybody have any suggestions for a work-around? Has anybody else encountered these issues?

Cheers, Mark

– Dr. Mark J. Fitzpatrick Assistant Professor Integrative Behaviour & Neuroscience Group Department of Biological Sciences University of Toronto Scarborough Toronto ON M1C 1A4 Canada

mark.fitzpatrick@utoronto.ca twitter: @blackbellied

mark.fitzpatrick@utoronto.ca

## ErnstMayr AwardContestants

The deadline to submit abstracts for the 2011 Ernst Mayr Award has been extended to April 22nd. The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meeting of the Society of Systematic Biologists, held in conjunction with the Evolution meeting. The award consists of $1000, a certificate, and a subscription to the journal Systematic Biology. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible.

Based on the submitted abstracts, the Mayr Awards Committee will select students for inclusion in the Ernst Mayr Symposium, held at Evolution 2011. Talks will be judged on creativity, quality, excellence of research, and quality of presentation. The winner of the award will be announced at the SSB business meeting and again during the banquet awards ceremony at the conclusion of the Evolution Meetings.

For more information on submission guidelines, please visit the website below:

http://systbio.org/?q=node/10 Please contact Dr. Sydney Cameron, SSB Awards Chair, at ssb-apps@life.illinois.edu if you have additional questions.

– Sydney A. Cameron Assoc. Prof. Department of Entomology and Program in Ecology, Evolution and Conservation Biology University of Illinois 320 Morrill Hall 505 S. Goodwin Ave. Urbana, IL 61801

ofc ph. 217-333-2340 lab ph 217-333-2170 cell ph 217 766-5631 scameron@life.illinois.edu

www.life.illinois.edu/scameron Sydney Cameron <scameron@life.illinois.edu>

## Eukaryote 18S primers answers

Dear EvolDir members,

Thank you all for your responses to my request about general eukaryotic 454 primers. I received some very informative answers, and quite a few people have expressed their interest in the question. I attach the three papers suggested by Scott Fay and Simon Creer here.

However, for my part, having checked the supposedly "general" primers on alignments of protozoa from the very diverse groups (Ciliates, cercozoans, bodonids, heterokonts), I would say that I am a bit skeptical about generality of the primers in some protozoan groups. But well, lets see - and certainly, there is sufficient variability in this region to enable a satisfactory taxonomic resolution from only 250 bp, let alone 500 bp. I guess I will simply have to give it a try and see how it plays out.

Best regards,

Christoffer

I wrote:

I am looking for a set of eukaryote specific 18S (SSU) primers amplifying a fragment about 3-400 bp long (i.e. suitable for 454 sequencing). So far those here (of Stoeck et al.) appear to be the best published ones (of about 250 bp)

http://icomm.mbl.edu/microbis/project_pages/-details/proposals/APP_propos al.pdf

Simon Creer wrote:

Hi Christoffer

I have checked F04 and R22 for eukaryotes that have meiobenthic representatives - likewise, they span the most variable region for metazoa in 18S. Watch out though, there is a typo in the ME F04 in text primer. Figure is right and cross check with Nat Comms....

250 bp is too short for Titanium sequencing.

Cheers and best

Si

–

Scott A. Fay wrote:

Hi Christoffer,

I too have been agonizing a lot over universal Euk primers for 454.

As you know, it's a new field. After looking at the sequences myself, I don't think there is a "magic bullet" to capture all of Euk diversity in one primer set.

I plan on using the Amaral-Zeller (V9) ones.

Can you please let me know what other responses you get? This is a topic that interests me.

Warm regards,

Scott

Christoffer Bugge Harder <cbharder@bio.ku.dk>

## EvoDevo texts answers

Dear friends,

Thanks to 30 people who wrote me indicating books and videos to use with undergrad classes about Evo Devo and these are the most cited material:

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The most cited books:

Endless Forms Most Beautiful for Evo Devo. By Sean Carroll. http://www.amazon.co.uk/Endless-Forms-Most-Beautiful-Science/dp/1849160481/ref=sr_1_1?ie=UTF8&qid01065731&sr=8-1. It would be a good introduction to get students interested. Very accessible.

>From DNA To Diversity: Molecular Genetics and the Evolution of Animal Design, 2nd ed. Carroll, Grenier, Weatherbee. 2005. Blackwell Publishing.

Wallace Arthur "Evolution. A developmental approach", which was just published by Wiley-Blackwell.

Hall BK, Olson WM: Keywords and Concepts in Evolutionary Developmental Biology. 2003:476.

—–

Other books:

There is a very nice chapter on the topic written by John True in Futuyma's textbook, Evolution (2nd edition).

"The Origin of Animal Body Plans" by Wallace Arthur

The evolution of developmental pathways. Wilkins.

Wray, G. A. 2010. Embryos and Evolution: 150 years of reciprocal illumination. In: Evolution Since Darwin: The Firt 150 Years, pp. 215-239, in M. A. Bell, D. J. Futuyma, W. F. Eanes, and M. A. Bell. Sinauer Associates, Sunderland.

Developmental plasticity and evolution. West-Eberhard. (lots of overview material)

Ontogeny and Phylogeny. Gould. (not exactly up to date, it's from 1977)

Evolution - The Extended Synthesis IT Press, 2010 http://mitpress.mit.edu/catalog/item/default.asp?ttype=2&tid173 Evolution, Development, and the Predictable Genome. David L. Stern (Author) http://www.amazon.com/Evolution-Development-Predictable-Genome-David/dp/1936221012/ref=sr_1_6?s=books&ie=UTF8&qid01078243&sr=1-6 Gilbert & Epel's "Ecological Developmental Biology: Integrating Epigenetics, Medicine, and Evolution

The shape of life. Raff

—–

VIDEOS:

"Ghost in Your Genes" (http://www.amazon.com/Ghost-Your-Genes-Nova/dp/B000XBPDYY/ref=sr_1_1?ie=UTF8&s=dvd&qid01077278&sr=8-1) "What Darwin Never Knew" both produced by the television show NOVA.

PBS video: http://www.pbs.org/wgbh/nova/body/epigenetics.html http://www.pbs.org/wgbh/nova/body/rnai-explained.html http://www.pbs.org/wgbh/nova/body/rnai.html http://www.hhmi.org/biointeractive/rna/rna_interference/01.html http://www.nature.com/focus/rnai/animations/index.html http://learn.genetics.utah.edu/content/epigenetics/rats/ —–

Website:

On ENSI site, there is a very nice Threespine Stickleback lesson that introduces elements of evo-devo: http://www.indiana.edu/ ˜ ensiweb/lessons/stickleback.html —–

Thanks for all of you and....... we need a website to organize references, links of videos and also a library of slides. We are always discussing about research but we need a place to centralize all material!

Prof. Dr. J. C. VOLTOLINI Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br ECOTROP (CNPq): http://dgp.cnpq.br/buscaoperacional/detalhegrupo.jsp?grupo46205IMB87W7 Currículo Lattes: http://lattes.cnpq.br/8137155809735635 Orkut ("Ensino de Ciência"): http://www.orkut.com.br/Main#Profile?rl=ls&uid608429643840608483 Fotos Artísticas: http://voltolini.album.uol.com.br/texturas . 'Siamo tutti angeli con un'ala e possiamo volare soltanto se ciabbracciamo'

jcvoltol@uol.com.br

## Evolution2011 UndergraduateDiversity

CALL FOR MENTORS: Undergraduate Diversity at Evolution 2011

Twenty-five undergraduates will be attending the 2011 Evolution Meeting in Norman, OK with support from the NSF-funded "Undergraduate Diversity at Evolution" program (in partnership with NESCent). We invite graduate students, postdocs, and faculty members to serve as mentors to the undergraduates. Mentors take pairs of students to attend talks with them, introduce them to colleagues, network and generally make the meetings a welcoming place for them. Although costs are not covered for mentors, it is an unusually rewarding experience.

Contact Dr. Rich Kliman (rmkliman@cedarcrest.edu) if you are interested in serving as a mentor.

Jory Weintraub <jory@nescent.org>

## Examples Population Mismanagement

Hello all,

I am looking for examples where a population has been over-harvested because it was incorrectly assumed to be part of a larger population. Or examples of where a management plan was implemented based on total numbers but resulted in the loss of a cryptic population segment (as opposed to the over harvesting of the entire species or population). I commonly use this story as a cautionary tale about why non-a priori methods for genetic analysis are important but I don't know of any published examples. Most examples I can think of are over harvesting because of other pressures and then realization after the fact when the area turns out to be demographically/genetically independent. For example, beluga whales in Eastern Hudson Bay were over harvested because of market demand not because the levels were thought to be sustainable at the time.

Any leads would be appreciated.

Thanks Stephen

alertstephen@gmail.com

"Petersen, Stephen D" <Stephen.Petersen@dfo-mpo.gc.ca>

## GoodGenes metaanalysis DataRequest

Dear All,

We are collecting data for a meta-analysis of good genes effects in sexual selection, based on literature AND unpublished results.

We are interested in studies reporting on - broadly understood - genetic correlations between male attractiveness-related traits and fitness components. Therefore, data on relationships between sire ornaments (or other measures of attractiveness) and offspring fitness components (viability, life history, physiological, behavioral - any type of traits really, as long as there is evidence, or at least a sound reason to believe, that they are related to fitness); data on heritability of ornaments (or other attractiveness measures), or data on genetic correlations calculated from full sib - half sib experiments or animal model - are of interest for us.

Should you have access to such data in any form - e.g. unpublished manuscript / thesis / unanalysed raw data file etc., but also published papers (we are conducting a Web of Science search but may not be able to retrieve each and every one relevant paper this way) - we would be most grateful if you could share it with us. We will obviously cite your contribution in the resulting publication.

We need the following information for our work:

- a measure and direction of the relationship in question (results of Pearson's correlation, regression, t test, ANOVA, chi square test, or any other test as long as the exact P value is given - or raw data),

- how were the attractiveness-related and fitness-related traits measured,

- number of sires and offspring included,

- breeding scheme (observational or experimental),

- whether paternity was certain (experimentally controlled or genetically confirmed) or if not, what is the frequency of extra-pairyoung in the population on which the study was conducted (if known),

- environmental conditions sires were raised in (natural/seminatural, benign laboratory or harsh laboratory conditions)

- environmental conditions offspring were raised in (as above)

- any other important details on study design

If you know other researchers who may have access to such data, please forward this e-mail to them.

Thank you very much in advance for any help you can provide.

Zofia Prokop (zofia.prokop@uj.edu.pl), Lukasz Michalczyk, Szymon Drobniak, Magdalena Herdegen & Jacek Radwan

–

Zofia Maria Prokop PhD student Molecular and Behavioral Ecology Group Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland

Zofia Prokop <zofia.prokop@uj.edu.pl>

## Gypsy database

Dear EvolDir members,

I am glad to announce that the second release of the Gypsy Database of mobile genetic elements (GyDB) has been recently launched. The GyDB is a research project devoted to the evolutionary dynamics of viruses and transposable elements based on their phylogenetic classification (per lineage and protein domain). It is powered by MediaWiki (Wikipedia's wiki platform) and open to all researchers interested in the field. Registration and use of GyDB is completely free of charge, and allows users to edit and add new articles, correct entries, or provide more information related to existing articles. The GyDB offers a peer-reviewed system ran by a staff of curators in order to keep the information accurate and up-to-date. All articles provide a "Discussion" tab where registered users may exchange ideas or provide the rationale for their contributions. Registration also gives you access to "GyDB People", a social network for GyDB collaborators, where you can customize your profile, create a blog or send and receive messages and chat online with other registered users. Additionally, users can choose to keep both their personal information and their articles public or private (this is especially useful for rough edits and works in progress).

You can access the GyDB with the following URL: http://gydb.org Feel free to explore the site. All the GyDB staff are looking forward to seeing you contribute and enrich the discussion on the site.

This second release of GyDB has an associated publication in Nucleic Acids Research: Nucl. Acids Res. (2011) 39(suppl 1): D70-D74 doi:10.1093/nar/gkq1061 http://nar.oxfordjournals.org/content/39/suppl_1/-D70.abstract – Alfonso Muñoz-Pomer Fuentes Polytechnic University of Valencia Department of Information Systems and Computation

alfonso.munozpomer@biotechvana.com

## Haplotype network using amino acid sequences

Hello

I am looking for a program which can be used to build a haplotype network using amino acid sequences rather than nucleotides. Any tips would be appreciated.

Best wishes

Alejandro

Alejandro Gonzalez Voyer Post-doc

Estación Biológica de Doñana (CSIC) Avenida Américo Vespucio s/n 41092 Sevilla Spain

Tel: +34- 954 466700, ext 1749

E-mail: alejandro.gonzalez@ebd.csic.es

Web-site: https://docs.google.com/-View?id=3Ddfs328dh_14gwwqsxcg alejandro.gonzalez@ebd.csic.es

## Isolation Microalgal DNA

Hello all,

I would be grateful to hear about effective protocols for the preservation of microalgal cultures for DNA analysis (for basic PCR and sequencing) and for isolation of microalgal genomic DNA (for those same types of applications).

Thanks in advance, Andres Lopez - jalopez2@alaska.edu

andresl.fish@gmail.com

## Kovalevskaja Award

Dear All,

There is a Sofja Kovalevskaja Award by the Alexander von Humboldt Foundation, "offering promising young researchers from all over the world attractive career prospects in Germany. Junior research talents of all disciplines from abroad are given the opportunity to establish working groups of their own at German research institutions." The Sofja Kovalevskaja Award is up to 1.65 million EUR and enables each winner valuable starting capital to spend five years pursuing an innovative research project at a research institute of his or her choice.

Outstanding junior academics of all disciplines who completed their doctorate less than six years ago are eligible to apply for the Sofja Kovalevskaja Award. German researchers have to have been working abroad for more than five years. Applications must be submitted by 1 September 2011.

Details of the application procedure for the Sofja Kovalevskaja Award can be found on our website at: www.humboldt-foundation.de/skp_en. For individual questions, you are also welcome to contact info@avh.de.

forwarded by: Klaus Reinhardt Advanced Fellow - VolkswagenStiftung University of Tuebingen http://www.uni-tuebingen.de/?id=14671 University of Sheffield Dept Anim & Plant Sciences http://e3.group.shef.ac.uk/people/klaus-reinhardt/ Klaus Reinhardt <k.reinhardt@sheffield.ac.uk>

## London LinneanLecture Apr14

The Fourth Annual Systematics Association/Linnean Society Biodiversity Policy Lecture

Dr Peter Bridgewater Chair, Joint Nature Conservation Committee "Seeing REDD: Science, Policy and Politics in Biodiversity and Climate Change

14 April 2011, 6pm Linnean Society of London, Burlington House, Piccadilly, London, W1J 0BF Tea will be served in the Library from 5.30pm and the lecture will be followed by a wine reception.

In late October 2010 The Convention on Biological Diversity held its tenth meeting, regarded as successfully achieving a new target for 2020, having missed the target set for 2010. As the abstract is being written preparations are in hand for the 16th meeting of the Framework Convention on climate Change, to be held in Cancun, December 2010. A key issue for both conventions is that or Reducing Emissions (of carbon) from Deforestation and (forest) degadation (REDD). This has morphed to REDD+ in recent discussions, where the plus includes conservation measures for forests. This has led to discussions about where the discussions and decisions on forest, carbon and biodiversity should be conducted within the UN system. And it ignores the inconvenient truth that while forests are a significant carbon moderator there are other ecosystems on earth! This lecture will explore the links between biodiversity and climate change, the avenues for sensible national and international discussion and the likely policy outcomes for biodiversity in the coming decades.

