# EvolDir

February 1, 2009

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

## AMNH NewYork Health and Environment Apr2-3

EXPLORING THE DYNAMIC RELATIONSHIP BETWEEN HEALTH AND THE ENVIRONMENT The Center for Biodiversity and Conservation Milstein Science Symposium American Museum of Natural History New York City, New York, USA April 2 and 3, 2009 http://cbc.amnh.org/health Health and the environment are deeply intertwined for populations, species, and ecosystems, as well as for human lives and livelihoods. Human endeavors in agriculture, energy and food production, transportation, and infrastructure development can have far-reaching and significant impact on the health of humans and the environment. Understanding these relationships is increasingly critical in the context of our changing world and the accelerating loss of biodiversity.

This two-day conference will present a diversity of viewpoints and experiences, spanning the natural, medical, and social sciences, as well as policy planning. Presenters will discuss knowledge/data gaps and the limitations of current approaches, and examine innovative methods that move beyond speculation to a grounded understanding of impacts and realistic solutions. Particular emphasis will be placed on consideration of multiple and interacting stressors and decision making for maximizing benefits to both health and the environment.

Call For Posters

Alimited number of posters will be accepted for presentation during the Symposium. Posters that address any aspect of the relationship between health and the environment will be considered. See the Symposiumâs main themes.

Supplementary topics may include, but are not limited to:

â Links between the health of plants, wildlife, domestic animals, and/or humans â Anthropogenic drivers of disease emergence â Environmental change and disease ecology â Environmental change and pathogen evolution â Pathogen discovery in natural reservoirs â Ecology of host-pathogen interactions â Climate change and health â Health-related ecosystem functions and services â Environmental sustainability and health â Health and biodiversity conservation â Capacity building in environment and health

Members of a Poster Selection Committee will determine which abstracts are to be accepted based on their relevance and general level of interest.

Abstract Submission Deadline: 30 January 2009

The Poster Session and Reception will be held on the evening of Thursday, 2 April 2009.

To be considered for the Poster Session, please submit an abstract (see Sample Abstract Submission). http://symposia.cbc.amnh.org/archives/-biocultural/pdf-docs/sample-abstract-submission.pdf Abstract Format Authors - List the contributing authors with the name of the presenting author in CAPITAL LETTERS. Order should be last name first for the first author, but first name first for all other authors. Write out full first names.

Addresses - List each contributing authorâs institutional affiliation, including its city, state/province, and country. For the presenting author only, include an email address in parentheses at the end of the address. If there are multiple addresses, indicate by superscript numeral.

Title - Titles are limited to 150 characters or less.

Abstract - The body of the abstract is limited to 300 words and should not exceed one paragraph. Begin with a statement of the problem or objectives and end with a clear conclusion.

Name of contact - Provide the name of the contact person for necessary correspondence, including notification of abstract acceptance. Include the contact personâs complete mailing address and country. Also provide an email address.

Abstracts may be submitted by email to posters@amnh.org. The subject line of the email should read âPoster Submission.â

Poster Abstract Submission Deadline: 30 January 2009

Selection Committee Notification: 9 February 2009

If you require a decision before January 30 (e.g., for visa requirements to travel to New York), please state so in your email and we will do our best to accommodate your request.

All poster presenters must register for the symposium by Friday, 13 February, to guarantee inclusion in the Poster Session and in the printed Program.

Please Note: The American Museum is unable to provide financial support to poster presenters for travel or accommodation. For a list of hotels, student centers, and hostels in the neighborhood of the Museum, visit http://cbc.amnh.org/health Sergios-Orestis Kolokotronis, PhD Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024 -USA- tel +1 212 313 7654 koloko@amnh.org http://softlinks.amnh.org koloko@amnh.org

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## AMNH NewYork PathogenEvolution Apr2-3

EXPLORING THE DYNAMIC RELATIONSHIP BETWEEN HEALTH AND THE ENVIRONMENT CALL FOR POSTERS: SESSION ON PATHOGEN EVOLUTION AND THE ENVIRONMENT The Center for Biodiversity and Conservation Milstein Science Symposium American Museum of Natural History New York City, New York, USA 2 & 3 APRIL, 2009 http://symposia.cbc.amnh.org/health Health and the environment are deeply intertwined for populations, species, and ecosystems, as well as for human lives and livelihoods. Understanding these relationships is increasingly critical in the context of our changing world and the accelerating loss of biodiversity. This two-day conference will present a diversity of viewpoints and experiences, spanning the natural, medical, and social sciences, as well as policy planning. Please visit http://-symposia.cbc.amnh.org/health for the list of confirmed speakers and the program so far.

Call For Posters

A limited number of posters will be accepted for presentation during the Symposium. Posters that address any aspect of the relationship between health and the environment will be considered; we would like to invite posters on the role of the environment on pathogen evolution. See the Symposium$B!G(Bs main themes at http://symposia.cbc.amnh.org/health .

Abstract Submission Deadline: 5 February 2009

The Poster Session and Reception will be held on the evening of Thursday 2 April 2009.

To be considered for the Poster Session, please submit an abstract (see sample). http://symposia.cbc.amnh.org/archives/biocultural/pdf-docs/sample-abstract-submission.pdf Abstract Format Authors - List the contributing authors with the name of the presenting author in CAPITAL LETTERS. Order should be last name first for the first author, but first name first for all other authors. Write out full first names.

Addresses - List each contributing author$B!G(Bs institutional affiliation, including its city, state/province, and country. For the presenting author only, include an email address in parentheses at the end of the address. If there are multiple addresses, indicate by superscript numeral.

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## Fribourg Switzerland Polyploidization Sep7-8

*MINISYMPOSIUM ANNOUNCEMENT*

POLYPLOIDIZATION, PLANT FITNESS AND TROPHIC INTERACTIONS

Fribourg Ecology & Evolution Days 2009

Fribourg(Switzerland), 7-8 September 2009

The evolutionary success and potential selective advantage of genome duplication through polyploidy is a widespread evolutionary phenomenon and a common speciation mechanism in plants. Recent studies indicate an association of polyploidy with successful weeds and plant invaders. Little is yet known about the manifold underlying mechanisms, and the relative importance of auto- vs. allo-polyploidisation, the latter including hybridization. Surprisingly, ecological and evolutionary effects of polyploidy on shaping interspecific interactions within natural communities are largely unknown, although changes in plant traits related to polyploidy have been exploited in agriculture to produce crop varieties that are also more resistant to natural enemies.

In this workshop, we will bring together scholars from both ecology and evolution, and from plant and animal biology to discuss concepts and new developments in this yet greatly under-researched, but highly promising field. (Flyer)

Confirmed invited speakers:

- Brian Husband (Univ. of Guelph, CA) - Zuzana Münzbergová (Charles Univ. Praha, CZ) - Scott Nuismer (Univ. of Idaho, Moscow, USA) - John Pannell (Univ. of Oxford, GB) - Yves van de Peer (Univ. of Gent, BE) - Kristina Schierenbeck (USDA-ARS, Reno, USA)

The meeting is open and there is no registration fee, but online registration is required.

Talk/poster submission deadline: 1 July 2009 Registration deadline: 1 August 2009

Info:heinz.mueller@unifr.ch

Web site and Registration: www.unifr.ch/biol/-ecology/Polyploidy09 Organisers Heinz Müller-Schärer, Patrik Mráz & Louis-Felix Bersier, Univ. of Fribourg, CH Jasmin Joshi, Univ. of Potsdam, D Urs Schaffner, CABI Delémont, CH

Please distribute this information to all researchers and students potentially interested!

Best wishes,

Louis-Félix Bersier

Prof Louis-Félix Bersier Unit of Ecology and Evolution Department of Biology, University of Fribourg Ch. du Musée 10 CH-1700 Fribourg, Switzerland

louis-felix.bersier@unifr.ch louis-felix.bersier@unifr.ch

## Galapagos GalapagosScienceSymposium Jul20-24

Galapagos Science Symposium: the role of science in developing a sustainable future

20-24 July 2009 Charles Darwin Research Station Galapagos, Ecuador

The meeting is in recognition of the 50th anniversary of the Charles Darwin Research Station and the Darwin anniversaries. Scientists, scholars and experts on Galapagos, evolution, Darwin, conservation and biodiversity will be featured.

Meeting flyer including a tentative program and speakers: http://www.darwinfoundation.org/files/-about-us/pdf/Symposium%202009%20PP %20-%20PC-Web-Distribute.pdf

Peter H Wimberger <pwimberger@ups.edu>

## IowaCity SMBE Jun3-7 Update

**SMBE 2009, Iowa City**

The 17th annual meeting of the Society for Molecular Biology and Evolution-SMBE 2009-will be held in Iowa City June 3-7, 2009, on the campus of The University of Iowa. Visit our meeting website (http://smbe2009.org) for the most current information.

REMINDER: Contributed Symposium Proposals due: Monday, January 12th

UPDATES: Registration opens: February 2nd (or sooner) Early registration closes: April 1st Abstract deadline for consideration as Fitch Prize: March 16th Abstract deadline for consideration as contributed talk: April 1st (all abstracts received after April 1st will be posters) Abstract deadline for inclusion in the program book: May 15th

On behalf of the organizers, we'll see you soon in Iowa City! John

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John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biology 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

email <john-logsdon@uiowa.edu> web < http://-ccg.biology.uiowa.edu><http://ccg.biology.uiowa.edu > < http://euplotes.biology.uiowa.edu><http://-euplotes.biology.uiowa.edu >

john-logsdon@uiowa.edu john-logsdon@uiowa.edu

## Irakleio Crete ConservationBiol Sep22-26

*Dear Sir,* *I am sending you this mail in order to announce the 1st Circular of the Scientific Conference "11 International Congress on the Zoogeography and Ecology of Greece and Adjacent Regions".*

* 1st Circular*

Dear colleague,

It is my pleasure to invite you to participate in the Scientific Conference "*/11^th International Congress on the Zoogeography and Ecology of Greece and Adjacent Regions/*", which will take place in Irakleio (Crete, Greece), September 22-26, 2009. Please, find attached information (First Circular) about this Scientific Conference. We hope that you or some of your colleagues will be interested to attend the Conference.

Sessions will convene in the mornings and early afternoons and will include lectures by invited speakers, as well as talks and poster presentations selected from submitted abstracts. The invited key speakers are:

*Prof. Robert Whittaker*, Biodiversity Research Group, Oxford University Centre for the Environment, UK

*Dr. Kevin de Queiroz*, National Museum of Natural History, Smithsonian Institution, USA

*Prof. Kevin N. Laland, * Centre for Social Learning and Cognitive Evolution, School of Biology, University of St. Andrews, Scotland

*Dr. Thord Fransson, *Swedish Museum of Natural History, Sweden

*Prof. Carlo Heip*, Centre for Estuarine and Marine Ecology (CEME) and General Director of the Royal Netherlands Institute of Sea Research, The Netherlands

*Prof. Fritz F. Steininger*, Research Institute and Natural History Museum Senckenberganlage, Frankfurt am Main, Germany

*Prof. Gary R. Carvalho, *School of Biological Sciences, University of Bangor, Environment Centre Wales, Bangor, UK

*We will appreciate very much also if you disseminate this information among your colleagues and encourage them to participate.* Further information can be found at: www.nhmc.uoc.gr/iczegar11 < http://www.nhmc.uoc.gr/iczegar11 >.

We are inviting abstract submissions for oral and poster presentations in the “11^th ICZEGAR”. Abstracts should be submitted online at www.nhmc.uoc.gr/iczegar11 < http://www.nhmc.uoc.gr/iczegar11 > by February 20, 2009. We will send a new message to re-announce the opening of registration and abstract submission. The deadline for receipt of abstracts, early registration, and hotel reservations will be May 31, 2009.