For further information see http://www.systass.org/news/index.shtml#BiodiversityPolicyLecture2011 james.cotton@sanger.ac.uk

## Macroevolutionary Videos

We hosted a Centre for Ecology & Evolution symposium on Integrating Ecology into Macroevolutionary Research on 9th March at the Zoological Society of London.

The event was filmed in association with the Wiley-Blackwell journal, Methods in Ecology & Evolution.

Most of the day's talks can now be viewed online at

www.vimeo.com/cee2011< http://www.vimeo.com/cee2011 >

Enjoy!

Lynsey McInnes & Albert Phillimore

Lynsey McInnes PhD Student Imperial College London Silwood Park Campus

http://www.bio.ic.ac.uk/research/apurvis/lynsey.htm http://www.justgiving.com/offset_silwood_carbon "McInnes, Lynsey" <lynsey.mcinnes01@imperial.ac.uk>

## Misinterpretation of molecular phylogenies

Dear colleagues,

Would you please provide me any examples when someone in his paper misinterpret results of molecular phylogenetic analysis published by other authors either challenging or accepting it. I need it for a lecture but can't use the examples that I know because they concern people who will attend this lecture.

Thank you very much in advance, Alexei Kostygov.

Laboratory of Molecular Systematics, Zoological Institute of the Russian Academy of Sciences Angliyskiy pr. 32 190121, St.-Petersburg, RUSSIA e-mail: kostygov@gmail.com tel.: +78127140404

kostygov@gmail.com

## MrBayes bug

Dear all,

I am having a weird problem with the sump command in MrBayes. Everytime I try to summerize the parameters it returns an error message "Non-matching headers in file 2. Error in command Sump". I know there is a patch for this bug. Compiling the source code and patching this is beyond my capabilities. I would apprecite if someone could email me an already patched executable.

Thank you very much,

Cheers, Kartik Sunagar * – Kartik Sunagar Research Fellow, Laboratory of Ecotoxicology, Genomics and Evolution University of Porto, Portugal Tel : (351) 933634324

Home Page: www.kartik.co.nr Wildlife Photography: http://kartiks.weebly.com/my-photography.html and www.flickr.com/photos/kartik_s The Snake Planet: www.snake-planet.co.nr Kartik Sunagar <anaturalist@gmail.com>

## MSI Faculty SabbaticalOpportunity

Sabbatical opportunity in evolutionary biology for MSI faculty

The US National Evolutionary Synthesis Center (NESCent) is an NSF-funded evolutionary biology research center in Durham, NC representing a partnership of Duke University, North Carolina State University and The University of North Carolina at Chapel Hill.

As part of NESCent's commitment to increasing diversity in evolutionary biology we offer targeted sabbatical opportunities to evolutionary biologists from Minority-Serving Institutions (MSIs) to undertake projects that will increase minority participation in evolutionary science and/or develop evolution education activities.

NESCent provides stipends up to the equivalent of a full salary (monthly stipend equal to 1/12th of a 9-month salary at home institution). A housing allowance up to $1,000/month can also be provided.

Deadlines for NESCent Targeted Sabbaticals are July 10th and December 1st each year. For more information and to apply, please see http://www.nescent.org/science/targetedsabbatical.php or contact Dr. Jory Weintraub (jory at nescent dot org).

Jory Weintraub <jory@nescent.org>

## NESCent CallforProposals

CALL FOR PROPOSALS - SABBATICAL SCHOLARS, WORKING GROUPS AND CATALYSIS MEETINGS

Proposals for Sabbaticals, Working Groups and Catalysis Meetings are now being accepted at The National Evolutionary Synthesis Center (NESCent). We are looking to support innovative approaches to outstanding problems in evolutionary science. In particular, proposals that have a clear interdisciplinary focus, or involve evolutionary concepts in non-traditional disciplines, are strongly encouraged, as are proposals that demonstrate international participation and a mix of senior and emerging researchers, including graduate students. Proposals are accepted twice a year, with deadlines on July 10 and December 1. Proposals for Sabbaticals may be for up to a full year. We also accept proposals for short-term visits (2 weeks to 3 months; deadlines on January 1, April 1, July 1 and September 1). For more information, please see our website at https://www.nescent.org/science/proposals.php . Craig R. McClain, Ph.D. Assistant Director of Science National Evolutionary Synthesis Center 2024 W. Main St., Suite A200 Durham, NC 27705 phone: 919-668-4590 cmcclain@nescent.org

Associate Editor for Journal of Biogeography: http://www.wiley.com/bw/journal.asp?ref=0305-0270&site=-

1 Deep-Sea News: http://deepseanews.com Homepage: http://www.duke.edu/˜cm171 McClain Craig <cmcclain@nescent.org>

## NESCent EvolutionVideoContest

Call for entries: NESCent announces Evolution Video Contest Application deadline: Friday June 10, 2011

Submit your best evolution-themed video for screening at this years Evolution meeting! The National Evolutionary Synthesis Center (NESCent) invites scientists of all stripes X graduate students, postdoctoral fellows and faculty X to enter the first-ever evolution video competition.

To enter, submit a video that explains a fun fact, key concept, compelling question, or exciting area of research in evolution in less than three minutes. Entries may be related or unrelated to your own research, and should be suitable for use in a classroom at any level (K-12, undergraduate, graduate...your choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini-documentaries are all fair game.

Selecting the winners A panel of reviewers from both NESCent and the science video community will select the semi-finalists, who will be notified by e-mail. The top finalists will then be screened at a film festival at the 2011 Evolution meeting in Norman, OK, from 6:30 to 7:30 PM on Monday June 20th. After screening the videos, the audience will vote for their favorites. Prizes will be awarded for the top entries.

Eligibility

You dont need to attend the conference to submit an entry. All videos submitted by Friday June 10th (5:00 p.m. ET) are eligible to win. For more information and full contest rules, please see http://www.nescent.org/eog/videocontest.php or contact Dr. Jory Weintraub at jory@nescent.org, or Dr. Robin Smith at rsmith@nescent.org.

Jory P. Weintraub, PhD Assistant Director, Education and Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200 Box 104403 Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub Web: www.nescent.org

Jory Weintraub <jory@nescent.org>

## PCR samples methylated spirits

Dear All,

We are experiencing problems with DNA extraction and PCR of beetle samples stored in methylated ethanol. The samples were collected as a part of citizen science project, and were stored in the type of ethanol-based fuel used in camping cookers. Rumour has it that other labs have had similar problems when using more exotic cocktails as storage agents, and that someone has invented a trick to solve this . If anyone knows more about it, please drop me a line.

The exact content of the stuff that we have used is the following: Ethanol 90-100 % Propan-2-ol 1-5 % Methyl ethyl ketone 2 % Methyl isobutyl ketone 2 %

Thank you for your help, Tomas Roslin

Dr Tomas Roslin, University Lecturer

Spatial Foodweb Ecology Group Department of Agricultural Sciences PO Box 27 (Latokartanonkaari 5) FI-00014 University of Helsinki Finland

Phone: +358 9 191 57659 Fax: +358 9 191 58582

web pages: http://www.helsinki.fi/science/metapop/foodwebs/ http://www.helsinki.fi/science/metapop/People/Tomas.htm Tomas Roslin <tomas.roslin@helsinki.fi>

## Phyloseminar Tues26

Please come to a free online seminar next week:

Mike Lin speaks Tuesday, April 26th at 12pm PST on “Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes”

Abstract: The degeneracy of the genetic code allows protein-coding DNA and RNA sequences to simultaneously encode additional, overlapping functional elements. A sequence in which both protein-coding and additional overlapping functions have evolved under purifying selection should show increased evolutionary conservation compared to typical protein-coding genes – especially at synonymous sites. We developed a method to systematically locate short regions within known ORFs that show conspicuously low estimated rates of synonymous substitution, based on phylogenetic codon rate models and likelihood ratio tests.

We applied this method to genome alignments of 29 placental mammals, resulting in more than 10,000 synonymous constraint elements (SCEs) with resolution down to nine-codon windows. These are found within more than a quarter of all human protein-coding genes and contain ˜2% of their synonymous sites. We collected numerous lines of evidence that the observed synonymous constraint in these regions reflects selection on overlapping functional elements including splicing regulatory elements, dual-coding genes, RNA secondary structures, microRNA target sites, and developmental enhancers. We also ruled out certain alternative explanations such as codon usage bias and neutral rate variation.

Our initial results show that overlapping functional elements are common in mammalian genes, despite the vast genomic landscape. Furthermore, anticipating the future availability of additional mammalian and vertebrate genomes, we are currently developing Bayesian codon modeling methods to measure synonymous rates at even higher resolutions, perhaps eventually allowing the detection of individual regulator binding sites embedded in protein-coding ORFs.

Japan 04:00 (04:00 AM) on Wednesday, April 27 New Zealand 07:00 (07:00 AM) on Wednesday, April 27 West Coast USA 12:00 (12:00 PM) on Tuesday, April 26 East Coast USA 15:00 (03:00 PM) on Tuesday, April 26 England 20:00 (08:00 PM) on Tuesday, April 26 France 21:00 (09:00 PM) on Tuesday, April 26

For more information on how to attend this and other seminars, visit www.phyloseminar.org . Erick Matsen <matsen@fhcrc.org>

## Pruning taxa across trees

Dear colleagues,

I would like to prune the same set of taxa from a sample of trees (˜5000) obtained with BEAST 1.6.1 but I don't seem to find an easy way to do this without having to remove the taxa in every tree one by one. I have tried using drop.tip function in R but does not seem to do the job; it does not recognise the set of phylogenies as a phylo object (either when loaded as nexus or newick format, which I guess is due to the file having more than one tree as drop.tip works fine with a single tree loaded), although R recognises correctly the number of phylogenetic trees. I have also tried the "sapply" function with drop.tip, but again when I try to save the supposedly pruned trees into a file, or plot any of them, I get an error message. So my question is simple, does anyone know how to prune taxa from a sample of trees in R or in any other Mac-friendly programme?

Thanks a lot.

Cheers,

Ramiro

–

Dr. Ramiro Morales-Hojas Molecular Evolution Lab Instituto de Biologia Molecular e Celular (IBMC) University of Porto Rua do Campo Alegre 823 4150-180 Porto Portugal

e-mail: rmhojas@ibmc.up.pt tel.: +351226 074 900 ext 1612

rmhojas@ibmc.up.pt

## RevBayes Icon Design Contest

A number of evolutionary biologists are working on the successor to the MrBayes program. The new program is to be called RevBayes. It has an R-like language for specifying evolutionary models and performs Bayesian estimation of the parameters (using Markov chain Monte Carlo to do the numerical summation/integration).

This is to announce a contest for an icon for the program. The winner of the best design will receive $500. Entries must be received by July 15, 2011. Please send your entry to johnh@berkeley.edu.

Keep in mind that the icon should be in digital form, of high quality, and be distinctive even when it is small. Contestants should look at Apple's icon design considerations:

http://developer.apple.com/library/mac/-#documentation/UserExperience/Conceptual/-AppleHIGuidelines/XHIGIcons/XHIGIcons.html
The judges will consist of members of the core RevBayes development team.

– The RevBayes Development Team

John Huelsenbeck <johnh@berkeley.edu>

## Roommate ASM

Greetings!

I will be attending the general meeting of the American Society for Microbiology in New Orleans, LA (May 21-24). It's been really difficult to find accommodation at this time so I am looking for an attendee who would be willing to share the costs of housing with me. If interested and to discuss specifics please contact me at rcguerr@emory.edu.

Thanks!

Ricardo C. Guerrero, PhD Emory University School of Medicine Division of Pediatric Infectious Diseases

Emory Children's Center 2015 Uppergate Dr NE, Suite 560 Atlanta, GA 30322 Lab: +1 404-727-3752 Office: + 1 404-727-0039 Dept. Office: +1 404-727-5642 Fax: +1 404-727-9223

"Guerrero, Ricardo C." <rcguerrero@emory.edu>

## RoyalSociety CommunityGenetics

Royal Society Publishing has just published Community genetics: at the crossroads of ecology and evolutionary genetics compiled and edited by Jennifer K Rowntree, David M Shuker and Richard F Preziosi. See - http://rstb.royalsocietypublishing.org/site/2011/community-genetics.xhtml for further details or you can go straight to the issue contents at http://rstb.royalsocietypublishing.org/content/366/1569.toc The print issue is available at the special price of Â£47.50. You can order this online via the above web page (enter special code TB1569 when prompted) or, alternatively, you can contact debbie.vaughan@royalsociety.org

PLEASE NOTE NEW POSTAL ADDRESS BELOW

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felicity@tou-can.co.uk

## Seminar questions

Dear all,

There was an evoldir discussion / post on a taxonomy of questions asked during seminar ("types of questions", or something to that effect). The discussion ran over 10 years ago, and now I don't seem to be able to find the text and whoever wrote it.

Does anyone know what I am talking about? Can you send it to me?

Sorry for the apparently frivolous posting, but it was a truly excellent write up and I wonder if someone still has that text.

Best,

Sarah

sarah.vogel.max@gmail.com

## Software AFLPOP v1 2

Dear evoldir members,

AFLPOP was designed primarily to solve the population allocation problem based on AFLP markers: Given an AFLP genotype and a set of candidate populations defined by AFLP samples, what population is the genotype most likely to belong to?

A new version (1.2) of AFLPOP is now available. The functionalities provided in AFLPOP 1.2 are exactly the same as those implemented in AFLPOP 1.1. However this new version may be run on a much broader set of operating systems (OS) and OFFICE versions.

Users are invited to make suggestions and report bugs by sending e-mails to either Pierre.Duchesne@bio.ulaval.ca or Julie.Turgeon@bio.ulaval.ca.

Also, the latest version of AFLPOP can be downloaded free of charge at:

http://www.bio.ulaval.ca/no_cache/departement/-

professeurs/fiche_des_professeurs/professeur/11/13/ (scroll all the way down to ≪ Téléchargement : ≫)

Julie Turgeon Pierre Duchesne Département de biologie Université Laval 1045 ave. de la Médecine (Vachon 3048) Québec, Québec Canada G1V 0A6 Tel: (1) 418-656-3135 Fax: (1) 418-656-2043 julie.turgeon@bio.ulaval.ca

## Software PAPA AFLP

Dear evoldir members,

We wish to announce the first version of the parental allocation program PAPA_AFLP (1.0).

PAPA_AFLP is designed to allocate parental pairs on the basis of AFLP genotypes. It is assumed that the allocation system is either closed or semi-closed. A closed allocation system is one in which all offspring have their two parental genotypes included in the parental files. A semi-closed allocation system is one in which the number of missing parental genotypes is small and is known precisely or nearly so for each parental file. An example of a semi-closed system: all putative parents have been kept in captivity prior to breeding but the genotypes of some of the parents are not available due to lab problems or mortality. The parental genotypes may be sexed or non-sexed. Also, they may come from one or two populations. This feature is especially useful when studying hybridization between pairs of populations. Both allocations of real offspring and simulations may be performed. Simulations provide an estimate of the proportion of correct allocations.

A User Guide is provided which describes the uses, working principle, procedures, formats and parameters in PAPA_AFLP. Its interface is user-friendly and similar to that of AFLPOP (Duchesne & Bernatchez 2002). Users are invited to make suggestions and report bugs by sending e-mails to either Pierre.Duchesne@bio.ulaval.ca or Julie.Turgeon@bio.ulaval.ca.

Potentials users may download free copies of PAPA_AFLP directly from: http://www.bio.ulaval.ca/no_cache/fr/departement/professeurs/fiche_des_professeurs/professeur/11/13/ (scroll all the way down to ≪ Téléchargement : ≫)

Reference: PAPA_AFLP was developed and first used in a paper currently in preparation and which is part of Marie-Claude Gagnon's PhD thesis at Université Laval (Quebec City, Canada). Please verify the final reference for this paper in order to cite PAPA_AFLP.

Julie Turgeon Pierre Duchesne Département de biologie Université Laval 1045 ave. de la Médecine (Vachon 3048) Québec, Québec Canada G1V 0A6 Tel: (1) 418-656-3135 Fax: (1) 418-656-2043 julie.turgeon@bio.ulaval.ca

## SouthAfrica 2 Volunteers SmallMammalEvolution

2 volunteers needed from July / August to November / December 2011 onwards

as field assistants for the project:

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

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to evolution, ecology and behavior before starting an MsC or PhD project.

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

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o‘ clock), and stops its activity with dusk (19 o‘ clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers are also expected to help with maintenance of the research station (water pump, solar power, etc.)

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

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1000 (around 150 US$, 110 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 190 US$, 140 Euro) per month applies. Students must buy their own food etc in Springbok (costs of about R 2250, approx. 340 US$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 550 US$, 450 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SSJARP in Switzerland).

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

When and how long: At the moment we are looking for 2 volunteers for the period July / August to November / December. Volunteers are expected to stay at least 4 months, but longer periods of up to 6months are possible.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@ieu.uzh.ch.

More information under http://www.ieu.uzh.ch/research/behaviour/endocrinology.html Contact via e-mail: carsten.schradin@ieu.uzh.ch

Dr. Carsten Schradin

Research Assistant, Department of Animal Behavior,

University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland.

Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences,

University of the Witwatersrand, South Africa.

WORKING AS A FIELD ASSISTANT IN GOEGAP NATURE RESERVE

A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

Blue skies without a single cloud for six weeks rocky mountains with little vegetation yellow, orange and pink fields of flowers in whatever direction you look small mammals, lizards and birds in our front yard and Mountain Zebras, Springbok and Ostrich right next door...

This was my time at the Succulent Karoo Research Station in Goegap Nature Reserve in South Africa! During six weeks from the beginning of July until the middle of August I've been living here, studying mice, experiencing nature like never before and being part of a small community where there was always something to laugh and joke about!

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I improved quickly shaking the mice out of the traps, weighing them and checking the number of the ear tag. Other duties like cleaning the cages of

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## Spectrophotometer LightSource

Dear all,

I'm currently considering purchase of Ocean Optics Jaz spectrophotometer but I'm wondering which light source would be the best? The main use of the spectrophotmeter will be reflectance measurements of bird plumage both in UV and VIS range. Two possible solutionas are tungsten-deuterium light source and xenon pulsed source, more less equally frequently reported in papers. I would really appreciate any recommendations and advantages of using either of these sources.

Cheers, sz.d. szymek.drobniak@uj.edu.pl

– Szymon Drobniak || Population Ecology Group Institute of Environmental Sciences,Jagiellonian University ul. Gronostajowa 7, 30-387 Kraków, POLAND tel.: +48 12 664 52 19 fax: +48 12 664 69 12

www.eko.uj.edu.pl/drobniak geralttee@gmail.com

## Spectrophotometer LightSource answers

Hi all,

about 2 weeks ago I posted several questions about JAZ OCean Optics spectrophotometer. I was wondering which light source (deuterium-tungsten or xenon pulsed) would be the most appropriate. First of all - I'd like to thank everyone who answered my concerns - you're comments were very useful and valuable :) From what I've received it seems clear that both light sources have pros and cons. Deuterium one: requires up to 30 min warm-up (which may be annoying) and generates significant amounts of heat, however offers very stable and smooth emission spectrum; xenon one is operational without warm-up and seems to require less power (which would be precious in field applications) but generates constant (although not very loud) noise and has more irregular emission spectrum. For me it's clear that PX-2 (xenon source) is better. As one of You mentioned, with PX-2 one has to be careful as the light seems to contain different amounts of shorter wavelengths right after turning on and later after several minutes so it's a good idea to take several measurements and average the spectra. Importantly I was reassured that JAZ with either PX-2 or DT does not require any additional powering module apart from the one powering the spectrophotometer.

Thanks for all your remarks! Cheers, szymek

– Szymon Drobniak || Population Ecology Group Institute of Environmental Sciences,Jagiellonian University ul. Gronostajowa 7, 30-387 Kraków, POLAND tel.: +48 12 664 52 19 fax: +48 12 664 69 12 szymek.drobniak@uj.edu.pl

www.eko.uj.edu.pl/drobniak geralttee@gmail.com

## Tree class

Anyone have experience in Python or in writing a tree class. I am particularly stuck on how to parse the tree (in newick format) and how to join the node class and edge class together. Can anyone help?

Aj

Wasiu Akanni <waakanni13@gmail.com>

## UNewSouthWales VolunteerAvianFieldAssistant

Two volunteer field assistants are needed to assist multiple PhD projects on the chestnut-crowned babbler during the 2011 breeding season. Primary duties will include assisting with mist-netting and field experiments, monitoring groups for breeding activity, and data entry. The work will often require starting before dawn and days off will be irregular and dependent on the weather.

The study site is located in western New South Wales, within a research station owned and run by UNSW. The station is approximately 90 minutes' drive from the nearest settlement, and visits there are generally limited to food and equipment shopping.

Successful applicants will need to be able to work independently and in a team, as well as being physically fit and having a tolerance for working in extreme environments. A positive attitude and enthusiasm for the work is essential. Previous experience working with birds, particularly mist-netting experience, would be an asset. The position would suit recent graduates from a relevant discipline that wish to develop their field experience or understanding of ecological research.

The dates of the position are approximately 20th July - 20th October with a possible extension into November depending on the quality of the breeding season.

There is no salary for the position, but food and accommodation at the station will be provided. Assistants must cover their own transport costs to and from the field station. To apply, email a letter of interest (include dates of availability), resume, and contact information for three referees to JAMES SAVAGE (jls59@cam.ac.uk). Applications will be reviewed as they are received; the closing date is Friday 6th of May.

James Savage <jls59@cam.ac.uk>

## Viral mutation rates

An on-line resource containing empirical estimates of the spontaneous mutation rate for viruses in now available at

www.uv.es/rsanjuan/virmut This dataset was published in a review paper last year (Sanjuán et al. 2010 J Virol 84: 9733-9748) and will be reguarly updated.

Please contact me if you know additional estimates and want them to be included.

Rafael Sanjuán, Ph.D. Institute Cavanilles for Biodiversity and Evolutionary Biology University of Valencia, Spain Tel: +34 963 543 270 E-mail: rafael.sanjuan@uv.es Web: www.uv.es/rsanjuan Address: Institut Cavanilles de Biodiversitat i Biologia Evolutiva Parc Cientific de la Universitat de Valencia C/ Catedratico Agustin Escardino n 9 46980 Paterna, Valencia Spain

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## Volunteer FieldAssist MadagascarLemurs

Volunteer Field Assistant for a Lemur Diet Study in Madagascar

Hiring Organization: PhD student, University of Southern California

Date Posted: 2011-04-13

Position Description: I am searching for a volunteer field assistant to work on a study of the diet of wild lemurs. This project, which is a part of my doctoral research, will study the effect of diet on the gut bacteria in two species of wild lemurs: the ring-tailed lemur (Lemur catta) and Verreauxâs sifaka (Propithecus verreauxi). Specifically, I will be investigating the effect of ingested plant chemical defenses on the lemursâ gut bacteria. The field assistant will be involved in observations of the lemurs, identifying plant species, recording their feeding behavior, as well as collecting samples of the plants they consume. The field assistant will also help collect fecal samples from the lemurs, which will be preserved for later analysis of the bacteria present. The assistant will be trained in all relevant data collection and archiving methods. This position provides an excellent opportunity to gain serious experience in fieldwork, animal behavior research, and behavioral ecology methods.

The work days will be long, heading into the forest around 7am and finishing around 6pm. We will come back to camp for a brief lunch around mid-day. Additional time entering the dayâs data may be required in the evening. We will work 6 days a week, with 1 day off to take care of laundry, relax, and read. Fieldwork will be from September 2011 through February 2012.

The field site, Beza Mahafaly special reserve, is a tropical dry forest in southwest Madagascar. The terrain is flat, but the wet season (approximately November through February) will be hot and humid, with brief rain daily. There is a grid system of trails through the forest (making it difficult to be lost for long), but we will often go off-trail to find and follow the lemurs. There are many plants with thorns and spikes in the forest, but there are few lethal creatures (you will definitely encounter some wasps and spiders). There are many groups of both lemur species in the forest and most individuals have been collared and tagged for easy identification. Two other species of lemur (the grey-brown mouse lemur and the white-footed sportive lemur), Indian civets, feral cats, tortoises, as well as many bird and insect species also live in the forest. Accommodations at the field site are rustic but adequate (tents, pit toilet, solar showers, well water, little solar electricity for charging electronics). A local cook will cook all of our meals (mostly rice and beans). Communication is limited at the field site. There is no internet and some cellphone reception can be gained by a 20-minute walk from camp. I am hoping to have a satellite phone for emergencies. There are several villages nearby, but the closest town with services is a 6-hour walk or cart ride.

Qualifications/Experience: Intended for undergraduates or early graduate level students specializing in Biology, Animal Behavior, or Anthropology. Other areas of specialization will be considered. This job presents the ideal opportunity for individuals with a Bachelorâs or Masters degree that are hoping to go on into postgraduate research but require field-experience. Existing fieldwork experience is therefore not required, but experience working in tropical forests, working with animals, and/or working in the outdoors will be beneficial. Successful applicants will have an excellent level of physical fitness and be able to work independently under isolated and demanding conditions (10 hour days, 6 days a week) in a hot and humid environment. The position is not ideal for someone who needs a lot of personal time, or for someone who easily feels lonely.

The ideal applicant will: â Have a strong interest in animal behavior or ecology; â Have experience working on a scientific research project, collecting and working systematically with data, ideally an observational/behavioral project and will understand the scientific method; â Be hardworking and motivated; â

Be comfortable being unplugged and a distance from easy communication with the outside world (limited phone and no internet access); â Feel comfortable being far away from family and friends for an extended period of time; â Have above average resistance to social/psychological stress with a tolerance towards local customs and beliefs and be comfortable with other conditions and risks that are simply part of tropical fieldwork, such as limited healthcare, monotonous diet, and rare confrontations with noxious plants or animals; â Be responsible, reliable, a team player able to work out any issues civilly, and able to follow field procedures carefully; â Have previous experience with animal behavior in general, or primates in specific; â Have experience traveling or living in a foreign country, preferably in developing countries;

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# PostDocs

## ArizonaStateU LizardGeneticVariation

Postdoctoral Fellowship in Mechanistic Niche Modeling and Climate Change Impacts School of Life Sciences, Arizona State University

A postdoctoral position is anticipated as part of a collaborative project to develop and evaluate mechanistic niche models that incorporate geographic variation in physiological traits of lizards. The post doc will be based in Michael Angilletta's laboratory at Arizona State University, but will interact with members of Lauren Buckley's lab at the University of North Carolina in Chapel Hill and Tim Keitt's lab at the University of Texas in Austin. The post doc will be expected to engage in modeling activities and coordinate lab studies of thermal physiology. Experience with mathematical modeling in C++, MATLAB, Python or R is beneficial and familiarity with environmental data and biophysical ecology is beneficial. The position will be awarded for one year with the possibility of renewal for additional years. To apply, please e-mail a single pdf file containing a cover letter, a curriculum vitae, a statement of research interests, representative publications, and a list of references to the following address: Michael.Angilletta@asu.edu. Review of applicants will begin immediately and will continue until the position is filled. This position is contingent on final approval of funding from NSF. A background check is required for employment. Arizona State University is an equal opportunity/affirmative action employer committed to excellence through diversity. Women and minorities are encouraged to apply https://www.asu.edu/titleIX/ .

Lauren Buckley UNC Chapel Hill, Department of Biology | www.unc.edu/˜lbuckley | buckley@bio.unc.edu | (919) 843-8732

“Buckley, Lauren Beth” <Buckley@bio.unc.edu>

## Bergen FishEvolutionaryGenetics

Post Doctoral position: Modeling genetic interactions between wild and farmed fish

The Institute of Marine Research has a two-year post doctoral research position available to work with modeling genetic interactions between wild and farmed fish. The position will be connected to the Population Genetics and Ecology research group in Bergen. The position will be linked to the modeling work-package in the Strategic Institute Project “INTERACT”, financed by the Norwegian research council. Building upon published data, current models and state-of the art, the work-package aims to advance models to quantify the interactions between wild and farmed fishes, for both Atlantic cod and Atlantic salmon. The ultimate aim is to identify “break points” for tolerance of genetic introgression in wild populations.

Together with members of the research team, the appointee will have responsibility for establishing, testing and publishing new models that shed light onto the consequences of farmed escapees and tolerable levels of introgression in wild populations. This will be achieved through developing models describing dynamics of wild salmon and cod populations that are interacting and potentially interbreeding with conspecific fish of aquaculture origin. Important parameters to be tested include numbers of escapees, fitness of hybrids, and behavioural interactions between wild and cultured fish.

We wish to appoint a highly motivated person with a PhD in modeling, statistical genetics, population ecology or related discipline. The appointee will need to be able to document experience of programming and use of models to study dynamical systems in biology. Previous experience with modelling of fish population dynamics is not necessary but is considered advantageous.

The Institute emphasises personal qualities such as good communication and cooperative skills, the ability to work independently and as part of an active research team. A record of publishing in this field will be considered and advantage.

We offer:

* a positive, challenging and creative work environment * the opportunity to work in a national institute with a high level of international contact * flexible hours, a good pension scheme and a wide range of welfare services. The Institute offers governmental regulated salaries as post doctor (code 1352 post doctor). Roughly, this salary equates to approximately 45 000 UK pounds per year (forty five thousand uk pounds).

For more information, please contact project leader Kevin Glover, email: Kevin.glover@imr.no, Tel: +47 4755236357 or research group leader Terje Svaasand, email: Terje.svaasand@imr.no, Tel: +47 55236891, or visit our web-site at www.imr.no The Institute of Marine Research is an “inclusive work-life” employer that encourages diversity, and we encourage all qualified candidates to apply for this position. Women are particularly encouraged to apply.

Please note that information about applicants may be made public even if an applicant has requested to be left off the list of applicants. Applicants will be notified about this in advance

Please apply in writing, enclosing a cover letter, full CV, copies of relevant recommendations and academic transcripts together with a set of publications, to: Institute of Marine Research, Personnel Division, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway. Application number: “11-11”. Closing date for applications: 27.04.11.

kevin.glover@imr.no

## Cardiff PopulationGenomics

Postdoctoral Research Associate in Population Genomics

A position is available for a Postdoctoral Research Associate to join the Bruford laboratory at Cardiff School of Biosciences, a multidisciplinary team focussing on understanding the determinants of genomic diversity and structure in endangered wild and domestic species.