I look forward to welcoming you in Irakleio (Crete) for a scientifically stimulating and socially enjoyable meeting.

With best regards,

On behalf of the Organizing Committee

Nikos Poulakakis

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11iczegar <11iczegar@nhmc.uoc.gr>

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## Irakleio Crete ConservationBiol Sep22-26 Corrected

*1st Circular*

Dear colleague,

It is my pleasure to invite you to participate in the Scientific Conference “*/11^th International Congress on the Zoogeography and Ecology of Greece and Adjacent Regions/*”, which will take place in Irakleio (Crete, Greece), September 21-25, 2009. Please, find attached information (First Circular) about this Scientific Conference. We hope that you or some of your colleagues will be interested to attend the Conference.

Sessions will convene in the mornings and early afternoons and will include lectures by invited speakers, as well as talks and poster presentations selected from submitted abstracts. The invited key speakers are:

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*Dr. Kevin de Queiroz*, National Museum of Natural History, Smithsonian Institution, USA

*Prof. Kevin N. Laland*, Centre for Social Learning and Cognitive Evolution, School of Biology, University of St. Andrews, Scotland**

*Dr. Thord Fransson*, Swedish Museum of Natural History, Sweden**

*Prof. Carlo Heip*, Centre for Estuarine and Marine Ecology (CEME) and General Director of the Royal Netherlands Institute of Sea Research, The Netherlands

*Prof. Fritz F. Steininger*, Research Institute and Natural History Museum Senckenberganlage, Frankfurt am Main, Germany

*Prof. Gary R. Carvalho, *School of Biological Sciences, University of Bangor, Environment Centre Wales, Bangor, UK

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I look forward to welcoming you in Irakleio (Crete) for a scientifically stimulating and socially enjoyable meeting.

With best regards,

On behalf of the Organizing Committee

Nikos Poulakakis

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11iczegar <11iczegar@nhmc.uoc.gr>

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## LeibnizInst ConservationEvolutionaryGenomics Sep21-24

On behalf of the Leibniz Institute for Zoo and Wildlife Research (IZW) and the European Association of Zoos and Aquaria (EAZA) I would like to invite you to the

"7th International Conference on Behaviour, Physiology and Genetics of Wildlife",

The Conference will be held between the 21st and 24th September 2009 in Berlin, Germany.

The aim of the meeting is to foster an exchange of ideas between wildlife scientists from different disciplines with an interest in both wild and captive mammalian species.

The main topics of the conference are:

- Life History & Maternal Effects

(Pat Monaghan, Universtity of Glasgow, UK)

- Stress & Disturbance

(Marco Apollonio, Universita Sassari, Sardinien)

- Reproduction Biology

(David Wildt, Smithsonian National Zoological Park, USA)

-Evolutionary Genomics in Conservation

(Pierre Taberlet, Université Joseph Fourier, Grenoble, France)

-Conservation Biology

(Eric Dinerstein, senior scientist WWF USA, Washington, USA)

The Conference offers several workshops: - Evolutionary Genomics in Conservation (Pierre Taberlet, Simone Sommer, IZW)

- Communication in Mammals and Birds (Francesco Bonnadonna, Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, France, Martin Dehnhard, IZW)

- Welfare and Conservation (Eric Dinerstein, senior scientist WWF USA, Washington, USA)

- Nutrition and Energetics (Carlos Martinez del Rio, University of Wyoming, USA, Sylvia Ortmann, IZW, Christian Voigt, IZW)

- Behavioural Rhythms (Serge Daan, University of Groningen, The Netherlands)

- Research by, in, with and for zoos, aquaria and other ex situ-institutions (Kirstin Leus, Zoo Antwerp, Belgium)

A practical training workshop on non-invasive monitoring of hormones will be run during the week before the conference (Martin Dehnhard, IZW).

You will find more information about the conference on our homepage at: http://www.izw-berlin.de/willkommen.html

Yours sincerely, Simone Sommer

Prof Dr Simone Sommer Evolutionary Genetics, Leibniz-Institute for Zoo- and Wildlife Research & Evolutionary Ecology, University of Potsdam Leibniz-Institute for Zoo- and Wildlife Research (IZW) Alfred-Kowalke Str. 17 D-10315 Berlin Tel. +49 30 5168 315 Fax +49 30 5126 104

SOMMER@izw-berlin.de

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## Leiden Systematics Aug10-14

Dear colleagues,

The National Herbarium of the Netherlands and the National Museum of Natural History Naturalis want to announce

"Systematics" BioSystEU 2009 10-14 August 2009

The combined:

First meeting of BioSyst EU

Seventh Biennial Conference of the Systematics Association

11. GfBS-Jahrestagung

BioSyst EU (www.biosyst.eu < http://www.biosyst.eu > ), the federation of European systematic societies, was founded in 2006. It aims to provide a European platform to:

* promote research, teaching, and training in all areas of systematic biology * encourage collaboration and interchange among researchers, coordinate national and international efforts * support and represent researchers in countries lacking formal systematic societies * represent systematic biology in the European parliament

Participarting societies include:

GfBS - Gesellschaft für Biologische Systematik (Germany)

NOBIS - Network of Biological Systematics Austria (Austria)

SFS - Société Française de Systématique (France)

Swiss Systematics Society (Switzerland)

The Systematics Association (UK)

The conference will be the first of a series of quadrennial European conferences for biological systematics. These meetings will encourage both formal and informal collaboration among systematic biologists and other interested researchers across Europe.

Sessions will include major themed symposia; timely 'how-to' talks on important emerging topics by leaders in the field, and generous time allocation for contributed papers or posters by students and established researchers on any topic in systematics.

The conference is open to everyone; we especially encourage participation of research students and researchers in the early stages of their careers.

Student Bursaries

To encourage student participation, competitive bursaries will cover registration, accommodation costs and the conference dinner (but not travel) for students presenting a paper on their own research work. For details and an online application form, see the Systematics Association website: www.systass.org . Deadline for Registration and Submission of Abstracts 30th June 2007. A late registration surcharge will apply after this date.

Conference venue

Leiden houses the major biodiversity collections of the National Museum of Natural History Naturalis and the National Herbarium of the Netherlands. It has one of the largest and most attractive historical town centres of the Netherlands, and is centrally located with excellent connections to Amsterdam, The Hague and Schiphol Airport. The conference venue is within walking distance of Leiden Central Station

For more information, registration and booking details, see www.biosyst.eu < http://www.biosyst.eu > or contact Peter Hovenkamp Hovenkamp@nhn.leidenuniv.nl <mailto:Hovenkamp@nhn.leidenuniv.nl> (National Herbarium of the Netherlands, Leiden University branch).

Prof. dr. E.F. Smets

Scientific Director National Herbarium of the Netherlands Leiden University branch P.O. Box 9514 2300 RA Leiden The Netherlands

www.nationaalherbarium.nl

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## Lyon EvolutionBehaviour Apr6-10

5th Â≪ Evolution & Behaviour Â≫ Meeting

Monday 6 - Friday 10 April 2009, Lyon (France).

The “Evolution & Behaviour” Meeting is an international meeting with the main purpose of promoting postgraduate research and interactions between young researchers in Behavioural Evolution. One specificity of this meeting, which is organized by the SERL PhD students association, is that it is free for all participants: you only have to pay for your trip to Lyon.

This year, the “Evolution & Behaviour” Meeting consists of four days of conferences divided into six themes: * Sexual Selection * Foraging * Parasitism and predation * Habitat selection and dispersal * Collective behaviour * Applied Behavioural ecology

Each session will be introduced by two invited professors specialized in this field of research, followed by 8-10 postgraduate student research presentations and discussions. In addition, poster sessions and three “theme evenings” designed for a broad public are planned.

The number of participants will be limited to 100 postgraduate students.

Participants are expected to give a 10-minute talk. In order to register please submit the abstract of your talk (or poster) (300 words maximum) on the website: http://serl2009.univ-lyon1.fr (see the website for supplementary information). Registration and submission of abstracts are opened until March 2nd.

Hope to see you in April,

SERL Association 2009.

oudenhove@biomserv.univ-lyon1.fr
oudenhove@biomserv.univ-lyon1.fr

## ManchesterU TropicalEvolution Mar30-31

Open to ecologists and evolutionary biologists working on tropical systems

3rd British Ecological Society -Tropical Ecology Group Early Career Researcher Meeting - FINAL CALL FOR ABSTRACTS - DEADLINE 31ST JANUARY

Held at: Manchester Metropolitan University, Manchester UK 30th & 31st March 2009

Plenary Speakers: Robin Chazdon (University of Connecticut) Charles Sheppard (University of Warwick)

Plus: Lloyd Peck - UK NERC Biodiversity theme leader will be speaking

Registration: £60 before 31st Jan 2009; £70 after this date (En suite B & B accommodation available for £39.50) Abstract closing date 31st January 2009 50% discount for students - limited availability, contact organizers NOW!

CONTACT: Francis Brearley (f.q.brearley@mmu.ac.uk) or Jenny Rowntree (jennifer.rowntree@manchester.ac.uk)

Facebook page: http://www.facebook.com/editevent.php?info&eid=3D40770566187#/event.php?eid@770566187

jkrowntree@mac.com

## Marseilles 13thEvolutionaryBiology Sep22-25

Dear All,

We are pleased to inform you that the 13th Evolutionary Biology Meeting at Marseilles will take place on 22-25 September 2009 and that you can register at http://sites.univ-provence.fr/evol-cgr The following subjects will be discussed:

- Evolutionary biology concepts and modelisations for biological annotation; - Biodiversity and Systematics; - Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogeny; - Environment and biological evolution; - Origin of Life and exobiology; - Non-adaptative versus adaptative evolution; - The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge.

For more information, do not hesitate to go on: http://sites.univ-provence.fr/evol-cgr

Best wishes and Happy New Year!

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

## Marseilles 13thEvolutionaryBiology Sep22-25 2

Dear All,

We are pleased to announce you that the early deadline of the 13th Evolutionary Biology Meeting at Marseilles 22-25 September 2009, Marseilles, France will be on 31st January.

For more information, do not hesitate to go on: http://sites.univ-provence.fr/evol-cgr Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

## Ottawa SystemsBiology Apr23-24

The Ottawa Institute of Systems Biology and the National Research Council are organizing a symposium entitled “Progress in Systems Biology Symposium: The Brain and Mind”. This Symposium will take place in Ottawa on April 23rd and 24th 2009. More information on the symposium is available at www.oisb.ca < http://www.oisb.ca > . I would appreciate if you could forward the information to other researchers that might be interested in this symposium.

Location: National Research Council of Canada, 100 Sussex Drive, Ottawa,Canada

Keynote Speakers

Dr. Seth Grant, Wellcome Trust Sanger Institute, Cambridge, England Dr. Hanfa Zou, National Chromatographic R&A Center, Dalian, China Dr. Arturas Petronis, University of Toronto, Toronto, Canada Dr. Alexandra Golby, Harvard Medical School, Boston, USA Dr. Frank Sharp, University of California, Davis, USA Dr. Freda Miller, University of Toronto, Toronto, Canada

Early Bird Registration Deadline and Poster Submission: March 1, 2009

For more information and to register, please visit: www.oisb.ca Contact information: sysbio@uottawa.ca or phone (613) 562-5800 ext. 8073

Regards, Daniel

Dr. Daniel Figeys Director, Ottawa Institute of Systems Biology Canada Research Chair in Proteomics and Systems Biology Professor, Department of Biochemistry University of Ottawa BMI department, room 4510D 451 Smyth Road Ottawa, Ontario K1H 8M5

(613) 562 5800 ext 8674 613-562-5655 (fax)

Rachel Figeys Assistant to the OISB Director Room 4510E, 451 Smyth Road University of Ottawa, Faculty of Medicine Ottawa, Ontario, K1H 8M5 Phone: 613-562-5800 x 8073 Fax: 613-562-5655 Email: sysbio@uottawa.ca <mailto:sysbio@uottawa.ca> or rfigeys@uottawa.ca <mailto:rfigeys@uottawa.ca> Website: www.oisb.ca < http://www.oisb.ca >

Daniel Figeys <dfigeys@uottawa.ca>

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## Shanghai MolSystemsBiol Jun21-25

11th International Conference on Molecular Systems Biology http://www.picb.ac.cn/icmsb2009 June 21-25, 2009 Chinese Academy of Sciences - Max Planck Society Partner Institute for Computational Biology, Shanghai, China

For the past years, active research in systems biology has generated many promising and intriguing experimental, theoretical, and computational results. At the 11th International Conference on Molecular Systems Biology (ICMSB'09, Shanghai), world experts from many relevant fields will meet in Shanghai to present and discuss recent advances and new applications in molecular systems biology, and exchange emerging research ideas. We strongly encourage participation by young researchers and graduate students from all over the world. The ICMSB'09 will be hosted by the CAS-MPG Partner Institute for Computational Biology (PICB). The city of Shanghai is a dynamic center of economy, commerce, science and technology in . It provides an excellent environment for scientists to interact and identify potential collaborations.