Funded by grant from the European Commission, the appointee will work in the Nextgen research project http://nextgen.epfl.ch/, undertaking population genomics analysis of livestock and their wild ancestors using a combination of high density SNP and whole genome data for cattle sheep and goats in a variety of environments and production systems. Specifically, the appointee will examine genome-level diversity and selection in wild and domestic sheep from North Africa and the Middle East

The successful candidate will have a PhD in population genetics or genomics, plus experience of handling genome-scale datasets and the major bioinformatics software packages for genomes.

The position is fixed term for a period to 31 March 2014, available immediately. Job specifications can be found at http://www.cf.ac.uk/jobs/ Salary: £29,972 &#8211; £35,788 per annum, (Grade 6).

Informal enquiries can be made to Professor Mike Bruford, BrufordMW@cf.ac.uk

Michael Bruford <BrufordMW@cardiff.ac.uk>

## DrexelU BacterialRolesInAntEvolution

Job description:

The Russell lab at Drexel University seeks a postdoctoral researcher for a position spanning June 2011-February 2014. This NSF funded research (NSF Award ID: DEB-1050360) will focus on symbioses between ants and bacterial gut associates, addressing the hypothesis that nutritional symbionts have facilitated the evolution of low-quality, herbivorous diets in the ants (for background, see Russell et al. 2009 at: http://www.pnas.org/content/106/50/21236.full). Through collaboration with PI Corrie Moreau (at The Field Museum of Natural History), one graduate student (at Drexel), and PI Jacob Russell, the postdoc will study microbial gut bacteria through the use of 454 amplicon sequencing of 16S rRNA genes, using the ant phylogeny and trophic classification to quantify the relationship between diet, relatedness, and gut community composition. The position will also involve microscopy and collaboration on experiments designed to identify the nutritional roles of gut bacteria.

Background in microbial ecology and evolution are preferable, while skills in microscopy, bioinformatics, and basic molecular biology are strongly preferred. Interested applicants should apply at www.drexeljobs.com/applicants/Central?quickFindt594, while also contacting Jacob Russell at jar337@drexel.edu to express their interest.

Dr. Jacob A. Russell Assistant Professor Department of Biology Drexel University Philadelphia, PA 19104 phone: 215-895-1643 e-mail: jar337@drexel.edu

jar337@drexel.edu

## DukeU BacteriaEvolutionaryGenomics

A Postdoc position is available in Jen Wernegreens lab at Duke University (Durham, NC) to study evolutionary and population genomics of bacteria. The project will explore the impacts of fundamental evolutionary forces (mutation, recombination, selection and genetic drift) on DNA sequences, proteins, and whole genomes of bacteria. We are especially interested in how these forces shift when bacteria adopt symbiotic lifestyles, ranging from parasitic to mutualistic. Potential projects are largely computational but may also include experimental approaches depending on interests.

Candidates should have strong training in evolutionary biology, population genetics, and/or bioinformatics, a working knowledge of UNIX/LINUX, programming skills, and familiarity with genomics software and databases. Knowledge of PERL is a plus. A Ph.D. is required before starting the position.

To apply, please email a statement of interest, CV, and names of 2-3 references to Jen Wernegreen (j.wernegreen@duke.edu).

Jennifer Wernegreen <j.wernegreen@duke.edu>

## Leipzig BacterialGenomics

Postdoctoral position: Genomic analysis of recombination and adaptation in bacteria

"Why do organisms have sex?" is a central question in evolutionary biology but one that has been difficult to study empirically. Bacteria and Archea represent the bulk of living organisms and import DNA from other strains into their genomes by diverse mechanisms. This project will use the 1000s of bacterial genomes that are becoming available to characterize the role of this recombination in adaptation. The project will make use of statistical genetic algorithms ClonalFrame and ClonalOrigin to identify individual recombination events and the genetic changes they introduce.

The project is a collaboration between Daniel Falush (Leipzig), Xavier Didelot (University of Oxford) and Eduardo Rocha (Pasteur Institute, Paris). The applicant will be based at the Max Planck Institute for Evolutionary Anthropology, Leipzig which is home to a diverse group of researchers interested in the genetics of adaptation. See: http://www.eva.mpg.de/genetics Desirable skills include knowledge of modern computationally intensive statistics, programming in C or C++, bioinformatics ability, knowledge of evolutionary biology and population genetics. However, applications are welcomed from any candidate with good quantitative skills and enthusiasm for the subject area. The initial period of employment is 2 years , with the possibility of extension. Please contact daniel_falush@eva.mpg.de to apply and for further information.

daniel_falush@eva.mpg.de

## MasseyU ComputationalBiology

Postdoctoral Position in Computational Biology (A118-11ZZ) Dr Murray Cox Institute of Molecular BioSciences, Massey University, New Zealand

A postdoctoral fellowship is now open for a highly motivated and productive researcher in the Computational Biology Research Group at Massey University, New Zealand. The successful candidate will study ways of improving the spatial and temporal resolution of genetic inferences about past human migrations. Although there is scope to accommodate existing research interests, the successful candidate will develop, implement and test new methods in statistical genetics, and apply these methods to genome-scale datasets. This research will initially be directed toward reconstructing aspects of prehistoric mobility in the Pacific region, a major focus of my research group.

This postdoctoral fellowship offers a rare opportunity to extend your research training within an internationally recognized computational biology research group, while taking advantage of New Zealand's unique natural and cultural environment. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located close to the North Island's central mountains, and presents regular opportunities for hiking, skiing, surfing and adventure sports, as well as experiencing New Zealand's unique indigenous culture. Nevertheless, my research group maintains extensive international connections, especially with colleagues in Australia, Indonesia, France and the United States, and is linked firmly into the international scientific community.

MINIMUM QUALIFICATIONS: - A Ph.D. in computational biology, bioinformatics, applied mathematics, computer science, population genetics, molecular evolution, or other relevant field. - Able to conduct independent cutting-edge research. - Proven research experience with a strong publication record. - Solid analytical, quantitative and mathematical skills. - Fluency in probabilistic modeling and statistical genetics. - Candidates should be comfortable working in a UNIX environment, have a strong programming background, and be proficient in working with large datasets.

PREFERRED QUALIFICATIONS: - Candidates with a background in interdisciplinary research, spanning both biological sciences and applied mathematics/computer science, are especially encouraged to apply. - Candidates will ideally be conversant in a compiled programming language (e.g., C or C++), a scripting language (e.g., Perl), and a statistical environment (e.g., R). - Experience with parallel computing on large clusters and/or parallel programming would be highly advantageous.

APPLICATION DEADLINE: Sunday 15 May 2011

Funding is available for two years. Preference will be given to candidates who, with the help of the Principal Investigator, are most likely to be successful in obtaining independent funding.

This position will remain open until filled, and informal inquiries may be sent to Murray Cox at <m.p.cox@massey.ac.nz>. To apply formally, please submit the following documents in PDF format at http://jobs.massey.ac.nz/ 1. A brief statement of research interests, qualifications and experience. 2. A brief statement describing i) how your career goals are consistent with the research area described above, and ii) possible directions for independent fellowship and/or grant applications. 3. A curriculum vitae, including a list of scientific publications. 4. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

Dr Murray P. Cox Institute of Molecular BioSciences Massey University Private Bag 11 222 Palmerston North 4442 NEW ZEALAND

http://massey.genomicus.com/
M.P.Cox@massey.ac.nz

## NHM London FishEvolution

THE NATURAL HISTORY MUSEUM DEPARTMENT OF ZOOLOGY

Postdoctoral Researcher Evolutionary diversification in an endangered biodiversity hotspot: the Southeast Asian peat swamp forest fish fauna'

We seek a highly motivated and productive postdoctoral researcher to work for the final year to complete a 3-year NERC-funded research project on the evolutionary history of the peat swamp forest ichthyofauna. The Southeast Asian peat swamp forests (PSF), found in the Sundaland biodiversity hotspot, are waterlogged forests that grow on a layer of dead plant material. PSF are characterized by a unique, vastly stenotopic freshwater fish community, which is adapted to highly acidic (pH as low as 3) black waters and comprises many miniature taxa and narrow range endemics, many of which have only been discovered in recent years. The successful candidate will use a multigene, molecular systematic approach to provide a robust phylogenetic framework of representative PSF fish clades, integrating relaxed molecular clock methodology and statistical phylogeography with geological and paleoclimatological data, in order to (1) reconstruct the time frame for the PSF fish diversification, (2) identify past demographic expansions and their taxonomic, geographic and temporal correlates, and (3) identify regions of elevated taxonomic and genetic diversity that contribute most to the evolutionary legacy of this unique ecosystem.

Applicants should have a broad interest in systematics and evolution and should have demonstrated the ability to work on complex and demanding projects. They should possess a PhD in molecular phylogenetics or associated areas, be physically fit enough and willing to participate in extensive fieldwork in Southeast Asia, together with a strong commitment to publication and collaborative research. The position requires experience in ichthyology, phylogenetic systematics, and population genetics, Outstanding molecular (PCR, cloning, sequencing), and computational skills are essential and knowledge of statistical phylogeography and GIS based approaches would be advantageous. The successful candidate will be supervised by Dr Lukas Rüber (Department of Zoology, The Natural History Museum), and co-supervised by Dr Ralf Britz (Department of Zoology, The Natural History Museum).

This NERC-funded position is available for 1 year with ideally a starting date of 1 July 2011, although there is some flexibility. The salary is GBP £27,339 per annum plus benefits.

Applications including a short CV, list of publications, names of three referees willing to provide a letter of recommendation upon request, and a brief statement of interest and qualification should be sent to l.ruber@nhm.ac.uk

Closing date for applications: Friday 20 May, 2011.

Dr Lukas Ruber Department of Zoology The Natural History Museum Cromwell Road London SW7 5BD UK

Tel: +44 (0)20 7942 6208 Fax: +44 (0)20 7942 5054 e-mail: l.ruber@nhm.ac.uk

www.lukasruber.com www.nhm.ac.uk/zoology
l.ruber@nhm.ac.uk

## OxfordBrookesU PrimateConservation

Hello!

I am running a research project at Oxford Brookes University and am advertising a post-doctoral position. My co-principal investigator Dr Bryan Fry suggested that your web site was an excellent place to announce this position. Would it be possible to provide a link via your site?

https://edm.brookes.ac.uk/-hr/hr/vacancies.do;jsessionid=-170804ac26f69216522904cdde16c55f873304369b10b0030ae0e896e91751
13603075 or

http://www.jobs.ac.uk/job/ACN676/post-doctoral-research-assistant-in-primatology/ If this is not the correct way to list the post please let me know! Thank you so much. With best wishes Anna Nekaris

– 2000-2010: Celebrating Ten Years of Primate Conservation at Oxford Brookes University

Dr K.A.I. Nekaris, MA, PhD Reader in Primate Conservation Course Tutor in Primate Conservation (MSc) Anthropology Field Chair

Oxford Brookes University Nocturnal Primate Research Group School of Social Sciences and Law Department of Anthropology and Geography Oxford OX3 0BP United Kingdom

++44 (0)1865 483767 anekaris@brookes.ac.uk loris on the web!! http://www.loris-conservation.org/database/index.html Anna Nekaris <anekaris@brookes.ac.uk>

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## RanchoSantaAna BotanicGarden GrassEvolution

Postdoctoral Research position in Evolutionary Biology / Chloridoid Grasses

General Information

A post-doctoral researcher is sought for a two-year, NSF-funded position beginning no later than 1 September 2011 to investigate the evolution of inflorescence development in chloridoid grasses (Poaceae, Chloridoideae). The study will involve molecular phylogenetics, characterizing inflorescence morphology and development, identifying genes potentially involved in inflorescence repatterning, and exploring gene expression in diverse inflorescence forms. Starting salary is $40,000 plus benefits.

Rancho Santa Ana Botanic Gardens Research Department is home to staff scientists who are also faculty members at Claremont Graduate University; four current postdoctoral fellows; up to 15 graduate students; and facilities that include laboratories (molecular and structural, including SEM); an herbarium of more than 1.1 million plant specimens, almost entirely of vascular plants; an excellent research library; and extensive plant growth facilities. For additional information about Rancho Santa Ana Botanic Garden and its Research Department, please visit http://www.rsabg.org . Qualifications

Candidates should have a Ph.D. in the plant sciences and experience with molecular techniques.

Responsibilities The successful applicant will conduct studies of inflorescence development in chloridoid grasses in a phylogenetic context. The post-doctoral scholar will also have opportunities to mentor graduate and/or undergraduate students, participate in phylogenetics discussion groups, and participate in faculty meetings.

To apply Applicants should submit a CV, a statement of interest and description of prior experience, and the contact information (names, email addresses, phone numbers) for three references. Review of applications will be completed by 15 June 2011.

Application materials and any questions should be submitted electronically to Dr. J. Travis Columbus (j.travis.columbus@cgu.edu). Dr. Columbus is conducting fieldwork until 1 June and will respond to email messages when he has access to the Internet. On Apr 7, 2011, at 5:03 PM, B. Golding wrote:

Linda Worlow <linda.worlow@cgu.edu>

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## StanfordU CacaoDomesticationGenomics

Hi all,

Juan Carlos Motamayor and I are hiring a post-doc to work on a USDA funded project in Cacao genomics. Details are below. Please email both of us with questions. To apply, send a CV in PDF format to both of us.

Carlos

MARS Bioinformatics Postdoctoral Fellowship at USDA/Stanford University

We are looking to hire a postdoctoral fellow at the USDA-ARS Subtropical Horticulture Research Station in Miami, FL in bioinformatics and computational genomics. The successful candidate will work with my lab at Stanford University, Juan Carlos Motamayors from MARS, and David Kuhn and Ray Schnell (USDA-ARS). The position is based largely in Miami with travel to Stanford several times per year.

The post-doc will make original contributions to a diverse set of scientific projects. The primary research topic will be the analysis of diverse cacao accessions to address question in domestication and agricultural genomics of the genus. S/he will also be tasked with analyzing gene expression and methylation data to generate a functional genomic maps across diverse environments including stress tolerance. The primary duties for this position are to design and implement pipelines for acquiring and assembling genomic data, to compare whole genome sequences and to analyze gene expression data. There will also be opportunities for building resources for research outreach in collaboration with Washington State University. This position requires an individual capable of communicating with students and researchers, handling and prioritizing duties across multiple projects, and working independently on critical tasks.

Desired Qualifications

- PhD in Biology, Statistics, Computer Science and 2+ years experience in bioinformatics.

- Excellent knowledge of high-throughput genomics technologies

- Experience with bioinformatic software for next-gen sequence analysis (e.g. GATK, SAMtools)

- Experience in programming C/C++ and Perl or Python, and experience with UNIX.

- Familiarity with cloud computing (Amazon AWS).

- Excellent problem solving and organization skills.

- Excellent communication and interpersonal skills.

- Excellent oral and written communication skills in English.

- Strong statistical background and experience with R.

- Proficiency with use of web databases including genome browsers.

Interested candidates should contact both: cdbustam@stanford.edu and juan.motamayor@effem.com

For more information on our research:

http://www.cacaogenomedb.org

"Carlos D. Bustamante" <cdbustam@stanford.edu>

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## Trentino Italy Biodiversity

The Department of Biodiversity and Molecular Ecology of the Research and Innovation Centre (CRI), Fondazione Edmund Mach, Trentino, Italy, is currently seeking to recruit an enthusiastic and highly motivated Post-doctoral Researcher to join the new Biodiversity and Environment Group.

This Group focuses or will focus on epidemiological and evolutionary aspects of interactions between pathogen and parasite communities and their animal vectors and hosts, including their microbiomes; however, the researcher's own interests will also be considered. Experience and interest in one or more relevant fields (molecular ecology, genetic epidemiology, virology, metagenomics and/or functional biodiversity) with relevant knowledge of laboratory and bioinformatics training is required.

Because this is a fairly senior position, applicants should have an internationally recognized track record. We are interested in having an experienced post-doc join this group who is particularly capable of drafting scientific papers and grant proposals (hence, fluent written English is essential); however, the candidate will also be expected to perform laboratory genetic, genomic and data analyses, learn new techniques and optimize them in our laboratory, take oral presentation of results to national and international conferences/workshops, supervise of young researchers (MSc and PhD students, technician), and spend some time in the field on sample collection. The Group is currently involved in projects on arthropod vectors, rodent-borne disease, speciation and conservation genetics.

Currently, CRI comprises over 250 staff, coordinates international PhD programmes and operates research programs fully integrated with state-of-the-art genetics, genomics, metabolomics and GIS platform technologies. Almost 20% of researchers are now non-Italian.

The Fondazione is a non-profit organization, with private legal status. Employment conditions are in line with prevailing European standards, including benefits and a highly competitive salary scheme. All openings are effective immediately (although starting date is flexible) and will be for three years initially, with a possibility of extension and/or transformation into permanent positions for exceptional candidates.

Set among the Dolomites, Trento is a particularly attractive province of Italy, offering a wide range of cultural and outdoor activities for all ages (please see www.apt.trento.it).

All candidates, with at least 2 years of Postdoctoral experience, proven ability to publish and attract funding, are invited to follow the application instructions at the link: http://www.fmach.eu/-sperimentazione_context2.jsp?ID_LINK=-3D4051&area=3D6 .See also Nature Jobs 28 April 2011.

Please also feel free to contact Heidi Hauffe (heidi.hauffe[at]iasma.it) for more information.

Closing date for applications: 31 May 2011.

– Heidi C. Hauffe Department of Biodiversity and Molecular Ecology, Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, 38010 S. Michele all'Adige (TN), Italy tel.: 0461-615558 cell.: 348-7263653 e-mail : heidi.hauffe@iasma.it

heidi.c.hauffe@gmail.com

## UAlabama EvolutionaryBiology

Postdoctoral Position in Evolutionary Biology

Dr. Leslie J. Rissler

Department of Biological Sciences, University of Alabama

A 1-year (possibly 2-year) postdoctoral position is available in the laboratory of Leslie Rissler at the University of Alabama. The successful candidate will work on projects involving biogeography, conservation genetics, and the landscape ecology of amphibians and reptiles. The candidate will also help the P.I. mentor graduate students, teach evolutionary biology or conservation biology classes, and manage an active lab working on diverse grant-supported projects. The candidate will have the opportunity to develop collaborative research project(s) that are linked to an ongoing NSF-funded project that examines the impact of the environment on neuroendocrine responses and genetic diversity across a latitudinal gradient in natural populations of the wood frog.

MINIMUM QUALIFICATIONS:

- A Ph.D. in biology or related field with a focus on evolution, population genetics, biogeography, ecology, conservation, behavior, and/or systematics. - Previous research experience and a strong publication record. - Field experience and familiarity with IACUC procedures. - Strong interpersonal skills and the ability to work as part of a team.

ADDITIONAL PREFERRED QUALIFICATION:

- Experience with GIS and modeling using Maxent or similar algorithms. - Molecular biology experience (microsatellites, SNPs, sequencing, etc. with associated skills in the analysis of these types of data). - Desire to teach undergraduate classes in evolution and conservation biology.

APPLICATION DEADLINE: 1 June 2011 (or until filled). Start date 1 August 2011.

To Apply: Apply online at the UA staff job application site: http://jobs.ua.edu/ The specific job is Requisition # 0804834. Applicants must have been awarded a Ph.D. degree by August 2011. Interested individuals should send a cover letter, a CV, a 2-page (maximum) statement of interest including research and teaching background and goals, and contact details for three individuals who could provide a confidential letter of recommendation.

Info on the University of Alabama can be found here: http://www.ua.edu/ Rissler's lab information can be found here: http://web.mac.com/ljrissler/lab/ Dr. Leslie J. Rissler Associate Professor Department of Biological Sciences Box 870345 MHB Hall University of Alabama Tuscaloosa, AL 35487

205-348-4052 (office) 205-348-4039 (lab) rissler@as.ua.edu http://web.mac.com/ljrissler/lab/ rissler@as.ua.edu

## UCaliforniaDavis PopulationGenetics

Postdoctoral fellowships are available in the Begun lab at UC Davis. Ongoing projects include genetic and phenotypic analysis of spatially varying selection in Drosophila, Drosophila population genomics and empirical investigation of de novo genes in Drosophila.

The Department of Evolution and Ecology is a stimulating place to study evolutionary genetics. The third floor of Storer Hall houses the labs of Begun, Coop, Kopp, Langley and Turelli. Several other laboratories studying evolutionary genetics can be found in the department and in other departments across campus.

Please send by email a CV, a brief statement of research accomplishments and interests and email addresses of three references.

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

David Begun Department of Evolution and Ecology & Center for Population Biology University of California, Davis

djbegun@ucdavis.edu

## UCaliforniaRiverside SilkEvolution

UCaliforniaRiverside_SilkEvolution

A postdoctoral opportunity is available to work on the evolution of spider silk. A broad range of projects can be pursued at or across the level of genes, proteins, organisms, and phylogeny. The ideal candidate will have expertise and strong interests in one or more of these areas: molecular evolution, functional genomics, biomechanics, bioinformatics, arachnology. A PhD is required and initial appointment is for one-year. To apply, email (to cheryl.hayashi@ucr.edu) your CV, statement of research interests and experience, representative reprints, and contact information for three referees. Review of applications will begin promptly and continue until the position has been filled.

Sincerely, Cheryl Y. Hayashi Professor of Biology University of California, Riverside

cheryl.hayashi@ucr.edu

## UdeProvence ClimateAdaptation

Dear all,

A postdoctoral position (3 years) is available in France to simulate genetic connectivity between marine protected area in the Mediterranean Sea under climate change scenarios.

Details of the position can be found on the link:

https://sites.google.com/site/stephaniemanel/projet File: PostdocConnectivity.

Stéphanie Manel, Pr, LPED Université de Provence Personal website: https://sites.google.com/site/stephaniemanel/ Laboratory website:http://www.lped.org/ stephanie.manel@ujf-grenoble.fr

## UGlasgow PlantMatingSystems

University of Glasgow

College of Medical, Veterinary and Life Sciences

Institute of Biodiversity, Animal Health and Comparative Medicine

Postdoctoral Research Assistant/Associate

Assessing the impact of plant mating system and ploidy on adaptation to parasitism in changing environments

Ref: M00131

Salary: Grade 6 £25,854 - £29,099 / Grade 7 £31,798 - £35,788 per annum

This job is part of a UK Natural Environment Research Council (NERC) funded project to investigate the influence of variation in host mating system and ploidy level on pathogen response systems and on the dynamics of host-parasite co-evolution. The project is run jointly with researchers at the University of Warwick (Prof. Eric Holub).

Although host distributions have been the focus of other studies, the impacts that mating system and ploidy have on pathogen response systems have been less well studied. We propose to use a wild host species that varies in these traits (Arabidopsis lyrata: Brassicaceae) and an important pathogen of crop plants in the Brassicaceae (oomycetes in the genus Albugo) as a model to investigate these types of interactions. Formerly considered as one species, it is now known that there are multiple species of Albugo that infect both wild and domesticated plants in the Brassicaceae. We propose to use this system to: 1) evaluate whether response to infection with Albugo varies by mating system, ploidy or geographic distribution of A. lyrata; 2) evaluate the extent to which wild populations of A. lyrata are naturally infected with the various species of Albugo; 3) assess levels of genomic variation between isolates of Albugo infecting various host species; 4) compare the relative performance of A. lyrata populations in response to Albugo epidemics caused by exposure to an Albugo strained carried by A. thaliana under semi-natural epidemic conditions; and 5) investigate the genetic basis for variation in resistance to Albugo in natural populations of A. lyrata.

The Glasgow PDRA would be primarily responsible for generating crosses to assess the genetic basis of host responses, for generating and analysing whole-genome scale sequence data, and investigating variation at candidate genes for resistance.

This post has funding for 24/28 months, depending on level of appointment. The preferred starting date is September, 2011.

You can apply online at www.glasgow.ac.uk/jobs Please direct informal enquiries to Barbara Mable (barbara.mable@glasgow.ac.uk)

Closing date: 15th May 2011

Dr. Barbara Mable Rm 404 Graham Kerr Building Institute of Biodiversity, Animal Health and Comparative Medicine College of Medical, Veterinary & Life Sciences University of Glasgow Glasgow, Scotland G12 8QQ Email: barbara.mable@glasgow.ac.uk Phone: +44 (0)141 330 3532 Fax: +44 (0)141 330 5971

barbara.mable@glasgow.ac.uk

## UMontreal 2 EnvironmentalGenomics

2 Postdocs are available at the Biodiversity Center of the University of Montreal.

The Biodiversity Centre at the University of Montreal would like to announce the availability of two Postdoctoral Fellowships available through a large scale Funds. The two projects will focus on the environmental genomics, genome sequencing and genome evolution of free-living and symbiotic bacteria and fungi in mixed organic and inorganic polluted soils.

Candidates must have a PhD degree in bioinformatics, computer science, genomics, population genetics, or other relevant fields of biology. All the positions are initially for three years.

Research experience (with strong first-author publications) in computational genomics, molecular evolution, population genetics, or a closely-related field. Should be comfortable in a linux/unix environment, with large data sets, computer clusters, and databases. Experience in analysis of DNA-seq and RNA-seq data, as well as experience constructing complex biological networks. Candidates with multidisciplinary background, spanning both life sciences and computer sciences are especially encouraged to apply.

The successful candidate will lead and coordinate the de novo assembly of several fungal and/or bacterial genomes and contribute to functional and evolutionary genomics analyses. In addition, the candidate is expected to help organize and analyze comparative transcriptomics sequence data obtained by next generation sequencing technologies.

CLOSING DATE: Open until filled, but applications, including a CV, a letter of motivation, list of published papers, and at least two letters of recommendation should be received by 30 of June 2011 to ensure full consideration.

The positions will start at the earliest possible date. Candidates should indicate the position topics and when they could take up the position.

Please send applications to : Mohamed.Hijri@umontreal.ca

Mohamed Hijri Institut de Recherche en Biologie Végétale (IRBV) Département de Sciences Biologiques Université de Montréal 4101 Sherbrooke est, Montréal, Qc, Canada, H1X 2B2 Phone: 514-343-2120 http://www.irbv.umontreal.ca/chercheurs/mohamed-hijri Mohamed Hijri <mohamed.hijri@umontreal.ca>

## UOregon TheoreticalEvolution

*Postdoctoral Position in Theoretical Ecology and Evolution*

University of Oregon Posting 11109

Jessica Green (http://biology.uoregon.edu/people/green/) and Brendan Bohannan (http://biology.uoregon.edu/ceeb/faculty_pages/Bohannan/) are currently seeking a postdoctoral researcher to collaborate on projectscombining theoretical and empirical approaches to explore fundamental questions in microbial ecology and evolution. Applicants should have a PhD with extensive quantitative training (e.g. in theoretical ecology/evolution, physics, or applied math), expertise in coding mathematical and statistical models, and strong writing skills. The successful candidate will play a key role in the Biology and Built Environment (BioBE) Center (http://biology.uoregon.edu/biobe/). The BioBE Center is training a new generation of innovators and practitioners at the /architecture-biology/ interface to understand the built environment microbiome - the diversity of indoor microbial life, their genetic elements and their interactions/. /The vision of this national research center, funded by the Alfred P. Sloan Foundation < http://www.sloan.org/ >, is to integrate recent advances in microbial genomics and biological theory to develop hypothesis-driven, evidence-based approaches to sustainable building design.

The position is available for 1 year with the possibility for renewal depending on performance. The start date is flexible. Applications will be considered starting on May 20, 2011. Please email questions regarding the position to Jessica Green (jlgreen@uoregon.edu).

*To apply*

A complete application will consist of the following materials:

(1) a brief cover letter explaining your background and career interests

(2) CV (including publications),

(3) names and contact information for three references.

_Sumbit materials to ceebjobs@uoregon.edu. Subject: Posting 11109_

To be assured full consideration, applications must be received by May 20, 2011/,/ but position will remain open until filled.

Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity. EO/AA/ADA institution committed to cultural diversity. http://hr.uoregon.edu/jobs/unclassified.php?id=3385
sara@uoregon.edu

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## UppsalaU DrosophilaEvolutionaryBiology

Post doc position in Evolutionary Biology: The role of non-genetic inheritance in adaptive evolution

Apart from DNA also non-genetic factors are transmitted from parent to offspring. Much evidence points to that these factors have a significant influence on the phenotype of offspring, but their ability to respond to selection and contribute to adaptive evolution has rarely been tested. Using the powerful model system of Drosophila melanogaster this project aims to select for paternal effects on a life-history trait and measure the response. Follow up experiments will try to tease apart through what mechanism(s) the paternal effects are mediated through.

We are now looking for a highly motivated post doc to lead this project. The ideal candidate has a background in evolutionary genetics and experience with Drosophila, as well as a strong interest in statistics. He/she should work well both as a member of a group and independently, and also be proficient in both written and spoken English. The successful candidate will join a research group led by Urban Friberg (http://www.ebc.uu.se/Research/IEG/evbiol/research/Friberg/). Applications should be written in English and include i) personal information/background, ii) a description of research interests (max 1-2 pages), iii) complete CV, iv) names and email addresses of 2-3 referees. Applications should be sent to Urban.Friberg@ebc.uu.se. For more information please feel free to contact Urban Friberg by email (Urban.Friberg@ebc.uu.se) or by phone (+46-18-4716415). The target date for receiving applications is May 1, 2011, but screening may continue if a suitable candidate has not been found by that deadline.

The Program in Evolutionary Biology (http://www.ebc.uu.se/Research/IEG/evbiol/) is situated in the Evolutionary Biology Centre (http://www.ebc.uu.se/) in central Uppsala, Sweden. The working atmosphere is international with English as working language. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm.

urban.friberg@ebc.uu.se urban.friberg@ebc.uu.se

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## USheffield PopulationGenetics

UNIVERSITY OF SHEFFIELD DEPARTMENT OF ANIMAL & PLANT SCIENCES

A Post-doctoral Research Associate with experience in population genetics/ bioinformatics is required to join the NERC Biomolecular Analysis Facility (NBAF) node in Sheffield (see http://nbaf.nerc.ac.uk/). You will assist facility users with study design, data analysis and training, and contribute to the node's research and development activities. Educated to PhD level or equivalent in population genetics or molecular ecology, you will have excellent analytical skills, preferably including experience of bioinformatic programming tools.

The post is fixed-term with an immediate start date. Note that although the initial appointment would be for one year, it would be renewable for 2 further years. Previous funding for the Facility has run continuously since 1998.

Salary on the Grade 7 scale (minimum UKP28,251 pa) Closing date: 20 May 2011

Informal enquiries may be made to Professor Terry Burke, Tel: 0114 222 0096 (e-mail: t.a.burke@sheffield.ac.uk).

Further information and details on how to make an application can be found at http://bit.ly/giHhP1 . (Post reference UOS002570)

t.a.burke@sheffield.ac.uk

## USouthampton MolecluarEvolution

Applications are invited for the post of Postdoctoral Research Fellow to work closely with Dr Richard Edwards on a BBSRC-funded project using molecular evolution to develop and apply computational tools for the prediction of protein motifs that mediate protein-protein interactions.