We are now open to accept contributed talks and posters for all areas in molecular systems biology including (but not limited to) the following topics:

* Mathematical modeling and simulation of biosystems and their evolution * Functional genomics and proteomics * Identification and analysis of gene regulatory networks * Identification and analysis of protein-protein interaction networks * Identification and analysis of metabolic networks * Computational approaches to complex genetic diseases * Synthetic biology and circuitry

ABSTRACT SUBMISSION DEADLINE

March 15, 2009

SCIENCE ADVISORY BOARD

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Tel: +(86)-21-54920460 Fax: +(86)-21-54920451 E-mail: lihaipeng@picb.ac.cn

## Switzerland EvolutionOfSexDetermination Jun17-20

We open registration for a 3-days meeting (June 17-20, 2009) on the evolution of sex-determination mechanisms. Brief description and address for registration at http://www.unil.ch/dee/page62605_fr.html Invited speakers include D.Charlesworth, W Rice, RH Devlin, F.Janzen, L.Beukeboom, M.Beye, and M.Kirkpatrick

The meeting will take place in a small village in the Swiss Alps (La Sage, Val d'Herens)

Fees are Euro 300.- , including inscription and full accommodation.

When registering, please send a short statement of research interests, and an abstract if you plan to contribute a talk.

Deadline 1st of March 2009

Nicolas Perrin Dept. Ecology & Evolution University of Lausanne (Switzerland) http://www.unil.ch/dee/page5090_en.html Tel (0041) 21 692 41 84 new mail: nicolas.perrin@unil.ch

Nicolas Perrin <Nicolas.Perrin@unil.ch>

## Turin ESEB2009 EvolutionaryTranscriptomics Aug24-29

We invite interested people to submit abstracts for oral/poster presentation in the symposium "Evolutionary transcriptomics", which will take place at the next congress of the European Society for Evolutionary Biology (24-29 August 2009, Turin, Italy)

This symposium will focus on genome-wide analysis of gene expression, with emphasis on the genetic mechanisms, ecological conditions, and selective forces responsible for expression variation within species and/or expression divergence between species.

To submit your abstract (deadline 15 February 2009) and get useful information about the congress, please go to http://www.eseb2009.it/uk EVOLUTIONARY TRANSCRIPTOMICS In recent years, the fundamental role of gene expression in shaping phenotypes has been recognized. The tempo and mode of expression of a particular gene, i.e. of a transcript, can influence an organism's morphology, physiology and behavior. As such, the regulation of gene expression is an important evolutionary process and variation in gene expression levels provides a substrate for natural selection. High-throughout methods, such as microarrays, have made it possible to investigate the expression level of all genes in the genome, i.e. the transcriptome. An increasing number of researchers are using these methods to evaluate the role of the transcriptome in phenotypic evolution. These include studies of gene expression polymorphism within populations to understand the forces that maintain/limit expression variation, as well as comparative studies that seek to identify the specific expression changes underlying phenotypic differences. There are many open questions in this field that researchers are only now beginning to address. Examples include the role of selective versus neutral forces in driving the evolution of gene expression, and the relative importance of cis- versus trans- regulation in transcriptome evolution. The aim of this symposium is to bring together leading experts to discuss and share information in this fast-growing area of research, which encompasses fields such as evolution, development and ecology.

Organizers: John Parsch, University of Munich, Germany (parsch@bio.lmu.de) Lino Ometto, University of Lausanne, Switzerland (lino.ometto@unil.ch)

Lino Ometto

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## Turin ESEB2009 SexualSelection Aug

There is a symposium to be held at the European Society for Evolutionary Biology Congress in Turin, Italy (August 2009) entitled âAre âGood Genesâ theories of sexual selection finally sinking into the sunset?â The rationale behind this symposium is described below.

Abstracts for oral or poster presentations need to be submitted to the main conference web site at http://www.eseb2009.it/uk/ by February 15th. Unfortunately, we cannot offer any financial help.

Rationale

âGood Genesâ models and interpretations of mate choice have dominated sexual selection since at least 1975, and much of the empirical research in behavioural ecology and evolutionary genetics has emphasised the maintenance of genetic variation of indicator traits and fitness. In the last ten to fifteen years, views of sexual selection have shifted to emphasise exploitation and sexual conflict, which predicts cheating and sexually antagonistic coevolution. Also, studies of genotype by environment interaction and indirect genetic effects have demonstrated that there are numerous ways in which genetic variation can be maintained for sexually advantageous traits and fitness. Many of these recent results make the maintenance of genetic variation in sexually selected traits easier to understand. However, in turn this raises the question of whether such genetic variation is likely to provide predictable genetic benefits for offspring. Can sexually antagonistic selection maintain adaptive mate choice? Is there any need to invoke good genes explanations for elaborate sexual traits any more? We encourage speakers from both sides of the argument to apply, and we hope that the deliberately provocative tone will prompt a lively exchange of views.

Invited speakers: Adam Chippendale (assessment of extent and significance of antagonistic genetic variation in Drosophila). Anna Qvarnström (empirical studies of natural genetic variation in birds)

Organisers: Mike Ritchie, University of St Andrews, Scotland. mgr'AT'st-and.ac.uk Nathan Bailey, University of California, Riverside, USA. nathanb'AT'ucr.edu

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Mike Ritchie School of Biology Dyers Brae House University of St Andrews St Andrews, Fife Scotland KY16 9TH

Phone 0 (44 outside UK) 1334 463495 Fax 0 (44 outside UK) 1334 463366

Website: http://bio.st-andrews.ac.uk/staff/mgr.htm PDFs etc: http://biology.st-and.ac.uk/supplemental/ritchie/papers.aspx Mike Ritchie <mgr@st-andrews.ac.uk>

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## Turin ESEB asexual Aug24-29

Conference: Turin.ESEB_asexual.Aug24.29

We invite submissions of abstracts for talks in our symposium 'The genetic consequences of reproductive modes: insights from asexual species', which will be held at the 2009 congress of the European Society for Evolutionary Biology (24-29 August, Turin, Italy).

For abstract submission and information, follow this link http://www.eseb2009.it/uk Submission deadline of abstracts is February 15th, 2009.

This Symposium will explore experimental work that has started to unravel the evolution of asexual reproduction at the genetic level.

Confirmed speakers

David Mark Welch, Marine Biological Laboratory, USA

Shannon Hedtke, Univeristy of Texas, USA

Given the overlap between our session and several others, please feel free to contact us regarding whether your abstract would be appropriate for our session.

Please send questions to both:

Karine Van Doninck, University of Namur, Belgium kvandoni@fundp.ac.be Diego Fontaneto, Imperial College London, UK d.fontaneto@imperial.ac.uk

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

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## Turin ESEB EarlyEvolution Aug24-29

Dear colleagues,

We would like to invite interested people to submit abstracts for oral and poster presentations for the symposium “EARLY EVOLUTION”, which will take place at the next conference of the European Society for Evolutionary Biology in Turin, Italy (24-29 August 2009).

Description: The molecular era has had a profound impact on our view of early evolution, notably by allowing reconstructing a tree of life describing the history of present-day organisms and their evolutionary relationships. Since the first trees of life based on comparison of ribosomal RNA sequences around thirty years ago, a number of hypotheses have been put forward on the origin of the three domains of life, Eukarya, Archaea, and Bacteria, as well as the nature of the last universal common ancestor (LUCA). Debate is still lively and continuously revived with the accumulation of genomic data and use of new analytical approaches, such as phylogenomics. The symposium is designed to put together scientists working on different aspects of early evolution. We will consider proposals in different areas of investigation, including the origin and evolution of the three domains of life and their relationships, the origin and evolution of early metabolic pathways and cellular structures, the mechanisms for genome evolution such as horizontal gene transfer and the origin of operons, and the evolution of regulatory signals and networks.

Invited speakers: Purification Lopez-Garcia (University of Paris Sud, France) Paola Londei (University of Rome La Sapienza, Italy)

To submit your abstract (deadline 15 February 2009) and obtain further information about the congress, please go to http://www.eseb2009.it/uk Organisers: Simonetta Gribaldo, Institut Pasteur, Paris, France simonetta.gribaldo@pasteur.fr Renato Fani, University of Florence, Italy renato.fani@unifi.it

simo@pasteur.fr simo@pasteur.fr

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## Turin ESEB EcoGenetics Aug24-29

We invite submissions of abstracts for talks in our symposium 'Ecological Genetics in the Genomic Era', which will be held at the 2009 congress of the European Society for Evolutionary Biology (24-29 August, Turin, Italy).

For abstract submission and information, follow this link (http://www.eseb2009.it/uk ) Submission deadline of abstracts is February 15th, 2009.

This session focuses on research integrating ecology, molecular biology, and evolution with the goal of understanding how genetic variation affects performance and fitness in the wild. Our emphasis will be on systems where the ecology is well understood and genomic resources are being developed and applied.

Confirmed speakers

Jon Slate, University of Sheffield, UK

Thomas Lenormand, Universite Montepellier, France

Given the overlap between our session and several others, please feel free to contact us regarding whether your abstract would be appropriate for our session.

Please send questions to either/both:

Christopher W. Wheat, Penn State Univ & University of Helsinki cww10@psu.edu

Jay F. Storz, School of Biological Sciences University of Nebraska jstorz2@ unl.edu Christopher W. Wheat, Ph. D.

http://www.christopherwheat.net Postdoctoral Fellow

Pennsylvania State University & University of Helsinki

Christopher W. Wheat, Ph. D.

http://www.christopherwheat.net Postdoctoral Fellow

Pennsylvania State University & University of Helsinki

cww10@psu.edu

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## Turin ESEB EvoDevo Aug24-29

Dear friends,

we invite you to consider the opportunity to contribute to the evo-devo symposium we are organizing at ESEB 2009, the congress of the European Society for Evolutionary Biology (Turin, Italy, 24-29 August 2009).

The congress website is at http://www.eseb2009.it/ Here is a short outline of our symposium:

31. The evolution of development across the species boundary

Organisers: Giuseppe Fusco, University of Padova, Italy (giuseppe.fusco@unipd.it) and Alessandro Minelli, University of Padova, Italy (alessandro.minelli@unipd.it)

This symposium will explore the hitherto neglected relationships between the evolution of development and microevolution, with emphasis on speciation. This approach is largely complementary to the traditional focus on comparisons between distantly related model organisms.

Invited speakers: Gregory Wray, Duke University, USA and Barbara Gravendeel, University of Leiden, The Netherlands

Deadline for registration and submission of abstracts is February 15.

Cordially yours

Giuseppe Fusco and Sandro Minelli

Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail giuseppe.fusco@unipd.it webpage http://-dept.bio.unipd.it/fusco

Giuseppe Fusco <giuseppe.fusco@unipd.it>

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## Turin ESEB EvolutionaryApplications Aug24-29

We are inviting abstract submissions for oral and poster presentations for the symposium "Evolutionary applications", which is sponsored by Wiley-Blackwell, to be held for a full day on August 26 2009 at the European Society for Evolutionary Biology (ESEB) meeting in Turin, Italy (August 24-29 2009).

Abstracts must be submitted online at http://-www.eseb2009.it/uk/ by February 15 2009 latest.

There will be time for 14 oral presentations including three by invited speakers (see below). The organizers will choose among the abstracts who will be accepted for both oral and poster presentations based on the quality and importance of scientific content of the abstracts. The organizers will communicate their decisions to the corresponding authors of abstracts by March 31st. Wiley-Blackwell as well as the chief and managing editors of the journal Evolutionary Applications will convey the senior author of all oral presentations for a diner in one of the fine restaurants of Turin.

DESCRIPTION OF SYMPOSIUM: The average rate of loss for animal and plant populations and their habitats is estimated to be 1% per year with two-thirds of the world's terrestrial land area now devoted to supporting human populations, either through agriculture, fisheries, urbanization or infrastructure. Growing empirical evidence indicates that these human activities are altering the evolutionary trajectories of species imperative to our natural heritage and economic wellbeing. While resource managers have largely focused on threats causing population declines and extinction, little attention is being paid to the consequences of altering the course of evolution of species found in these human altered environments. In this context, the main goal of this symposium is to highlight the growing relevance of utilizing concepts from evolutionary biology to address biological questions of health, social and economic relevance. We feel that such symposium is particularly timely given the current general trend to limit resources available for conducting basic research in evolution compared to other research disciplines.

CONFIRMED INVITED SPEAKERS: Dieter Ebert, Univeristy of Basel, Switzerland Juha Merilä, University of Helsinki, Finland Steve Stearns, Yale University, USA

We are looking forward to seeing you in Turin. The organizers : Louis Bernatchez, Université Laval, Canada (Louis.Bernatchez@bio.ulaval.ca) Dany Garant, Université de Sherbrooke, Canada (Dany.Garant@USherbrooke.ca)

Dany.Garant@USherbrooke.ca
Dany.Garant@USherbrooke.ca

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## Turin ESEBi Ecol Selection Aug24-29

Dear EvolDir,

We would like to invite abstract submissions for oral and poster presentations at the upcoming European Society for Evolutionary Biology meetings in Turin this summer (http://www.eseb2009.it/uk/) for a symposium entitled:

The phenotype-fitness map re-visited: agents of selection and the importance of ecology in evolutionary studies.

This symposium aims to assemble evolutionary studies that seek to identify, understand and describe the agents of natural and/or sexual selection, and the specific environmental factors, such as food resources, social environments, predation, among others that shape the selective landscape. We would especially like to highlight studies that illustrate how knowledge of specific ecological factors plays an important role in understanding the process of selection in the wild.

The symposium will be open to 5 oral presentations from submitted abstracts and will also feature two invited speakers:

Stevan Arnold (Oregon State University, Corvalis)

Craig Benkmann (University of Wyoming, Laramie).

For pre-submission enquires, please email the organizers:

Alexis Chaine: <mailto:alexis.chaine@ecoex-moulis.cnrs.fr> alexis.chaine@ecoex-moulis.cnrs.fr

Erik Svensson: Erik.Svensson@zooekol.lu.se

Alexis Chaine <alexis.chaine@EcoEx-Moulis.cnrs.fr>

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## Turin ESEB KinSelection Aug24-29

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We are inviting abstract submissions for oral and poster presentations for the symposium "Recent Advances in Kin Selection", to be held on August 29 2009 at the European Society for Evolutionary Biology (ESEB) meeting in Turin, Italy (August 24-29 2009).

For abstract submission and further information, please visit http://www.eseb2009.it/uk/ by February 15 2009.

DESCRIPTION OF SYMPOSIUM

The aim of this symposium is to discuss recent advances in Kin Selection Theory, including the evolution of altruism and spite, intragenomic conflict, and social evolution.

INVITED SPEAKERS

Alan Grafen, Oxford University http://users.ox.ac.uk/~grafen Stuart West, Oxford University http://westgroup.biology.ed.ac.uk ORGANIZERS

Francisco Ubeda, University of Tennessee, USA Email: fubeda@utk.edu Web: http://www.tiem.utk.edu/~fubeda/ Andy Gardner, University of Edinburgh, UK Email: andy.gardner@ed.ac.uk Web: http://www.biology.ed.ac.uk/research/groups/gardner – Andy Gardner Royal Society University Research Fellow

Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road Edinburgh EH9 3JT United Kingdom

Email: andy.gardner@ed.ac.uk Tel: +44 (0) 131 535 4110 Fax: +44 (0) 131 650 6564

http://www.biology.ed.ac.uk/research/groups/gardner/ The University of Edinburgh is a charitable body, registered in Scotland, with registration number

andy.gardner@ed.ac.uk andy.gardner@ed.ac.uk

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## Turin ESEB MaleFemaleCoevolution Aug24-29

ESEB conference, Turin, 24th-29th August 2009

We invite abstracts for oral and poster contributions to a symposium: - Male-female coevolution - from molecules to species' to be held at the 12th Congress of the European Society for Evolutionary Biology from the 24th-29th of August in Turin, Italy. For further information and to register, please see: http://www.eseb2009.it/uk/ Confirmed invited speakers: Mariana Wolfner (Cornell); Kerry Shaw (Cornell); Mohamed Noor (Duke).

Symposium summary: The study of male- female coevolution has gained increasing attention in evolutionary ecology and is of particular interest given the potential roles of sexual selection and sexual conflict in species formation. Sexual selection, occurring at the premating or postmating level has been shown to shape a number of morphological and physiological traits. These changes can ultimately reduce gene flow and lead to the evolution of reproductive isolation. Our understanding of phenotypic trait evolution due to male-female coevolution is currently being rapidly augmented by studies of the underlying genes and molecules involved. Advances in molecular biology, and particularly genomics, are now allowing researchers to observe the evolutionary processes resulting from interactions between the sexes. In this symposium we aim to provide a synthesis of the current knowledge of male-female coevolution from the level of the gene to the whole organism. This symposium will provide a synthesis of recent advances in our understanding of male - female coevolution, covering evolution in molecular, morphological and physiological traits and the role of sexual selection and sexual conflict in driving these changes will be investigated.

We look forward to meeting you in Turin

Claudia Fricke and Tracey Chapman

School of Biological Sciences, University of East Anglia, UK e-mail: c.fricke@uea.ac.uk; tracey.chapman@uea.ac.uk

"Chapman Tracey Dr (BIO)" <Tracey.Chapman@uea.ac.uk>

## Turin ESEB meeting Aug24-29

The 12th Congress of the European Society for Evolutionary Biology will be held in Torino, Italy, August 24 -29, 2009

The structure of the congress is similar to previous meetings, each day starting with a plenary keynote speaker, followed by 30 parallel symposia. Other events will be the traditional John Maynard Smith lecture and the presidential address of the new President of ESEB, prof. Siv Andersson, University of Uppsala.

The congress will cover the field of evolutionary biology in a wide sense, but with emphasis on processes and mechanisms of evolutionary phenomena. For description of symposia, abstract submission, hotel accommodation, social events and updates please visit the congress website www.eseb2009.it < http://www.eseb2009.it/ >

Registration is now open. No more that 1200 participants can be accepted. Deadline for early registration (reduced price) and submission of abstracts is 15th of february 2009. Gabriella Sella & Cristina Lorenzi

– Maria Cristina Lorenzi

Dipartimento di Biologia Animale e dell'Uomo, Universita' di Torino Via Accademia Albertina 13, 10123 Torino, Italy tel. +39 011 670 4512 fax. +39 011 670 4508

e-mail: cristina.lorenzi@unito.it

Cristina Lorenzi <cristina.lorenzi@unito.it>

## Turin ESEB NaturalVarition Aug24-29

Dear Colleagues,

We invite submissions of abstracts for talks or poster presentations for our symposium on âFunctional analysis of natural variationâ at the 2009 congress of the European Society for Evolutionary Biology (24th-29th August, Turin Italy).

For abstract submission and information about the congress, please go to http://www.eseb2009.it/uk Note that the deadline for submission of abstracts is February 15th 2009.

Our symposium is aimed at researchers in the fields of evolution, population genetics and development and will discuss the application of the latest technology to identify adaptive natural variation and the functional characterization of natural variation in a range of organisms.

Organisers: Jean-Michel Gibert (Jean-Michel.Gibert@zoo.unige.ch), Alistair McGregor (alistair.mcgregor@vu-wien.ac.at) and Christian Schlötterer (christian.schloetterer@vu-wien.ac.at)

Functional analysis of natural variation

It is well understood that natural populations carry a wealth of molecular variation. While it has been assumed for a long time that most of this variation is neutral, there is increasing evidence that a large proportion is functionally different and thus subjected to different evolutionary forces.

After the first phase in the genomics projects, which were focusing on the sequencing of one genome for each species, the emphasis has now shifted to the genome wide characterization of natural variation. In particular the new generation of sequencing technology (454, Solexa etc.) is contributing to a hitherto unprecedented wealth of information about naturally occurring sequence variation. Nevertheless, the advances in cataloging natural variation are not matched with our advances in understanding the functional differences among the naturally occurring alleles.

Compared to classic forward genetics, which typically isolated mutations with strong effects, naturally occurring alleles are expected to show only subtle differences in function, which may nevertheless have dramatic effects in nature. Hence, the analysis of natural variation requires new approaches and tools to understand the functional differences of naturally occurring alleles.

The symposium aims to gather researchers using the latest technology to identify adaptive natural variation and those using a broad range of methods to functionally characterize natural variation in a range of organisms.

Alistair P. McGregor

Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Vienna Austria

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McGregor_website/mcgregor_home.html Alistair McGregor <alistair.mcgregor@vu-wien.ac.at>

## Turin ESEB OriginsOfNovelty Aug24-29

Dear Colleagues,

We would like to invite interested people to submit abstracts for oral and poster presentation in the symposium "ON THE ORIGINS OF NOVELTY IN DEVELOPMENT AND EVOLUTION: FROM CRYPTIC GENETIC VARIATION TO GENETIC ACCOMMODATION", which will take place at the next congress of the European Society for Evolutionary Biology (24-29 August 2009) in Turin, Italy

To date, speakers include Andreas Wagner (University of Zurich, Switzerland), Susan A. Foster (Clark University, USA), and Ian Dworkin (Michigan State University, USA).

To submit your abstract (deadline 15 February 2009) and get further information about the congress, please go to http://www.eseb2009.it/uk To learn more about the goals of this symposium please see the a summary of the symposium proposal below.

>>>> ON THE ORIGINS OF NOVELTY IN DEVELOPMENT AND EVOLUTION: FROM CRYPTIC GENETIC VARIATION TO GENETIC ACCOMMODATION

The origins of novel features is both one of the oldest and, at the same time, one of the most poorly understood frontiers in evolutionary biology. While evolutionary biologists have developed powerful theoretical frameworks and experimental tools to understand the evolutionary modification of existing traits, we know remarkably little about the ecological, genetic, and developmental mechanisms, and the interactions between them, that mediate the origin of novel features. In fact, even the terminology is often misleading and considerable debate exists regarding exactly what constitutes novelty in evolution. Where does variation end and innovation begin?

Recent progress in evo-devo and allied disciplines may now allow us to move beyond current roadblocks in our understanding of the mechanics of innovation. Specifically, the canalizing nature of development, the accumulation of cryptic genetic variation free to drift within populations until freed by above-threshold environmental or genetic perturbations and the process of evolution by genetic accommodation, provide a set of interrelated mechanisms of much unexplored potential to explain rapid diversification, recurrence of lost phenotypes as well as the origins of novel features.