Many protein-protein interactions are mediated by Short Linear Motifs (SLiMs): short stretches of proteins (5-15 amino acids long), of which only a few positions are critical to function. These motifs are vital for biological processes of fundamental importance, such as signalling pathways and targeting proteins to the correct part of a cell. The primary objective of this project is to integrate a number of leading computational techniques to predict novel SLiMs and, in so doing, add crucial detail to protein-protein interaction networks.

The project will use a number of computational and sequence analysis techniques. Basic programming skills are essential. Experience with database design, HPC and web programming are highly desirable. You will be required to develop a thorough knowledge of SLiM-mediated protein-protein interactions and should therefore be comfortable with biological literature, biochemistry, molecular evolution and structural biology. Please note that the project is 100% computational.

A background in either computer science or biology, with a PhD in a relevant subject area, is essential. Previous research experience (PhD or Postdoctoral) in computational biology is highly desirable. Candidates with a computer science background must demonstrate an interest and aptitude for molecular biology. Similarly, candidates with a biology background must demonstrate an interest and aptitude for computer programming. Project management skills and independent research experience are desirable. You should be an enthusiastic researcher, a good team worker and an excellent communicator.

The position is full-time and available immediately for a period of three years. Start date is flexible but the successful candidate must be in post by September 2011. The application deadline is 16 May 2011.

You can apply online at: http://-www.jobs.soton.ac.uk/soton/jobboard/-JobDetails.aspx?__ID=*9A7F829596E7D333 Informal enquiries are encouraged. Please quote reference number 5441-11-F on all correspondence.

More information about the lab can be found at: http://www.southampton.ac.uk/ ˜ re1u06/index.html . Dr Richard Edwards Senior Research Fellow (Bioinformatics) School of Biological Sciences University of Southampton B85/3041, Life Sciences Building Highfield Campus Southampton SO17 1BJ Tel: +44(0)23 8059 4344 email: r.edwards@southampton.ac.uk www.southampton.ac.uk/biosci

R.Edwards@soton.ac.uk

## UToronto AirwayMicrobeEvolution

A postdoctoral/research associate position is available immediately to investigate the airway microbiome in cystic fibrosis. This research will be conducted as part of a collaborative, multidisciplinary team funded by the Canadian Institutes of Health Research and the National Sanitarium Association, and involves both culture-independent and culture-based approaches to characterizing the microbiome and its impact in adult and pediatric patients with cystic fibrosis. The successful applicant will be based at the Toronto General Hospital Research Institute of the University Health Network (UHN), a fully affiliated teaching hospital of the University of Toronto, with opportunities to collaborate with team members at other hospitals and at the University of Toronto.

Qualifications/Requirements:

Ph.D. or equivalent degree in microbiology or a related field, with strong proficiency in microbiological and molecular biologic techniques.

Experience in microbiome/metagenomic research, bioinformatics, or epidemiology is desirable.

Self-motivated, with strong organizational skills and ability to work independently.

Excellent interpersonal, analytical and communication skills (both written and verbal).

To apply, please send your curriculum vitae and 3 references to Dr. David Hwang (David.Hwang@uhn.on.ca), Department of Pathology, Toronto General Hospital, 11th floor, 200 Elizabeth Street, Toronto, ON, Canada M5G 2C4.

David Guttman <david.guttman@utoronto.ca> David Guttman <david.guttman@utoronto.ca>

## UWisconsinMadison EvolutionaryGeneticsGenomics

Postdoctoral Position in Evolutionary Genetics/Genomics

A postdoctoral position is available immediately in the Laboratory of Professor Carol Lee in the Center of Rapid Evolution (CORE) at the University of Wisconsin, Madison to work on a project in collaboration with Joana Silva at the Institute for Genome Sciences.

The research focuses on the evolutionary genetics and genomics of invasive populations. We are exploring the systematic and functional composition of microbial communities associated with an invading host, the copepod Eurytemora affinis, and how microbial-host interactions shift following habitat invasions. The project will make extensive use of microbiome and metagenome methodologies to study the microbiota, and of transcriptome sequencing and analyses to characterize metabolic shifts within the copepod host.

Requirements for this position include a Ph.D., a strong background in molecular biology/genomics and strong analytical and quantitative skills. Applicants should email a cover letter, CV, a brief statement of research interests and experience, and up to three representative publications to: carollee@wisc.edu.

The University of Wisconsin, Madison provides an intellectually vibrant research environment, with ~37 biology departments and ~800 biology faculty, including a strong community of evolutionary biologists and geneticists. The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html carollee@wisc.edu

## UWyoming 2 BrassicaEvolutionaryGenetics

Genetic and ecophysiological analyses of natural variation in the control of water use efficiency and response to drought stress in Brassica rapa.

Two post-doctoral positions are available to study ecophysiological and genetic mechanisms of adaptation to atmospheric and soil drought stress in the labs of Cynthia Weinig and Brent Ewers at the University of Wyoming. These positions are associated with a five-year multi-investigator NSF project that includes collaborators from Dartmouth College, University of Wisconsin-Madison and Oregon State University. The overarching aim of the project is to identify the traits and genes involved in adaptation to atmospheric and soil drought stress, including the role of the circadian clock in regulating plant ecophysiological traits. Research questions include: What are the structural and ecophysiological traits that confer adaptation to soil and atmospheric drought stress? What QTL and genetic loci underlie variation in the expression of adaptive ecophysiological traits? What role does quantitative variation in the circadian clock play in regulating ecophysiological traits? To what extent does the clock model developed in Arabidopsis translate to other species?

Preference will be given to candidates with a strong background in ecophysiology (working in the Ewers lab) or evolutionary genetics (working in the Weinig lab). Each position will present opportunities to learn new measurement and analytical techniques in alternative disciplines through collaboration with other labs. Activities of the different labs will include development of Nested Association Mapping populations (NAM), quantitative-genetic analysis and QTL mapping of drought responses in RILs and natural accessions of B. rapa, fine-scale mapping and transgenic rescue to clone QTL for the ecophysiological components of water-use efficiency, ecophysiological analyses at multiple scales of the connection between plant gas exchange and hydraulics in response to atmospheric and soil drought, and development and dissemination of B. rapa genetic resources for enhancing K12 and undergraduate education. In addition, each position requires data analysis, publication of manuscripts and participation in workshops on career development.

Applicants should send a Curriculum Vitae, a brief letter stating specific research interests, research accomplishments, and future research objectives as well as the names and contact information for three professional references as a single pdf file to both Cynthia Weinig (cweinig@uwyo.edu) and Brent Ewers (beewers@uwyo.edu). A Ph.D. is required by the time the successful applicants start a position. Review of applications will begin April 21st and continue until suitable candidates are identified. The start date is negotiable, and salary will be competitive with full benefits.

Cynthia Weinig <cweinig@uwyo.edu>

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## UZurich PlantNGS

Open Position in Plant Evolutionary Biology at the University of Zurich, Prof. Elena Contis research group, Institute of Systematic Botany.

Position description: Applications are open for one 6-yr. position (3 yrs., renewable for a second 3 yr. term) at the level of advanced post- doc (Oberassistant, in the German-speaking countries) in the research team of Professor Elena Conti (http://www.systbot.uzh.ch/-Personen/ProfessorenundDozenten/ElenaConti.html ). The position is aimed at bringing next generation sequencing/ genomic approaches into Contis research group and at our Institute to investigate evolutionary, phylogenetic, and/or population genetic questions in plant biology, including, but not limited to, the molecular genetic control of plant reproduction, speciation, introgression, gene coalescence and polyploidization. Salary will be commensurate to experience.

Requirements: The successful candidate will have a proven record of academic achievement, with publications in high-quality, peer-reviewed journals. Evidence of successful application to competitive research funds is desirable. Demonstrated experience with next generation sequencing technology and comparative genomic approaches is required; expertise in bioinformatics will be highly valued in the screening process. Applicants must hold a Ph.D. degree. Previous, successful post-doctoral experience is desirable. The selected candidate will be expected to acquire extra-mural funding for his/her research and contribute to the teaching goals of the institute of Systematic Botany by offering the equivalent of one course per year (for a total of six credit points) that complements current topics offered at our Institute and University.

Facilities: The University of Zurich is one of the leading European Universities in Biology. We offer a modern research environment with up-to-date molecular infrastructure, excellent opportunities for collaboration among evolutionary biologists, molecular geneticists and ecologists, and access to competitive funding sources both at the national and European level. For further information on facilities, research and teaching activities at the Institute of Systematic Botany, see http://www.systbot.uzh.ch/index.html. The University of Zurich is associated with the Functional Genomics Center Zurich (http://www.fgcz.ch/ ).

How to apply: Send the following documents by email AS A SINGLE PDF FILE to Prof. Elena Conti, ContiElena@access.uzh.ch: I) a two- to three- page summary of your research goals and how your research will complement current projects in Prof. Contis group, leading to productive collaboration; II) a one- to two-page summary of courses that you would like to teach, explaining how they would complement current offerings at our Institute; III) your detailed curriculum vitae, including a list of scientific publications and grants obtained from competitive funding sources; IV) a copy of your graduate academic records and Ph.D. degree certificate; V) please, include the names and full addresses of three referees and have them send in their confidential assessment of your scientific achievement and potential directly to my email address.

Deadline for application: Applications will be screened as they arrive, thus we encourage each applicant to send in his/her pdf file as soon as possible. The target date for receiving applications is May 15, 2011, but screening may continue if a suitable candidate has not been found by that deadline.

Starting date: The ideal starting date is September 1, 2011, but alternative dates can be negotiated, if necessary.

Prof. Elena Conti, Director

Institute of Systematic Botany and Botanic Garden University of Zurich

Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 44 634 8424 Fax: 0041 44 634 84 03 email: elena.conti@systbot.uzh.ch

http://www.systbot.uzh.ch/Personen/-ProfessorenundDozenten/ElenaConti.html Elena Conti <ContiElena@access.uzh.ch>

# WorkshopsCourses

## Copenhagen PlantMarkerAnalysis

Course: Molecular marker analysis of plant population structure and processes

Copenhagen 22-08-2011 - 26-08-2011

This PhD course provides participants with practical and theoretical knowledge on analysis of genetic population structure, mating patterns, and population processes in plant populations, using molecular marker data. The course includes theoretical lectures, exercises and practicals with various computer programmes as well as discussions of student projects. The course is taught by staff at University of Copenhagen and other Danish Universities as well as Professor Peter Smouse, Rutgers University, one of the developers of GenAlEx, a widely used software for population genetic analysis. Course content Estimation of genetic diversity, F-statistics, inbreeding level, gene flow, population and paternity assignment, population admixture, hybridization. Assumptions and limitations of methods, and practical exercises with relevant computer programmes, such as: GenAlEx, Structure, Cervus, Two-gener, Population Graph, Geneland, Split tree, New Hybrids, AFLPOP, GeneClass2. Exact which programmes that will be used is to be decided. Discussion of selected student projects.Course credit 3 ECTS points. Requirement for obtaining credit: approval of a written synopsis of the course content. Course material Articles and lecture notes. All course material will be available through a restricted web site. Practical information Maximum number of participants is twenty. PhD students have preference, remaining seats are open to non-PhD students. The course will take place at University of Copenhagen, Frederiksberg Campus (within Copenhagen). Computers with the relevant software will be available for all. Travel, lodging, and accommodation are to be organised and paid by the participants themselves; suggestions for hostels and hotels will be posted on the web.Course fee: 150 Euro Organisers and teachers Ole K. Hansen, Associate Professor in Forest Genetics; Erik D. Kj©r, Professor in Forest Genetics, Thure Hauser, Associate Professor in Plant Ecology; Gunter Backes, Associate Professor in Plant Breeding; Peter Smouse, Professor in Ecology, Evolution and Natural resources.

okh@life.ku.dk

## Edinburgh PlantNGS Oct18-19

Dear all,

I'm pleased to announce that Royal Botanic Garden Edinburgh will be hosting a two day workshop on how next generation sequencing technologies can be used to study plant ecology and evolution. This event will take place on the 18th and 19th October, and features an exciting programme of international speakers. For more information, registration (from £40) and further details please see the website: http://www.botanical-society-scotland.org.uk/Next-Generation-Plant-Ecology-and-Evolution-workshop-2011 Sessions include how to use next generation sequencing to:

Estimate gene flow and population level genetic differentiation (Leader: TBC) Understand adaptation and fitness (Leader: Michael Arnold, University of Georgia) Sample diversity of environmental samples (Leader: Eric Coissac, Université Joseph Fourier) Obtain the genes for a specified phenotype (Leader: Ian Baldwin, Max Planck Institute) Generate more informative phylogenetic markers (Leader: Mark Chase, Royal Botanic Garden Kew) Understand the genetic changes of speciation (Leader: Pam Soltis, University of Florida)

Keynote speakers:

Christian Lexer (University of Fribourg) Douglas Soltis (University of Florida)

Please forward this email to colleagues you think may be interested, and apologies for the mass mailing.

Best wishes, Alex Alex Twyford - Tropical Diversity PhD student Royal Botanic Garden Edinburgh, 20A Inverlieth Row, Edinburgh EH3 5LR Email: a.twyford@rbge.org.uk Telephone: +44(0) 131 248 2899

randomalt@hotmail.com

## FortCollins NGS analysis Jul10-23

Workshop on Comparative Genomics, North America 2011

Fort Collins, Colorado, USA

10 - 23 July 2011

Application Deadline: 15 May is the preferred application deadline, however, later applications are accepted.

http://www.molecularevolution.org/workshops/WCG Scott A. Handley, Michael Cummings and Kendra Nightingale, Co-Directors

The Workshop on Comparative Genomics consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of comparative genomics focusing on next-generation sequencing data. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in comparative genomics. Included among the faculty are developers and other experts in the use of computer programs and packages such as ABySS, bowtie, velvet, bioperl, Scripture, GMOD, Gbrowse, Galaxy, PyCogent, QIIME who provide demonstrations and consultations. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of short-read sequence data, analytical methods, comparative structure of genomes, metagenomics, genome visualization tools and related areas are encouraged to apply for admission. Lectures and computer laboratories total ~96 hours of scheduled instruction. Admission is limited. No programming experience is required, however, detailed instruction suitable for the novice will be provided during the early days of the Workshop on the use of the command line, editing tools and basic scripting.

Topics to be covered include: - Linux command line usage and scripting for next-generation sequence analysis - Sequencing technologies and study design - Sequence data quality control - Assembly and alignment - Functional annotation - Transcriptomics - Metagenomic analysis - Evolutionary genomics - Population genomics

2011 Fee: 1800 USD does not include other meals or housing. Special discounted housing and meals are available on the campus of Colorado State University.

For more information and online application see the Workshop web site -

http://www.molecularevolution.org/workshops/WCG and for housing and payment information see -

https://regstg.com/Registration/RegForm.aspx?rid=-3Dd41e4a6a-bf9f-40f0-8b0a-74fba75088b4&action=add The Workshop on Molecular Evolution is also being offered immediately after the Workshop on Comparative Genomics.

http://www.molecularevolution.org/workshops/WME mike@umiacs.umd.edu

## Hinxton HumanGenomeAnalysis Jul23-29

Application Deadline Soon - friday 15 April

Human Genome Analysis: Genetic Analysis of Multifactorial Diseases 23-29 July 2011

Wellcome Trust Genome Campus, Hinxton, Cambridge Deadline for applications: 15 April 2011

http://www.wellcome.ac.uk/Education-resources/-Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Advanced-Courses/-WTX026851.htm Course summary An intensive, residential, computer-based course aimed at scientists actively involved in genetic analysis of multifactorial traits.