The proposed symposium is designed to make two important contributions. (1) First, on a general level it is intended to bring together scientists whose work focuses on the evolution of developmental mechanisms underlying evolutionary novelties and adaptive radiations, and the ecological mechanisms driving such evolution. In this context, the symposium hopes to foster a discussion on (a) what constitutes innovation in evolution, (b) the developmental properties that facilitate as well as constrain evolutionary innovation, and (c) the population-genetic and ecological forces that guide such evolution in natural populations. (2) On a more specific level, this symposium will explore the causes and consequences of cryptic genetic variation and its contributions to evolutionary diversification and innovation. In this context the symposium hopes to (a) facilitate a better understanding of the interplay between developmental processes, environmental variation, and genetic properties of populations as well as (b) design strategies to evaluate the importance of genetic accommodation in nature.

Lastly, the symposium is designed to facilitate an integration of micro- and macroevolution (by focusing on both population-level evolution and cladogenesis), to transcend taxonomic boundaries (by including presentations across phyla as well as on organismal interactions) and conceptual boundaries (by integrating across morphology, behavior, physiology, genetics, and genomics). As such this symposium hopes to make an important contribution towards a better understanding of the nature of innovation in evolution including its causes, mechanisms, and consequences.

Organizers: Armin Moczek, Indiana University, Bloomington (armin@indiana.edu) Emilie Snell-Rood, Indiana University (emcsnell@indiana.edu)

emcsnell@indiana.edu emcsnell@indiana.edu

## Turin ESEB ParasiteEvolution Aug24-29

We are inviting abstract submissions for oral and poster presentations in the symposium "Integrating ecology with parasite evolution" to be held on August 28

2009 at the European Society for Evolutionary Biology(ESEB) meeting in Turin, Italy (August 24-29 2009).

Abstracts should be submitted online at http://www.eseb2009.it/uk/by February 15 2009.

DESCRIPTION OF SYMPOSIUM: The enormous abundance of parasites and their effects on wild populations, agriculture and human health have given rise to a rapidly growing field centered on using evolutionary principles to understand infectious disease. This field does not only significantly contribute to our general understanding of evolutionary theory, but also has the potential to provide new ways of tackling disease. The last few decades have seen much progress in understanding general evolutionary processes in parasite biology, and have also revealed the important role of genetic interactions between hosts and parasites. However, much less attention has been paid to the effect of the ecological conditions under which hosts and parasites interact. This is a serious problem, because empirical studies are increasingly showing that in-host and external environmental factors (e.g. temperature, host diet and the presence of competitors) can shape parasite virulence, life-histories, within-host dynamics and transmission. The aim of this symposium is to bring together theoreticians and empiricists to explore how ecology influences the evolution of parasites. This will not only advance understanding of the basic processes by which parasites evolve, but also provide a basis to predict the consequences of human interventions on infectious disease.

INVITED SPEAKERS: Mike Boots, University of Sheffield, UK Anna-Liisa Laine, University ofHelsinky, Finland

ORGANIZERS: Sarah Reece, University of Edinburgh, UK (Sarah.Reece@ed.ac.uk) Jacobus de Roode, Emory University, USA (jacobus.deroode@emory.edu)

jderood@emory.edu jderood@emory.edu

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## Turin ESEB PollinatorSelection Aug24-29

You are invited to submit abstracts for oral / poster presentation in the symposium "Pollinator-mediated selection in floral evolution", which will be held in the ESEB meeting in Turin, Italy, at August 29th 2009. Please submit your abstract through the website http://www.eseb2009.it/ . Deadline for abstract submission and early registration - 15 February 2009.

Symposium description Pollination biology is an exciting field at the nexus of evolutionary genetics, ecology, behavior and plant and animal phylogenetics. Many pollination studies have accumulated in the last century on many plant species, and researchers are starting to bridge the gap between population-level processes (e.g., pollinators and plants communities), lineage-scale phenomena (e.g., adaptive divergence, male/female function), and the molecular genetics underlie them. It is an ideal time to assess the progress to date in developing a cohesive framework for understanding the role of pollinators in floral evolution and to lay the groundwork for future research directions. There is a solid evidence for selection on floral traits that is mediated by pollinators' preferences and flower-pollinator fit. Evolution in response to pollinator-mediated selection is a multi-layer process. First, it depends on the flower's ability to evolve - the genetic variation of floral traits and its constraints. Second, pollinators' preferences and behavior is influenced by many factors, some of which are floral traits. Finally, phylogenetic and biogeographical patterns affect both floral divergence and plant-pollinator communities. In short, pollination should be considered as an evolutionary process that involves many components simultaneously - from quantitative genetics to community ecology. This symposium will bring together researchers whose work represents methodological and theoretical advances in the discipline. It will provide a forum for the synthesis of the results from several areas of evolutionary research, and will produce comprehensive view of the evolutionary aspects of pollination. First, the genetic basis of floral evolution will be examined from the plant point of view. Second, the interface of floral traits, pollinator's behavior, and selection will be investigated. And third, pollination systems will be explored in the broad context of phylogeny and biogeography.

Invited speakers Thomas Hansen, University of Oslo, Norway Rebecca Irwin, Dartmouth College, USA

Symposium organizers Scott Armbruster, University of Portsmouth, UK. scott.armbruster@port.ac.uk Yuval Sapir, Tel Aviv University, Israel. sapiryuval@gmail.com

sapiryuval@gmail.com

## Turin ESEB Polyploidy Aug24-29

We'd like to invite you to submit an abstract for our symposium entitled "Polyploidy at the population level: ecological and population genetic consequences in plants and animals", which will take place at the next ESEB conference (24-29 august, Turin, Italy). We will have space for five contributions besides the two invited contributions.

ORGANISERS:

Marc Stift (m.stift@bio.gla.ac.uk), University of Glasgow http://www.gla.ac.uk/departments/ecologyevolutionarybiology/researchinterests/pdra/marcstift/ Barbara Mable (b.mable@bio.gla.ac.uk), University of Glasgow http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PQdGnd SUMMARY

Our symposium will focus on the effects of polyploidy on ecological adaptation, with the goal of bringing together researchers that work on polyploidy in different groups, including (but not necessarily limited to) plants, fishes, amphibians, planarians and crustaceans.

INVITED SPEAKERS

Brian Husband (plants), University of Guelph http://www.uoguelph.ca/ib/people/faculty/husband.shtml James Bogart (amphibians), University of Guelph http://www.uoguelph.ca/ib/people/faculty/bogart.shtml SUBMISSION

To submit your abstract (deadline 15 February 2009) and information about the congress, please go to http://www.eseb2009.it/uk POLYPLOIDY AT THE POPULATION LEVEL: ECOLOGICAL AND POPULATION GENETIC CONSEQUENCES IN PLANTS AND ANIMALS

Polyploids (individuals with more than two genomes) are common in many groups of organisms, including plants, amphibians, fish, reptiles and crustaceans. In addition, recent genome analyses indicate that many extant diploids have a polyploid history. The potency of genome duplications to drive evolution can be explained by the mere fact that polyploids inherently contain more (redundant) genetic material for selection to work on than diploids.

Research on polyploids has been strongly biased towards plants, and has tended to focus on genomic questions concerning differences in gene expression and epigenetics between diploids and polyploids. Unfortunately, such studies are limited to model organisms with a well known genome, and often to a limited number of samples within these. An ecological approach is more universally applicable, and may therefore provide more insights into the differences and similarities of polyploid evolution in a wide range of organisms.

With our symposium, we would like to offer the ESEB community a platform to discuss what is known about the effects of polyploidy on ecological adaptation. To achieve this, we intend to bring together researchers that work on polyploidy in different groups, including (but hopefully not limited to) plants, fishes, amphibians, planarians and crustaceans.

Marc Stift Barbara Mable

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## Turin ESEB Selection Aug24-29

Dear all,

We would like to invite abstracts for oral and poster presentations for our symposium "From the selfish gene to species extinction: levels of selection in evolution". This will tale place at the 2009 ESEB meeting in Turin between the 24th and 29th of August 2009. We have space for 10 oral presentations, including two by invited speakers. Please see below for a description of the symposium.

Abstracts must be submitted online at http://www.eseb2009.it/uk/ by the 15th of February 2009 at latest.

INVITED SPEAKERS Professor David Sloan Wilson, University of Binghampton, NY, USA (http://evolution.binghamton.edu/dswilson/ ) Professor Samir Okasha, University of Bristol, UK (http://www.bristol.ac.uk/philosophy/department/staff/so.html )

DESCRIPTION OF SYMPOSIUM Evolution is by its very nature a hierarchical entity. Genes are arranged in individuals, which form part of groups within populations of various species. The levels of selection debate has resurfaced recently in the field of social evolution.

In some part, this resurfacing has reinvigorated old debates in social evolution. However, there are also major unanswered questions, including whether there is true group adaptation in nature and how often selection acts at levels above kin groups. In particular, we are just beginning to appreciate how selection on multiple species can lead to the evolution of mutualisms, and how extinction and speciation can affect the distribution of species properties that we see in nature.

We wish to draw a range of evolutionary biologists, such as those working on speciation, ecologists interested in species extinction as well as sociobiologists interested in group and kin selection to address these questions. We also hope to foster discussion between empiricists and theorists to ask how multilevel selection can be addressed in the laboratory and the field. The renewed recent interest in the role of levels of selection in evolutionary biology has implications for all areas of evolutionary biology, particularly to those studying social evolution, mutualisms, speciation and macroevolution. We therefore expect our symposium to attract a wide range of interest from across all areas of evolutionary biology.

REGISTRATION AT: http://eseb2009.it/uk/-page.asp?PID3 The Organisers, Daniel Rankin (University of Zurich - d.rankin@bioc.uzh.ch) Kevin Foster (Harvard University - kfoster@cgr.harvard.edu)

— Dr Daniel J. Rankin Department of Biochemistry University of Zurich Building Y27, Winterthurstrasse 190 CH-8057 Zurich, Switzerland

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## Turin ESEB SexualConflict Aug24-29

We invite interested people to submit abstracts for oral/poster presentation in the symposium “Intralocus Sexual Conflict: Detection, Resolution and Consequences”, which will take place at the next congress of the European Society for Evolutionary Biology (24-29 August 2009, Turin, Italy)

Organizers: Adam Chippindale, Queen’s University, Canada (chippind@queensu.ca) Steve Chenoweth, University of Queensland, Australia (s.chenoweth@uq.edu.au).

Summary

The symposium explores the proposition that sex-specific selection on loci shared by females and males creates a genetic load that depresses the fitness of sexual populations, and that a distinct suite of genetic mechanisms have evolved to remediate this conflict.

Confirmed Invited Speakers

William Rice, University of California at Santa Barbara
Barry Sinervo, University of California at Santa Cruz

To submit your abstract (deadline 15 February 2009) and get useful information about the congress, please go to < http://www.eseb2009.it/uk > http://-www.eseb2009.it/uk INTRALOCUS SEXUAL CONFLICT

Females and males are often selected to pursue different strategies to maximize reproductive success, resulting in two distinct forms of evolutionary conflict. First, there may be direct conflict over the timing of reproduction and control of fertilization. Such interlocus conflict appears to be widespread and associated with intersexual coevolution of reproductive structures and behaviours, potentially via an ’arms race’ dynamic between loci. A second kind of conflict can arise within a locus, either when the fitness rank of segregating alleles differs between the sexes, or when optimal gene expression levels differs between the sexes. This intralocus sexual conflict is intrinsic to the evolution of dimorphic sexes but appears soluble, insofar as the genome can quarantine sexually antagonistic alleles and regulate gene expression in a sex-specific way.