Confirmed 2011 Guest speakers Professor William O. Cookson (Imperial College London, UK) Professor Elizabeth R. Hauser (Duke University Medical Center, USA) Professor Aarno Palotie (Wellcome Trust Sanger Institute, UK) Professor Mingyao Li (University of Pennsylvania School of Medicine, USA) Professor Sebastian Zöllner (University of Michigan, USA)

Course organisers * Daniel Weeks (University of Pittsburgh, USA) * Mark Lathrop (Centre National de Genotypage, Evry, France)

Course instructors * Heather Cordell (Institute of Human Genetics, University of Newcastle upon Tyne, UK) * Janet Sinsheimer (University of California, Los Angeles, USA) * Eric Sobel (University of California, Los Angeles, USA) * Joe Terwilliger (Columbia University, New York, USA) * Chad Garner (University of California, Irvine, USA) * Simon Heath (Centre Nacional d'Anàlisi Genòmica (CNAG), Barcelona, Spain)

Programme This advanced course covers statistical methods currently used to map disease susceptibility genes, with an emphasis on (but not limited to) methods that can analyse family data or a combination of families and individuals. Discussions of the latest statistical methodology are complemented by practical hands-on computer exercises using state-of-the-art software. The statistical basics behind each method will be carefully explained so that participants with a non-statistical background can understand.

With a focus on family data, we will discuss fundamental issues needed to increase success in gene mapping studies including: optimal study design, power to detect linkage and association, determining the most appropriate statistical methods and software, interpretation of statistical results and trouble shooting. We will also cover the basic principles of statistical inference, hypothesis testing, population and quantitative genetics and Mendelian inheritance. Our interactive and intensive educational program will enable one to better carry out sophisticated statistical analyses of genetic data, and will also improve one's interpretation and understanding of the results. All the software used is freely available, so that skills learned can be easily applied after the course.

Janet@mednet.ucla.edu

## Irapuato Mexico EvolutionaryGenomics Jul19-22

EVOLUTIONARY GENOMICS OF NON-MODEL SPECIES: NEXT GENERATION SEQUENCING, DATA MANAGEMENT, & HYPOTHESIS TESTING.

Announcing an NSF-Funded US-Mexico Workshop: Evolutionary Genomics of Non-Model Species: Next Generation Sequencing, Data Management, & Hypothesis Testing. http://www.theaga.org/2011/?page_id=-3D207 To be held at the Laboratorio Nacional de Genómica para al Biodiversidad (Langebio) http://-/www.langebio.cinvestav.mx/?pag=3D50 Irapuato, Mexico. July 19-22, 2011

Being held in conjunction with the 2011 AGA symposium, July 23-26, Guanajuato, Mexico. July 23-26, 2011. http://www.theaga.org/2011/

OVERVIEW:

We have received NSF funding for a workshop to precede the AGA symposium 2011 "Genomics and Biodiversity." The workshop is for graduate students and postdoctoral researchers looking to learn more about using next- generation sequencing technologies to address evolutionary questions with non-model organisms. There will be morning, afternoon, and evening sessions including hands-on computer sessions. We will cover a variety of topics and start with an introduction to NGS technologies and their applicability for different questions. We will also discuss hypothesis testing, data organization, data analysis pipelines with emphases on phylogeography, phylogenomics, and transcriptomics. In addition to the faculty listed below we will have guest speakers from the AGA symposium present case studies. Please see our website to download a flyer and for more details on eligibility, funding, and application procedures. Applications are due by May 13, 2011!

FACULTY INCLUDE:

-Bryan Carstens, Louisiana State University

-Ken Jones, University of Colorado School of Medicine

-Cei Abreu-Goodger, Langebio

-Scott Edwards, Harvard University

-Stacey Lance, UGA Savannah River Ecology Lab

ELIGIBLE APPLICANTS:

-Any US citizen currently enrolled in a MS or PhD program or working as a postdoctoral researcher in the US may apply to attend with funding to cover travel and lodging

-Any Mexican citizen currently enrolled in a MS or PhD program or working as a postdoctoral researcher in Mexico may apply to attend. Lodging will be covered via shared rooms with funded US participants.

-If space is available others may apply to attend but funding will not be provided

US PARTICIPANTS WILL BE EXPECTED TO:

-Share a hotel room with a Mexican student attending the workshop

-Partner with a Mexican student to write & present a short research proposal using NGS technologies on a non-model organism

Attend the AGA symposium 2011 “Genomics and Biodiversity” following the workshop

For more information and application procedures please see our website or contact Stacey Lance (see below).

Sincerely,

Bryan Carstens, Ken Jones, Cei Abreu-Goodger, Scott Edwards, and Stacey Lance

Stacey L. Lance, Ph.D. Assistant Research Scientist University of Georgia Savannah River Ecology Laboratory PO Drawer E Aiken, SC 29802

lance@srel.edu

803.725.0988

lancestacey@gmail.com

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## MemorialU MathematicalBiol Jun2-29

2011 AARMS Summer Course in Mathematical Biology

www.aarms.math.ca/summer/2011/index.html This is a four week course on mathematical biology. The first two weeks are dedicated to the mathematics of evolutionary biology. A range of applications of mathematics to evolutionary biology will be considered, including topics drawn from classical population-genetics, quantitative-genetics, game theoretic and optimization models, and adaptive dynamics. The last two weeks will focus on the design and analysis of models for the spread of diseases in human populations as well as within human hosts.

Instructors:

Part I: Professor Troy Day, Queen’s University, Canada (http://www.mast.queensu.ca/˜tday/).

Part II: Professor Abba Gumel, University of Manitoba, Canada (home.cc.umanitoba.ca/˜gumelab).

Course Outline

Part I, Weeks 1-2: Some of the following will be explored: the Price Equation; Single and multi-locus population-genetics models, including some aspects of differential geometry and tensor calculus; Stochastic models in population genetics (Wright-Fisher and Moran Models), including some aspects of stochastic differential equations, multi-type branching processes, and diffusion approximations; Spatial models of evolution, including Fisher’s PDE model for the spread of advantageous alleles, traveling wave solutions and migration-selection balance; Optimization approaches, evolutionary game theory, Nash equilibria, adaptive dynamics and evolutionary branching;

Part II, Weeks 2-4:

Purpose of modeling; compartmental modeling; classical epidemic models (SIR, SIS, SEIR); existence and stability of equilibria; modeling vector-borne diseases; determining optimal control strategies; advanced autonomous and non-autonomous models for disease spread (including models with vertical transmission, resistance development, periodicity, staged-progression, differential infectivity; age structure and co-infection models); models for assessing control strategies (quarantine, isolation, vaccination, anti-virals); within-host models; structured models (age-structured and risk-structured models); bifurcation analysis.

Prerequisites: Although no specific prerequisites are required, students should have the equivalent of a basic undergraduate degree in mathematics.

Application deadline is April 30, 2011.

For more information please see www.aarms.math.ca/-summer/2011/index.html troy.day@mac.com

## Montana CONGEN Sep27-Oct1

CONGEN COURSE IS BACK

We are pleased to announce and invite you to the forthcoming edition of ConGen!

5th ConGen- Population Genetics Data Analysis Course: Recent Approaches for Estimation of Population Size, Structure, Gene-flow, Selection Detection focusing on conservation and beyond

27-Sep/1-Oct 2011, Flathead Lake Biological Station, Montana, USA

Applications for 2011 edition are now open!

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program).

Deadline for application is 30 July, 2011

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

For detailed information see http://popgen.eu/-congen2011/

congen@popgen.eu

albanobp@fc.up.pt

## Montpellier ModelsEvolutionaryEcol Jun8-10

Dear EvolDir colleagues,

Please find below an update of the invitation to the seminar “Models in Evolutionary Ecology”

Student workshop: “Models in Evolutionary Ecology”. Montpellier (France), June 8-10, 2011 http://www.seminar-mee.org/ < http://www.seminar-mee.org/ >

Pre-registration deadline : April 29th 2011

Application deadline: May 13th 2011

We are pleased to invite you to the second edition of the workshop “models in evolutionary ecology”. This workshop is organized by PhD students and postdocs, and is dedicated to students (PhD students, postdocs, undergrads) but also to researchers interested in theoretical approaches in evolutionary ecology and has three objectives:

- give a broad overview of modelling techniques used in evolutionary ecology and their relationship with experimental work - encourage dialogue between PhD students using different approaches - discuss on how to communicate on the models and their meaning to the general public

The workshop is intended to favour exchange as much as possible, and consists in a series of methodological sessions by invited researchers, talks by researchers and students, journal clubs, poster sessions and roundtables. The detailed program is here: http://www.seminar-mee.org/home/programme Registration to the workshop is free, but we strongly recommend all participant to present their work or project in a talk or with a poster.

For organization purposes, it would be great if you could pre-register quickly (before the end of April). You can then take your time to complete your registration before May, 13th by submitting an abstract.

http://www.seminar-mee.org/home/inscription

Confirmed faculty:

Thomas Broquet Vincent Devictor Richard Gomulkiewicz

Sonia Kéfi Sébastien Lion Guillaume Martin Denis Roze

We look forward to seeing you in June!

The organizers, Ronan Becheler, François Blanquart, Benoit Goussen, Etienne Loire and Timothée Poisot.

http://www.seminar-mee.org/

GOUSSEN Benoit THESARD <benoit.goussen@irsn.fr>

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## Montpellier ModelsEvolution Jun8-10

Student seminar: "Models in Evolutionary Ecology". Montpellier (France), June 8-10, 2011 http://www.seminar-mee.org/ Application deadline: May 13th 2011

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For organization purposes, it would be great if you could pre-register quickly (i.e., before the end of April). You can then take your time to complete your registration before May, 13th by submitting an abstract. http://www.seminar-mee.org/home/inscription Confirmed faculty:

Thomas Broquet Vincent Devictor Richard Gomulkiewicz Sébastien Lion Guillaume Martin Denis Roze

We look forward to seeing you in June!

The organizers, Ronan Becheler, François Blanquart, Benoit Goussen, Etienne Loire and Timothée Poisot.

http://www.seminar-mee.org/ Francois.BLANQUART@cefe.cnrs.fr

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## MountDesertIsland EvolutionMedicine

*Course announcement* Evolutionary Foundations for Medicine and Public Health, Mount Desert Island Biological Laboratory, August 8-12, 2011

*Faculty* William Aird, Harvard University Gillian Bentley, Durham University, UK Carl Bergstrom, University of Washington Peter Gluckman, University of Auckland Peter Ellison, Harvard University Randolph Nesse, University of Michigan (Course Director) Chris Reiber, SUNY Binghamton Stephen Stearns, Yale University

*Participants* This course will be limited to 40 participants. It will be appropriate for those with a background in biology and/or medicine at diverse levels. While special expertise in evolutionary biology is not required, those with background in evolutionary biology will have specialized opportunities. To maximize benefits to this developing field, admission preference will be offered to professors who teach or anticipate teaching courses on the subject and to members of minority groups who may be eligible for support from the National Evolutionary Synthesis Center. Researchers and students from advanced undergraduates to postdocs will be warmly welcomed if there is space.

*Course description* This intensive one-week course will introduce strategies for applying core principles of evolutionary biology to problems in medicine and public health by focusing on selected examples. The relevant principles include life history theory, evolutionary genetics, host pathogen co-evolution, the regulation of defenses, developmental plasticity, and trade-offs shaping reproductive strategies. They will be applied to clinically relevant topics including aging, antibiotic resistance, clinical management of fever, endothelial disease, prenatal experience and metabolic syndrome, and reproductive cancers. This course will have extensive special expertise available on topics related to reproduction.

Mornings will be devoted to lectures and structured discussions. In the early afternoons, participants will work in small groups with faculty and others who share specialized interests. Most groups will investigate a specific disorder, for instance, metabolic syndrome, multiple sclerosis, or breast cancer. Each group will develop a possible research project, for presentation on Friday. Individuals are also free to create their own projects. Late afternoons (except Monday) are not prescheduled, allowing participants to pursue individual interests or organize their own additional discussions and projects.

For more information see

http://www.mdibl.org/courses/-Evolution_and_Medicine/296/ Judy Stone <jstone@colby.edu>

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## MtDesertIsland EvolutionaryMedicine Aug8-12

August 8 to August 12, 2011

Mount Desert Island Biological Laboratory One-Week Summer Course

Evolutionary Foundations for Medicine and Public Health

Full info at: http://www.mdibl.org/courses/-Evolution_and_Medicine/296/ Faculty

William Aird - Harvard University Gillian Bentley - Durham University, UK Carl Bergstrom - University of Washington Peter Gluckman - University of Auckland Peter Ellison - Harvard University Randolph Nesse - University of Michigan (Course director) Chris Reiber - SUNY Binghamton Stephen Stearns - Yale University

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CME credit CME credit will be available. This activity has been planned and implemented in accordance with the essential areas and policies of the Accreditation Council for Continuing Medical Education through the joint sponsorship of Colby College and the Mount Desert Island Biological Laboratory. Colby College is accredited by the ACCME to sponsor continuing medical education for physicians.

As an institution accredited for CME, Colby College designates this educational activity for a maximum of 29 AMA PRA Category 1 Credits. Physicians should only claim credit commensurate with the extent of their participation in the activity.

Travel: The Mount Desert Island Biological Laboratory is located in the village of Salisbury Cove, Maine, a short distance from Bar Harbor and Acadia National Park. Travel information and suggestions are available here: http://www.mdibl.org/traveling.php Housing and Dining: Lodging is available at local motels within walking distance, with choices available at various price levels. Hotel blocks will be posted on the course web page (see URL below). Limited on-campus housing may be available. All meals are provided except for Wednesday dinner.

For more information and To Apply http://www.mdibl.org/courses/Evolution_and_Medicine/296/ Two course fellowships will be available to underrepresented minorities in science. Please indicate on the course application if you wish to be considered for a course fellowship. A $500 deposit is due upon acceptance.

Support This course is made possible by support from MDIBL and The National Evolutionary Synthesis Center.

nesse@umich.edu

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## NorthCarolinaStateU PracticalProgrammingForBiol Jun6-15

Application deadline April 15, 2011

Title: Practical Computing for Biologists

Instructors: Steven Haddock and Casey Dunn

When & Where: June 6-15, 2011 at North Carolina State University, Raleigh, NC

Website: https://academy.nescent.org/wiki/Practical_computing_for_biologists As part of the new NESCent Academy initiative, NESCent is pleased to accept applications for Practical Computing for Biologists. This course covers the simple but powerful skills that all scientists should know in a world of increasingly complex analyses. This is not a typical bioinformatics course, although the lessons are applicable to molecular data. The skills are applicable to any subdiscipline where gathering and analyzing moderate to large data sets are involved. The specific sections include working with text files, command-line operations, scripting and Python programming, creating scientific graphics, working with servers (remote login, software installation), and a bit about the web and data-acquisition hardware.

This course is timely because biologists and other researchers are expected to analyze larger and more complex data sets, but using inadequate tools like spreadsheets. Although the examples will be shown making use of Mac OSX and its Unix underpinnings, all of the tools discussed are cross-platform and freely available. Participants will be able to take the techniques and skills they learn back to their labs to continue making their own research easier and more effective. The target audience for the course is anyone with data: grad students, post-docs, technicians, and faculty.

Practical Computing for Biologists is based on the book of the same name by Steven Haddock and Casey Dunn. The course is co-sponsored by the NESCent and the Department of Genetics / Initiative in Biological Complexity at North Carolina State University.

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Karen Cranston Training Coordinator and Informatics Project Manager nescent.org

Karen Cranston <karen.cranston@nescent.org>

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## Portugal RNABioinformatics May9-11

Deadline for applications May 1st

The Bioinformatics Training Course RNA11 is OPEN for applications

RNA11 Application Deadline RNA Bioinformatics May 1st 2011 with Lars Barquist (Sanger) and Anton Enright (EBI) Course dates: May 9th-11th 2011

An introduction to tools for identifying and characterizing RNA sequences

Course description:

Overview

This course will give an overview of RNA and the informatic challenges associated with studying RNA. This course will be run as a mixture of lectures and hands-on problem solving sessions.

Objectives

The course is practical in nature. After participating attendees will be aware of the difficulties in dealing with RNA. Current methods for addressing these challenges and the limitations of each approach. They should be able to predict RNA secondary structures, be able to use state of the art RNA homology search tools, predict RNA:RNA interactions, and use comparative methods for studying RNA structure.

Course Pre-requisites: Basic Molecular Biology. Graduate level understanding of Molecular Biology. A basic level of computer knowledge will be assumed.

Target Audience: Biologists interested in applying computational tools for RNA sequence analysis to their research.

Course fee: 240.00 (for 3 days at Euro 80.00), lunch is included for non-campus people.

more information at

http://gtpb.igc.gulbenkian.pt/bicourses/RNA11
Information on all GTPB courses at http://gtpb.igc.gulbenkian.pt – Pedro Fernandes GTPB Coordinator

Pedro Fernandes <pfern@igc.gulbenkian.pt>

## Poznan Bioinformatics Jul11-15

9th Poznan Summer School of Bioinformatics

Faculty of Biology, Adam Mickiewicz University, Poznan, Poland

11th-15th July 2011

Advanced Techniques in Genome Analysis

Poznan Summer School of Bioinformatics is a comprehensive course of bioinformatics. The course is best prepared for those who have little knowledge in bioinformatics and find it necessary/interesting to learn more in this field. It is therefore aimed to give the opportunity to find out how to use some basic bioinformatic tools and how to perform bioinformatic analyses in your research.

The course consists of lectures (by scientists from Poland and abroad) and hands-on - this combination should fit best your needs as you have a chance to try the methods out yourself. We cover the following subjects (which we find most interesting and up-to-date):

* Population genetics in the genomic era * Next generation sequencing technologies * Sequence assembly * Genome wide association studies * miRNAs and their targets * Genome wide analysis of repetitive elements * Tools for genome annotations and analysis * Gene complexity and alternative splicing * Reactome - reactions, pathways and biological processes

Details can be found at the workshop website: http://lemur.amu.edu.pl/bioinfo Please forward this announcement to anyone who might be interested.

Visit Poland! Enjoy bioinformatics!

Best regards,

PSSB Organizing Committee

Contact: genomics@amu.edu.pl

Bioinfo School <genomics@amu.edu.pl>

## SaintLouisU GISTraining Jun22-24

Aquatic GIS Training Workshop Announcement GIS Applications in Aquatic Ecology and Evolutionary Biology

An NSF supported three day aquatic GIS training workshop will be offered at Saint Louis University on June 22-24, 2011 and August 17-19, 2011. A general goal of this workshop is to train and establish an interactive group of researchers and educators applying GIS techniques in aquatic systems. Applicants with all levels of GIS experience are welcome; however, the workshop will be presented for aquatic biologists with little to no background in GIS techniques.

The tentative schedule of topics includes: 1) basic acquisition and manipulation of GIS data, 2) GIS data sources for aquatic research, 3) quantification of species habitat use at multiple spatial scales, 4) species distribution modeling, and 5) development and application of hydrologic data to studies of aquatic systems. More details on the specific schedule will be provided in the near future. The majority of the training will be conducted using ArcGIS 10.0; however, other software options will be presented. Computer space will be provided for each attendee.

The workshop is open to Faculty, Research Scientists, Postdoctoral Researchers, and Graduate Students conducting research in aquatic systems. There is no cost for the workshop; however, participants will be responsible for meals, travel, and lodging. Details and updates will be available at http://pages.slu.edu/faculty/jknouft/index_files/Page304.htm . To apply, please email a statement of application including a description of your research interests (maximum 1 page) and a

CV to Dr. Jason Knouft at aquaticgis@slu.edu. Review of applications will begin on April 30, 2011. GIS experience is not a prerequisite for the workshop. A total of 20 spots are available for each workshop. Please indicate the dates you would like to attend (June 22-24 or August 17-19). If you are available for both dates (one or the other), please indicate this in your application.

Jason Knouft <jknouft@slu.edu>

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## UCopenhagen MarkerAnalysis when

Course: Molecular marker analysis of plant population structure and processes

This PhD course provides participants with practical and theoretical knowledge on analysis of genetic population structure, mating patterns, and population processes in plant populations, using molecular marker data. The course includes theoretical lectures, exercises and practicals with various computer programmes as well as discussions of student projects. The course is taught by staff at University of Copenhagen and other Danish Universities as well as Professor Peter Smouse, Rutgers University, one of the developers of GenAlEx, a widely used software for population genetic analysis. Course content Estimation of genetic diversity, F-statistics, inbreeding level, gene flow, population and paternity assignment, population admixture, hybridization. Assumptions and limitations of methods, and practical exercises with relevant computer programmes, such as: GenAlEx, Structure, Cervus, Two-gener, Population Graph, Geneland, Split tree, New Hybrids, AFLPOP, GeneClass2. Exact which programmes that will be used is to be decided. Discussion of selected student projects.Course credit 3 ECTS points. Requirement for obtaining credit: approval of a written synopsis of the course content. Course material Articles and lecture notes. All course material will be available through a restricted web site. Practical information Maximum number of participants is twenty. PhD students have preference, remaining seats are open to non-PhD students. The course will take place at University of Copenhagen, Frederiksberg Campus (within Copenhagen). Computers with the relevant software will be available for all. Travel, lodging, and accommodation are to be organised and paid by the participants themselves; suggestions for hostels and hotels will be posted on the web.Course fee: 150 Euro Organisers and teachers Ole K. Hansen, Associate Professor in Forest Genetics; Erik D. Kj©r, Professor in Forest Genetics, Thure Hauser, Associate Professor in Plant Ecology; Gunter Backes, Associate Professor in Plant Breeding; Peter Smouse, Professor in Ecology, Evolution and Natural resources. Registration and questions Write an e-mail to Ole Hansen, okh@life.ku.dk, containing the following information: Full name, e-mail address, phone no., institution, full mailing address, country, whether you are a Ph.D. student, title of present research project, education in genetics (courses + experience) and whether you would like to present your project during the course; in that order and on separate lines.

okh@life.ku.dk

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## UMichigan EvolutionaryEpidemiology Jul25-29

Evolutionary Epidemiology and Public Health

The University of Michigan School of Public Health Graduate Summer Session 2011

July 25-29, 2011

Betsy Foxman and Randolph Nesse

Course Description: New applications of evolutionary theory to medicine are growing and helping to explain apparent paradoxes, such as rapidly increasing rates of breast cancer, increased asthma vulnerability in certain populations and the metabolic syndrome (For details see The Evolution Network at http://-evolutionandmedicine.org). Epidemiologists have begun to apply these principles and ask new questions, such as do genes that vary by latitude explain hypertension, and how might public health interventions for infectious disease be 'evolution-proofed' This course will explore how epidemiologists and other public health workers can make use of these advances in their own work. Applying evolutionary theory can sharpen research questions, raise new possible explanations for observed phenomena and identify new types of exposure and outcome measures.

Pre-requisites: No prior training in evolutionary biology is assumed.

For more information and registration: http://-www.sph.umich.edu/epid/GSS/ nesse@umich.edu

## Valencia MEPPA 2011 May30-Jun3 2

SECOND ANNOUNCE

DEADLINE FOR APPLICATIONS: April 29th, 2011

Dear mailing list member,

Registration is now open for:

MEPPA11 - Molecular Evolution, Phylogenetics, Phylogenomics, and Adaptation

Please visit the Course website for details:

http://bioinfo.cipf.es/courses/mol_evol_phylo_6ed/ This course is likely to be very competitive for seats. Our maximum capacity is 25 seats. Early application is recommended!

Instructors: Hernan Dopazo, Toni Gabaldon, François Serra, Jaime Huerta- Cepas, and Salvador Capella

Invited Instructors: David Posada, University of Vigo (Spain) and Rafael Zardoya, MNCN-CSIC (Madrid, Spain)

Duration: 5 days. May 30 to June 03, 2011

Course Fee: Eur 380, include meals. A limited number of grants will be available.

Place: Centro de Investigacion Principe Felipe. Valencia. Spain. http://www.cipf.es/ Course description:

Currently, the simplest Bioinformatics analysis uses species comparisons in order to hypothesise the function of a novel biological sequence. Moreover, in most Molecular Biology labs, evolutionary and phylogenetic concepts are constantly being used with more or less formality: homology, similarity, evolutionary rates, long branch attraction, rooted and unrooted trees, monophyletic group, molecular clock, adaptation, lineage effects, neutralism, cladograms, phylograms, etc. The course aims to provide the necessary background to understand the basic concepts from comparative and evolutionary biology that are frequently used in molecular biology and bioinformatics analyses. The course consists in five full-day sessions with an adequate balance between theory and computer practice, oriented to solve frequent problems and hypothesis testing. The program covers the basic and advanced analysis of Phylogenetic reconstruction, Phylogenomic analysis of genomes and Maximum likelihood tests for molecular adaptation. The software resources that will be used in the practical sessions include: Phyml, Phylip, MEGA, TreePuzzle, MrBayes, PAML, Modeltest-Protest, Jmodeltest and the Phylemon 2.0 web server. (phylemon.bioinfo.cipf.es)

Please feel free to pass this information to colleagues in your community.

Co-ordinators: Hernan Dopazo and François Serra

Hernan Dopazo <hdopazo@cipf.es>

Hernán J. Dopazo, PhD Head of the Evolutionary Genomics Unit Bioinformatics & Genomics Department Centro de Investigación Príncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanográfico) 46012, Valencia, España Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es http://hdopazo.bioinfo.cipf.es/ Hernan Dopazo <hdopazo@cipf.es>

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## Valencia Spain MEPPA 2011 May30-Jun3 3

LAST ANNOUNCE

DEADLINE FOR APPLICATIONS: April 29th, 2011

Dear mailing list member,

Registration is now open for:

MEPPA11 - Molecular Evolution, Phylogenetics, Phylogenomics, and Adaptation

Please visit the Course website for details:

http://bioinfo.cipf.es/courses/mol_evol_phylo_6ed/ This course is likely to be very competitive for seats. Our maximum capacity is 25 seats. Early application is recommended!

Instructors: Hernan Dopazo, Toni Gabaldon, François Serra, Jaime Huerta- Cepas, and Salvador Capella

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Please feel free to pass this information to colleagues in your community.

Co-ordinators: Hernan Dopazo and François Serra

Hernán J. Dopazo, PhD Head of the Evolutionary Genomics Unit Bioinformatics & Genomics Department Centro de Investigación Príncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanográfico) 46012, Valencia, España Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es http://hdopazo.bioinfo.cipf.es/ Hernan Dopazo <hdopazo@cipf.es>

## Vienna EvolGenetics Sep20-23

Evolutionary genetics is central to a wide range of biological questions, and is expanding dramatically with the flood of DNA sequence data. This intensive four-day course will give a thorough introduction to the subject, showing its broad scope, and teaching a variety of techniques that can be used to model the evolutionary process, and that can be applied to diverse problems.

The course is aimed at graduate students with diverse backgrounds - both in evolutionary biology, and coming in from different fields. Teaching will be a combination of lectures, discussion groups, and worked examples; simulation software will be provided.

For details, see http://pub.ist.ac.at/courses/2011/-evogen Faculty

Nick Barton, Jon Bollback (IST Austria) Reinhard Bürger, Joachim Hermisson, Ines Hellman (U Vienna) Magnus Nordborg (Gregor Mendel Institute, Vienna) Christian Schlötterer (Vetmeduni Vienna)

This workshop is a joint initiative between IST Austria and the Vienna Graduate School of Population Genetics. For more information, see www.popgen-vienna.at/ and www.univie.ac.at/evolvienna/ Dates

20 - 23rd September 2011. The course runs for four days, with students arriving for a welcome reception on the evening of Monday 19th September.

Costs The course fee is euro 350,-. This includes lodging on the IST campus, meals, course material, and social events.

Location The course will be held at the campus of IST Austria, which is just outside Vienna. Accommodation will be in the Guesthouse on campus.

Registration Application deadline is May 30, 2011. Successful applicants will be notified by mid-June

n.barton@ed.ac.uk

## Yunnan China Biodiversity Jun27-Jul1 2

Genomics of Tropical Biodiversity - Working Session I

(Second announcement)

Time and Venue: June 27-July 1 2011 Xishuangbanna Tropical Botanical Garden, Yunnan, China

The workshop is designed to be the first step in developing long-term working groups and collaborations focused on the genomic diversification of tropical plants. Registered participants will have access to available Illumina data obtained from whole genome samples of numerous species of tropical tree, primarily in the genus Ficus (figs) and the family Fagaceae (oaks, stone oaks, chestnuts and beeches). Whole transcriptome data from developing flowers is expected to be available for some fig samples. During the workshop, participants will make further plans for manuscripts, analyses, proposals, and future meetings.

Prior to the workshop, a brief summary of the sample species and their biological characteristics will be provided, so the participants can familiarize themselves with the biological framework of the samples. Additionally, sets of draft questions and analyses will be provided through Google Docs (if you need to set up a Google account, please let us know), allowing participants to become familiar with the specific objectives of the workshop, to comment on the questions and analyses, and propose new ones. The list of confirmed participants below will potentially lead discussion of specific topics that will then break out into working groups each day.

Confirmed participants and their expertise Mike ARNOLD, University of Georgia and Kunming Institute of Zoology - Genomics of speciation Jeff BOORE, University of California, Berkeley, and Genome Project Solutions, Inc. - Comparative genomics and phylogenomics Chuck CANNON, XTBG and Texas Tech University - Reference-free analytical approaches David GALBRAITH, University of Arizona - Biotechnology and genomics Manuel LERDAU, University of Virginia and XTBG - Phenotypes and genomics Christian LEXER, University of Fribourg - Genomics of phenotypic adaptation RUAN Jue, Beijing Institute of Genomics - de novo analysis of next-gen data Yann SURGET-GROBA, University of California, Santa Cruz and XTBG - transcriptomes and biodiversity

Registration

At the moment, we can still accept 4-5 additional participants but you must contact us before April 15, 2011, when the participant list will be finalized. Please contact Chai-Shian KUA (kuacs@xtbg.ac.cn ) or Chuck CANNON (chuck@xtbg.ac.cn) to register.

Fees, due upon arrival 950 RMB for Chinese professional scientists and 550 USD for foreign scientists 500 RMB for Chinese students and 250 USD for foreign students

Accommodation: 700 RMB for 4 nights at the garden hotel.

Visit our website for more details, including a draft agenda and research topics: www.ecologicalevolution.org/training chuck@xtbg.ac.cn

# Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. …plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

# Afterword

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