Recently several quantitative genetic analyses, spanning a diverse range of taxa (e.g. dioecious plants, insects, and terrestrial vertebrates), have pointed to substantial levels of intralocus sexual conflict in both wild and domesticated populations, manifested most often as a negative intersexual genetic correlation for fitness. With this recent flood of empirical work, several unexpected consequences have emerged that require further consideration. For example, intralocus sexual conflict may compromise the operation of ’good genes’ processes in sexual selection, maintain genetic variance for fitness, influence the evolution of sex chromosomes, and drive the evolution of genomic imprinting alongside other genetic mechanisms of sex-specific gene regulation and ontogeny. Finally, failure of the genome to resolve intralocus conflict reduces mean population fitness by sustaining genotypes that are maladapted to their current sexual environment of expression, a phenomenon that has been dubbed the ’gender load’, adding to the list of costs to sex.

With the recent surge of interest in intralocus sexual conflict and many empirical challenges remaining, the symposium dedicated specifically to this form of sexual conflict, will provide an excellent opportunity to bring together both empiricists and theoreticians to explore these emerging issues. We particularly encourage early-career researchers to apply.

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s.chenoweth@uq.edu.au s.chenoweth@uq.edu.au

## Turin ESEB Speciation Aug24-29

We invite abstract submissions for oral and poster presentations in the symposium “Frontiers in Speciation Research: proximal and causal mechanisms of behavioural divergence” to be held on August 28 2009 at the European Society for Evolutionary Biology (ESEB) meeting in Turin, Italy (August 24-29 2009).

Abstracts should be submitted online at http://www.eseb2009.it/uk/ by February 15 2009. Unfortunately, we cannot offer any financial support.

Description of the symposium: Three-quarter day symposium, on the 28th of August 2009 150 years after the publication of Darwin’s seminal work ’On the Origin of Species’, how new species arise remains an unresolved and fascinating riddle. The aim of this symposium is to cover new challenges in speciation research, addressing in particular the evolution of behavioural divergence involved in reproductive isolation. It will bring together researchers working on different types of behaviour involved in premating isolation (e.g. mate choice, habitat choice, pollinator choice) and developing various approaches (e.g. behavioural ecology, neurophysiology, genomics) to explore the mechanisms favouring behavioural divergence and reproduction isolation. A key point of this symposium will be to illustrate the more integrated view of behavioural divergence that is nowadays emerging, which combines consideration of the causal with the proximal mechanisms of receiver and/or signal divergence. Particular attention will be given to studies addressing the genomics of behavioural divergence, the role of non-genetic mechanisms in promoting the evolution of premating isolation (cultural transmission, imprinting, epigenetics etc.) and the neurophysiological basis of behavioural divergence.

Invited speakers: ESEB invited speaker: Jeffrey Feder, University of Notre Dame, USA. Mark Blows, University of Queensland, Australia. FroSpects (European Science Foundation) invited speakers: Glenn-Peter Sætre, University of Oslo, Norway. Florian Schiestl, ETH Zürich, Switzerland. Katie Peichel, Fred Hutchinson Cancer Research Center, Seattle, USA

We expect to have 5 contributed talks. There is no limit on the number of poster presentations. Organisers: Carole Smadja, University of Sheffield, United Kingdom (c.smadja@sheffield.ac.uk) Anneli Hoikkala, University of Jyväskylä, Finland (anneli.hoikkala@jyu.fi) Axel Meyer, University of Konstanz, Germany (axel.meyer@uni-konstanz.de) Roger Butlin, University of Sheffield, United Kingdom (r.k.butlin@sheffield.ac.uk)

Carole Smadja, PhD Marie Curie Research Fellow Website: http://www.carole-smadja.staff.shef.ac.uk < http://www.carole-smadja.staff.shef.ac.uk/ >

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Email: c.smadja@sheffield.ac.uk Telephone: +44 (0)114 2220112 Fax: +44 (0)114 2220002

C.Smadja@sheffield.ac.uk

## Turin ESEB SubdividedSelection Aug24-29

*Symposium 14: SELECTION IN SUBDIVIDED POPULATIONS*

Dear EvolDir members,

We are pleased to invite you to submit abstract for our symposium at ESEB 2009, the congress of the European Society for Evolutionary Biology (Turin, Italy, 24-29 August 2009 http://www.eseb2009.it/ < https://mpizmail.mpiz-koeln.mpg.de/egroupware/redirect.php?go=http%3A%2F%2Fwww.eseb2009.it%2F >). Our symposium will bring together people interested in how selection interacts with population structure to shape phenotypic and molecular variation of ecological importance. Both experimental and theoretical contributions are welcome.

Organizers: J. de Meaux (demeaux@mpiz-koeln.mpg.de <mailto:demeaux@mpiz-koeln.mpg.de>) and P. K. Ingvarsson (par.ingvarsson@emg.umu.se <mailto:par.ingvarsson@emg.umu.se>)

*Invited speakers: Johanna Schmitt (Brown University, USA) and Jerôme Goudet (University of Lausanne, Switzerland). *

Deadline for registration and submission of abstracts is February 15.

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## Turin ESEB SystemsBiol Aug24-29

We are inviting abstract submissions for oral and poster presentations for the symposium "Evolutionary systems biology", to be held for 3/4 of a day on August 25 2009 at the European Society for Evolutionary Biology (ESEB) meeting in Turin, Italy (August 24-29 2009).

Abstracts must be submitted online at http://www.eseb2009.it/uk/ by 15 February 2009 latest.

Our symposium is aimed at researchers with an interest in bridging the genotype-phenotype gap with mechanistic models. These models may quantify aspects of any level of the adaptive landscape with a view towards connecting empirical evidence from different levels. This can be done using theoretic, computational, genomic, experimental, systems biology or other approaches and might target anything from very specific molecular systems to whole organisms.

Confirmed invited speakers: Laurence Hurst, University of Bath, UK Roy Kishony, Harvard University, USA

We are looking forward to seeing you in Turin.

The organizers Laurence Loewe, CSBE, University of Edinburgh, UK (Laurence.Loewe@evolutionary-research.net ) Balázs Papp, Biological Research Center of the Hungarian Academy of Sciences, Hungary (pappb@brc.hu)

About evolutionary systems biology

Evolutionary genetics has a long history of successful quantitative modelling, especially in areas where functional details can be abstracted by selection coefficients. Molecular biology has a long history of uncovering functional details and has recently started to engage in quantitative modelling at a larger scale, giving rise to current systems biology. We propose to bring these two fields together to help elucidate some fundamental problems in evolutionary biology. Such a synthesis has the potential to provide a mechanistic basis for in silico predictions of many important parameters of evolution, including distributions of mutational effects, robustness and epistasis. Central to this approach is the definition of fitness correlates that can be computed using mechanistic models of individuals. One possible aim for modelling in evolutionary systems biology could be to define computable fitness correlates that can be calibrated experimentally by measuring mutant properties.

This ambitious goal can inspire experimental and theoretical work at many levels of the adaptive landscape. These levels include: 1. Changes in genotypes impact predicted molecular structures (like protein structures). 2. Changes in molecular structures impact predicted molecular functions (like enzyme reaction rates). 3. Changes in molecular functions impact predicted properties of reaction networks (see systems biology). 4. Changes in reaction network properties impact predicted fitness correlates (need to be defined for each model). How fitness correlates are mapped to fitness is defined at even higher levels (see life-history evolution). All levels ultimately need to be brought together to facilitate computational predictions of realistic mutational effects, robustness, epistasis and adaptive evolution.

In this symposium we aim to bring together researchers with an interest in the adaptive landscape at any level and researchers who want to contribute towards a synthesis of evolutionary genetics with mechanistic models of life. We believe that the new excitement in systems biology is an excellent opportunity for progress in many fundamental evolutionary questions, if the new models that are being constructed can be extended to include fitness correlates that turn them into powerful tools for investigating the adaptive landscape. We also expect systems biology to benefit from including the rich quantitative approaches that have been developed within evolutionary genetics.

Laurence.Loewe@ed.ac.uk Laurence.Loewe@ed.ac.uk

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## Turin ESEB TradeOffs Aug24-29

We invite interested people to submit abstracts for oral and poster presentations in the symposium " Genetic trade-offs in fitness-traits: theory, evidence, and implications", to be held at the 2009 congress of the European Society for Evolutionary Biology (24-29 August 2009, Turin, Italy)

Bringing together theoreticians, geneticists and evolutionary ecologists, this symposium will examine the genetic relationships among fitness related traits and discuss their role for selective trade-offs, evolutionary trajectories, and the maintenance of genetic diversity; with examples spanning laboratory systems and natural populations.

Abstracts must be submitted by February 15 2009 latest. For full details of the ESEB congress and online registration see http://www.eseb2009.it/uk/ Symposium outline:- Selective trade-offs are fundamental to our understanding of many fields in evolutionary biology; from life history theory to behavioural ecology and social evolution. However, while routinely assumed in optimality modelling approaches, there has been surprisingly little scrutiny of the genetic mechanisms assumed to underly fitness trade-offs. Consequently, even where the selective forces can be measured, important questions remain. How generally do selective trade-offs between traits serve as evolutionary constraints? How do trade-offs between sexes or across spatial or temporal environments determine evolutionary trajectories? To what extent can trade-offs act to maintain genetic diversity for phenotypic traits, or for fitness itself? The aim of this symposium is to address such questions by bringing together theoreticians, geneticists and evolutionary ecologists. We will have a particular emphasis on the need to examine the genetic relationships among traits involved in selective-trade offs, with examples spanning laboratory systems and natural populations.

Organisers:- Alastair Wilson, University of Edinburgh, Alastair.Wilson@ed.ac.uk Kathi Foerster, University of Lausanne, Katharina.Foerster@unil.ch

– Alastair J Wilson NERC Research Fellow

Alastair.Wilson@ed.ac.uk

http://wildevolution.biology.ed.ac.uk/index.html http://wildevolution.biology.ed.ac.uk/awilson/-index.html tel. 0131 6513608

Institute of Evolutionary Biology School of Biological Sciences The University of Edinburgh Ashworth Laboratories The King's Buildings West Mains Road Edinburgh EH9 3JT, UK

Alastair.Wilson@ed.ac.uk Alastair.Wilson@ed.ac.uk

## Turin ESEB Transitions to social life Aug24-29

We would like to invite abstract submissions for oral and poster presentations at the upcoming European Society for Evolutionary Biology meetings in Turin this summer (http://www.eseb2009.it/uk/) for a symposium entitled: Selective forces shaping transitions to social life

Organisers: Trine Bilde, University of Aarhus, Denmark (Trine.Bilde@biology.au.dk) Patrizia d'Ettorre, University of Copenhagen, Denmark (pdettorre@bio.ku.dk)

Description: This symposium aims at identifying and integrating the general principles underlying transitions to social life across a broad range of taxa, in order to advance our understanding of both the proximate and ultimate forces underlying these major transitions in evolution.

Confirmed speakers: Ashleigh Griffin, University of Edinburgh, UK Jacobus J. Boomsma, University of Copenhagen, Denmark

For submission of abstracts see http://www.eseb2009.it/uk/ Trine Bilde <trine.bilde@biology.au.dk>

## UFloridaGainesville SEEC Mar27-29

Abstracts for papers and posters are now being accepted for the Southeastern Ecology and Evolution Conference (SEEC), to be held March 27-29, 2009 at the University of Florida in Gainesville. Graduate students, undergraduate students, and postdoctoral researchers are invited to submit an abstract for SEEC. Presenters should be affiliated with a college or university in the southeastern United States, or with a school from outside the region but doing their research in the southeast. Abstracts related to ecology and evolution are welcomed. Examples of topics from previous conferences are: behavior, biodiversity, conservation, functional morphology, population ecology, and systematics.

Abstracts should be no more than 250 words, and may be sent to seec2009@gmail.com.

Along with your abstract please submit the following:

Name

Institutional affiliation

Status (undergraduate, graduate, or postdoc)

Whether the abstract is for a paper or poster presentation

If you would like to volunteer to moderate paper presentations

Abstracts will be reviewed by the SEEC 2009 Program Committee, and presenters will receive notification with further details about the presentations (time, format, etc.). Awards will be given for the best talk and best poster at the conclusion of the conference.

The deadline for submitting abstracts is *Tuesday, February 10, 2009*.

Registration information and further details about the conference may be found at our website, http://snre.ufl.edu/seec . seec2009@gmail.com

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## UFlorida SEEC Mar27-29 CallForAbstracts

Abstracts for papers and posters are now being accepted for the Southeastern Ecology and Evolution Conference (SEEC), to be held March 27-29, 2009 at the University of Florida in Gainesville. Graduate students, undergraduate students, and postdoctoral researchers are invited to submit an abstract for SEEC. Presenters should be affiliated with a college or university in the southeastern United States, or with a school from outside the region but doing their research in the southeast. Abstracts related to ecology and evolution are welcomed. Examples of topics from previous conferences are: behavior, biodiversity, conservation, functional morphology, population ecology, and systematics.

Abstracts should be no more than 250 words, and may be sent to seec2009@gmail.com.

Along with your abstract please submit the following:

Name

Institutional affiliation

Status (undergraduate, graduate, or postdoc)

Whether the abstract is for a paper or poster presentation

If you would like to volunteer to moderate paper presentations

Abstracts will be reviewed by the SEEC 2009 Program Committee, and presenters will receive notification with further details about the presentations (time, format, etc.). Awards will be given for the best talk and best poster at the conclusion of the conference.

The deadline for submitting abstracts is *Friday, January 30, 2009*.

Registration information and further details about the conference may be found at our website, http://snre.ufl.edu/seec . SEEC 2009 <seec2009@gmail.com>

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## Uruguay Darwin200 Sep3-6

Dear Colleagues,

Is with great pleasure that we would like to invite you to the meeting “150 years of Darwin’s Evolutionary Theory: a South American Celebration” to celebrate the 150 years of Darwin’s theory, together with 200 of his birth. The event will take place in Uruguay between the 3 and 6 of September 2009. We have chosen the location of Punta del Este-Maldonado to host this meeting not only for the natural beauty of this place, but also because its symbolic meaning since Charles Darwin spent more than 10 weeks there during the southern fall and winter of 1833 as part of his voyage in the HMS Beagle.

This meeting is part of a series of meetings convened by the International Union of Biological Societies (IUBS) and supported by UNESCO that are being announced worldwide. We are expecting to host several researchers, particularly young researchers, from South America and all over the world. We are convinced that this event will evolve in a unique opportunity to exchange ideas of the different issues of the evolutionary theory and related topics between a wide and diverse audience.

The main meeting will count with plenary lectures delivered by first line researchers in the field, up to now the confirmed speakers are:

Prof. Giorgio Bernardi, Stazione Zoologica Anton Dohrn, Italy Prof. Daniel Dennett, Tufts University, USA Prof. Douglas Futuyma, Stony Brook - State University of New York, USA Prof. Takashi Gojobori, National Institute of Genetics, Japan Prof. Eviatar Nevo. Weissman Institute, Israel Prof. Emile Zuckerkandl, Institute of Molecular Medical Sciences, California, USA.

Several Symposia will be also organized, the confirmed ones are:

Evolutionary Genomics and Molecular Evolution (Co-Chairs: Fernando Alvarez and Hugo Naya) Evolutionary Physiology (Chair: Francisco Bozinovic) Viral Evolution (Chair: Juan Cristina) Darwinism and Society (Chair: Amilcar Davyt) Paleontology and Evolution (Co-Chairs: Richard Fariña and Sergio Martínez)

Finally Poster Sessions covering all areas of Evolution will take place during the meeting.

The surroundings of Punta Del Este are rather extraordinary, with sea, countryside and sierras. Several social activities before and after the meeting will be organized including a horse ride following Darwin's path through the sierras.

Darwin in his daily accounts of his voyage commented colourfully several anecdotes as well as scientific data collected in these lands. According to these records, Darwin spent a productive time in this place, as he put it:

"[last days have been employed]... in arranging & writing notes about all my treasures from Maldonado".

We will be very happy to receive you next september in Uruguay.

Yours evolutively,

Dr. Daniel E. Naya

On behalf of the organizing comitee

For more information follow this link: www.darwin200.edu.uy

or send questions to: darwin200@fcien.edu.uy

Dr. Daniel E. Naya Seccion Evolucion, Universidad de la República, Uruguay & Centro de Estudios Avanzados en Ecología y Biodiversidad, P. Universidad Católica de Chile, Chile

"Daniel E. Naya" <dnaya@fcien.edu.uy>

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## USheffield Evolution of insect immunity Jul15-17

Royal Entomological Society International Symposium

Insect Infection and Immunity: Evolution, Ecology and Mechanisms

followed by contributed sessions on e.g. comparative genomics, evolutionary ecology of predation

In Sheffield, UK, July 15-17 2009

The meeting, organized by Stuart Reynolds (Bath, UK) and Jens Rolff (Sheffield, UK) will consist of three plenary sessions running in the morning of each day on insect immunity. Speakers include:

Bruno Lemaitre (EPF Lausanne, CH) Mike Kanost (Kansas State University, USA) David Schneider (Stanford University, USA) George Dimopoulos (John Hopkins Malaria Research Institute, USA) Fotis Kafatos (Imperial College, UK) Greg Hurst (University of Liverpool, UK) Jean-Michel Drezen (University of Tours, France) Jean Luc Imler (Institut de Biologie MolÃ©culaire et Cellulaire, Strasbourg, France) Jacob Koella (Imperial College, UK) Shelley Adamo (Dalhousie, Canada) Lex Kraaijeveld (University of Southampton, UK) Brian Lazzaro (Cornell University, USA) Paul Schmid-Hempel (ETH Zurich, CH) Mike Siva-Jothy (University of Sheffield, UK)

The afternoon, organized by Klaus Reinhardt, Roger Butlin and Mike Siva-Jothy (all Sheffield, UK), will see thematic sessions with the opportunity to contribute talks and posters on:

Insect Immunity (chair Petros Ligoxygakis, Oxford)

Comparative Genomics (chair Casey Bergman, Manchester) Invited Speaker: Jack Werren, Rochester, USA

General Entomology (chair Mike Siva-Jothy, Sheffield) Stanislav Gorb, Kiel, Germany Paul Buckland, Sheffield, UK

Predation (chair Dirk Mikolajewski, Sheffield) Johanna Mappes, Jyväskylä, Finland Robby Stoks Leuven, Belgium

Range Expansion (chair Janis Antonovics Virginia/Sheffield) Jane Hill, York, UK Rosa Menendes, Lancaster, UK

Chemical Ecology (chair Stephen Martin, Sheffield) Tbc

The conference dinner will be in a Victorian museum and pre-ceded by a plenary talk by Naomi Pierce from Harvard.

The Society offers excellent support for students: students can apply for support of up to 50% of all costs (travel, accommodation, registration). Also, as conference dinners are very good networking opportunities, the dinner is only Â£15 for students. Early application is strongly recommended. Applications must be made by letter or email (bill@royensoc.co.uk) to the Registrar at the RES office and the deadline for receipt is 1st May 2009.

Daytime childcare is available on request (childcare.ento2009@sheffield.ac.uk).

Registration and details http://www.royensoc.co.uk (there is a link to Ento â09 in the middle of the page) General questions: Vi Nguyen ento2009@sheffield.ac.uk. Kirsty Whiteford kirsty@royensoc.co.uk Scientific programme: Klaus Reinhardt: ento2009@sheffield.ac.uk

Jens Rolff <JOR@sheffield.ac.uk>

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## Zurich NicheEvolution Jul3-4

*CONFERENCE ANNOUNCEMENT*

NICHE EVOLUTION - A unifying concept for systematics, ecology, palaeontology and conservation biology

3-4 July, 2009. Excursion on 5 July. Zurich, Switzerland

www.systbot.uzh.ch/niche MOTIVATION Evolution of ecological niches, in their various guises, has become a central theme in several research fields of biology. We argue that niches, how they evolve, and the consequences of their evolution, affect a wide range of disciplines in organismal and evolutionary biology, and as such could be seen as a unifying thread.

In this meeting we will explore the interdisciplinary impact of evolving niches, and so bring together systematists, invasion biologists, biodiversity specialists, ecologists, and palaeontologists. We want to explore the commonality of evolving niches. The focus is more on concepts than methods (although, of course, the methods used will impact massively on the concepts). The emphasis is more on how to understand the evolution of a niche, rather than the definition of the niche. There will be some talks on the basics of niches to set the stage for the topics of niche evolution. The idea is to bring people together working in this field and to provide a forum to discuss developments, prospects and needs with various users and specialists. Therefore, the program is structured to provide ample time for discussions between and after the sessions.

PLACE The meeting will take place at the Institute of Systematic Botany of the University of Zurich, situated in the botanical garden of the University of Zurich, within easy reach of public transport.

TALKS Only invited talks will be given, and contributions as posters are welcome. There will be an evening poster session.

Invited speakers include William Bond, Jeannine Cavender-Bares, Alastair Culham, Catherine Graham, Antoine Guisan, Sabine Jakob, Jennifer Lau, Peter Linder, Signe Normand, Peter Pearman, Townsend Peterson, Bob Ricklefs, Nicolas Salamin, Walter Salzburger, Harald Schneider, Jonathan Silvertown, Wilfried Thuillier and Niklaus Zimmermann.

POST-CONFERENCE ONE-DAY EXCURSION There will be an excursion for Sunday, 5 July, into the Alps. We will cross the Susten Pass (2'250 m). On Susten Pass we will visit the Steingletscher glacier, which has shown a dramatic reduction in the past decades, thus exposing much new habitat. We will be able to see the plant successions into these newly exposed habitats. This shows very dramatically the effect of climate change, and the potential new habitats exposed.

ORGANISERS Peter Linder, Alexandre Antonelli, Rafael Wüest (Systematic Botany, University of Zurich), Niklaus Zimmermann and Peter Pearman (Institute of Forest, Snow and Landscape Research, WSL, Zurich), Harald Schneider (Natural History Museum, London), Frank Blattner (IPK Gatersleben) and Nicolas Salamin (Computational Phylogenetics, University of Lausanne)

REGISTRATION IS OPEN, at www.systbot.uzh.ch/-niche Please distribute this information to all researchers and students potentially interested!

Best wishes,

Dr Alexandre Antonelli Institute of Systematic Botany Zollikerstrasse 107 CH 8008 Zürich Switzerland Ph: +41 (0)44 634 8416 Fax: +41 (0)44 634 8403 alexandre.antonelli@systbot.uzh.ch

Alexandre Antonelli <alexandre.antonelli@systbot.uzh.ch>

# GradStudentPositions

## LausanneU GenomicsEvolutionSymbiosis

PhD studentship in Lausanne: Genomics, Evolution & Symbiosis

We are seeking a highly motivated student with an interest in molecular biology, genomics and/or evolutionary ecology to join our group working on symbiotic mycorrhizal fungi. These important fungi form mutualistic symbioses with most plants, improving plant growth and influencing diversity of ecosystems. Although the fungi grow clonally, they have a highly unusual genome organization, harbouring genetically different nuclei that are passed from one generation to the next (see Hijri & Sanders, Nature 2005; Kuhn, Hijri & Sanders, Nature 2001). The main goals of our research are to understand how selection, drift, genetic exchange and recombination act on these fungi and how this can be used to create more beneficial strains of the fungi for use in sustainable agriculture. A selection of possible projects include: - Stability/heritability of fungal traits associated with improved growth of rice - Evolutionary genomics and population genomics of AM fungi - Population genetics of mycorrhizal fungi in natural or agricultural systems - Linking quantitative changes in genetically different nuclei with important phenotypic traits The candidate should be familiar with molecular biology or genomics/ bioinformatics and have an interest in applying this knowledge to evolutionary & ecological questions. He/she should also be willing to interact with the other group members working on evolution and population biology of mycorrhizal fungi (see list of recent publications on our web site). The successful candidate must have a Masters degree (MSc) in order to qualify for our PhD program. We are located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland). The Dept. of Ecology and Evolution in Lausanne is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment and a strong PhD program. It is also one of the largest institutions in Europe for research in ecology and evolutionary biology, comprising 17 different research groups. A genomics research centre also exists at the same site.

The studentships are for a period of 3 years. Starting date ideally by late spring 2009 but this date can be extended for exceptional candidates. Closing date for application is 15 February 2009. To apply, applicants should send a CV plus a letter of motivation by EMAIL to Ian Sanders, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: ian.sanders@unil.ch: Tel: +41 21 692 4261. More details can be found about our group at: http://www.unil.ch/dee/page7238.html

iansanders@me.com

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## LundU Internship SexualSelection

Internships available

Internships are available for students interested in evolutionary ecology in general, and sexual selection and speciation in particular.

We are looking for highly motivated and enthusiastic students, with a strong interest in ecology and evolution, and who are prepared to work independently, both in the field and the laboratory. Students will work in close collaboration with PhD-students at the Department of Animal Ecology, Lund University. 1-2 studentships are available for a project with Skyros wall lizard (the project is described in more details below), field work will be conducted in Greece.

Fieldwork will take place between late February and late April (2 months). It would be of advantage if you have a driver's license. You are expected to work on a schedule that is flexible and organized by your advisor, and be able to coordinate between the other team members in the group. Time and length of stay can be agreed on personal preferences. We provide housing and travel costs, but students are expected to find as cheap flights as possible to Athens, where we will meet up. The working language of the group is English. If you are interested, please send us an e-mail announcing your interest no later than the 20th of January 2009.

1) Detailed project description Main Coordinators: Anna Runemark (Anna.Runemark@zooekol.lu.se) and Erik Svensson (Erik.Svensson@zooekol.lu.se)

Skyros wall lizard Podarcis gaigeae is a lizard species endemic to the island of Skyros. They are common on both the main island and the islets surrounding it. On at least two of the surrounding islets, the lizards have developed island gigantism with significantly larger body size than the ones on the mainland.

Previous work from our lab has shown that the islet populations also differ from the population on the main island in frequency of the six throat colour phenotypes which are present in the species. Mate preferences also seem to differ between the two studied islets and the main island. Other selection pressures, such as predation, have also been shown to differ between these populations.

Our fieldwork aims are to investigate if the larger body size on the islets is a general phenomenon and if there is a consistent pattern in the frequency of throat colour phenotypes on the islets. Indirect quantification of predation pressure in the populations will also be a part of the fieldwork. Our study populations are found on the island of Skyros, Greece, where the field work will be based.

The populations on the main island are within a short distance from the field base (1-2 hours by car) whereas transportation to the islets will be done with the help of local boat owners and is weather sensitive. We will visit several populations repeatedly during the field season. At each population, we will first catch about 30 lizards. For some populations, morphological measures and photographs as well as DNA samples will be taken in the field. Some populations will be brought into the laboratory for recording of morphological data and sampling of DNA.

At the field sites, basic data to describe the ecological setting of the population (ground cover, possible predators, etc.) will be recorded, and measurements of the reaction distances (proxy of predation pressure) of the lizards will be done. For a subset of the study populations mate choice experiments will be done in the laboratory. Finally, the ecological and morphological data will get entered into a database and analysed.

Anna Runemark <Anna.Runemark@zooekol.lu.se>

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## MaxPlanckInst HostParasite CoEvolution

Graduate position: 2 PhD positions in host-parasite co-evolution

There are openings for two 3-year PhD positions at the Max Planck Institute for Evolutionary Biology to work in the field of host-parasite co-evolution.

The specific goal for these positions is to identify evolutionary pressures exerted by parasites on the host immune system and how such interactions could lead to the maintenance of sexual reproduction. Research will be conducted using our established model organism, the three-spined stickleback.

Depending on the scientific interest of the candidates, the work can be extended to the molecular level of host-parasite (e.g. MHC, virulence genes) interactions.

The successful candidates should be highly motivated and have a background in evolutionary biology. The candidates will collaborate with the team working on immunogenetics, immunology, population genetics, parasitology, speciation and behavioural ecology both in the lab and in the field. Details about the department's research activities can be found under: http://www.evolbio.mpg.de/english/-abteilungen/evolutionsoekologie/index.html The Institute is located in Plön (Northern Germany, between Hamburg and the Baltic Sea) and offers a stimulating research environment dedicated to evolutionary biology with links to the Christian Albrechts University Kiel, and the Leibniz Institute for Marine Sciences (IFM-Geomar) in Kiel. The Institute provides state-of-the-art laboratories and equipment, including facilities for genome analysis.

To apply, students are required to have a Diplom/Master degree (or equivalent). Please send your application including a CV and address of two references by e-mail (milinski@evolbio.mpg.de). The positions will remain available until filled.

We encourage also foreign students to apply since the working language in the group is English. The Max Planck Society is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply.

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Prof. Manfred Milinski Executive Director Max-Planck-Institute for Evolutionary Biology (former Max-Planck-Institute of Limnology) Department of Evolutionary Ecology August-Thienemann-Strasse 2 D-24306 Ploen, Germany

direct: +49-(0)4522 763 254 Sec: +49-(0)4522 763 253 Fax: +49-(0)4522 763 310 email: milinski@evolbio.mpg.de http://www.mpil-ploen.mpg.de/ milinski@mail.evolbio.mpg.de

## MemorialU EvolutionaryEcolCod

PhD/MSc opportunities - Evolutionary Ecology of Farmed/Wild Cod

Funded graduate student projects are available with the evolutionary ecology of fishes research groups lead by Dr. Ian Fleming & Dr. Craig Purchase at Memorial University. These projects will also involve collaborators from Fisheries & Oceans Canada (Dr. Ed Trippel [St. Andrews] and Dr. John Brattey [St. John's]).

Project 1 (preferably PhD level): Mating experiments to determine the potential for interbreeding between farmed and native wild cod, and thus the potential for the introduction of aquaculture/non-native traits into the wild where they may have a negative impact.

Project 2 (preferably PhD level): Determination of the likelihood of inbred cod reproducing within cages, and the subsequent quality of embryos released into the environment. Lab experiments to determine if hybrid offspring between farmed and wild populations will have depressed growth and survival relative to native fish, and whether such effects may be mitigated by using farmed stocks derived from local populations.

Project 3 (MSc level): Determination of factors which may reduce the motivation of cod to escape from cages. Tagging studies to determine the fate of escaped fish and whether they can be easily recaptured.

All projects have flexibility and the scope to address additional questions. Start dates are from March to September 2009. Major scholarship holders will receive generous top-ups to their awards.

Information on our research groups can be found at http://www.ucs.mun.ca/ ˜ cfpurchase/ and http://www.mun.ca/osc/ifleming/bio.php Information on graduate studies at MUN can be found at http://www.mun.ca/sgs/home/ Prospective candidates should email a cover letter, CV, official transcripts and contact information for three people who can serve as references. Review of applicants will begin Feb 1/09 and continue until the positions are filled.

Dr. Craig Purchase Assistant Professor, Biology Department Memorial University of Newfoundland

St. John's, Newfoundland, A1B 3X9, Canada T: (709)737-4452, F:(709)737-3018 craig.purchase@mun.ca www.ucs.mun.ca/ ˜ cfpurchase cfpurchase@mun.ca cfpurchase@mun.ca

## Muenster Germany HostParasiteCoevolution

Graduate position: Muenster (Germany) - Ecological Immunology and Host-Parasite Coevolution

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

We are seeking highly motivated students with a background in evolutionary ecology, immunology or parasitology. Experience with molecular techniques is advantageous. Successful candidates will work in the field of ecological immunology and host-parasite coevolution. Research goals will include the evolution of specific memory and phenotypic plasticity in immune responses, using the red flour beetle Tribolium castaneum as a model organism. Working language of the lab is English.

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

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

Prof. Joachim Kurtz, Institute for Evolution and Biodiversity, University of Muenster, Huefferstr. 1, DE-48149 Muenster, Tel. +49 251 83 24 661, joachim.kurtz@uni-muenster.de

Closing date is February 22nd, 2009.

Prof. Dr. Joachim Kurtz

University of Muenster Institute for Evolution and Biodiversity, Animal Evolutionary Ecology Group Huefferstr. 1, D-48149 Muenster, Germany Phone: + 49 251 83 24661 Fax: + 49 251 83 24668 joachim.kurtz@uni-muenster.de http://www.uni-muenster.de/Evolution/ joachim.kurtz@uni-muenster.de

## Munich EvolutionaryGenomics

PhD Student Position: Evolutionary/Functional Genomics

A PhD student position in Evolutionary and Functional Genomics is available at the University of Munich. The student will join a collaborative research group studying natural selection in structured populations and be enrolled in the Munich Graduate School for Evolution, Ecology and Sytematics (EESLMU).

The project involves the analysis of gene expression variation in natural populations of Drosophila. This includes a microarray survey of gene expression variation, with particular focus on adaptive regulatory changes between ecologically differentiated populations. It also includes DNA sequence analysis and transgenic experiments to study the evolution of gene regulatory elements.

The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. We have an international group and the everyday working language is English. The Department of Biology is housed in the new, state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at:

http://evol.bio.lmu.de/EvoGen.html PhD students will receive a salary according to the German pay scale (E13/2 TV-L). Applicants should have a master's degree or equivalent in biology or a related field. In addition, laboratory experience in molecular biology and/or genetics is desired. Interested candidates should send a CV, statement of interest, and contact information of two potential referees as a single PDF file to Prof. John Parsch (parsch@bio.lmu.de).

Review of applications will begin on Feb. 20, 2009 and will continue until the position is filled.

The University of Munich is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

John Parsch <parsch@zi.biologie.uni-muenchen.de>

## NHN-Leiden PlantSystematics

Faculty of Mathematics and Natural Sciences

Vacancy number 8-251

The National Herbarium of the Netherlands, Leiden University branch (NHN-L) and Hortus botanicus Leiden are offering a position for a:

PhD-candidate in Plant Systematics (fulltime, 38 hours per week)

The NHN-L houses one of the leading herbarium collections in Europe and has two active, internationally oriented scientific research groups. The PITA group (Plant diversity of the Indo-Pacific and tropical Asia) has a strong focus on the flora of South-East Asia, and the PCNE group (Phanerogams and Cryptogams of the Netherlands and Europe) focuses on the flora of the Netherlands and groups as the algae, mosses and macrofungi. The Hortus botanicus provides a rich collection of living plants with special emphasis on Orchidaceae, Apocynaceae (Dischida, Hoya), myrmecophytic Rubiaceae, and carnivorous plants.

Our collections are par excellence useful for anatomical and molecular/evo-devo (incl. ancient DNA) studies, and for bioinformatics research.

Who fits the shoe?

You must have a degree (drs./MSc) in Biology and a strong interest and experience in plant taxonomy preferably including molecular and/or SEM/TEM techniques. To obtain the available position you have to write a research proposal of max 2 pages, preferably based on the collections available and the research performed at the NHN and/or botanical garden. Other research projects are also welcomed if the main focus is on morphology, anatomy and phylogenetics. As a person you are a driven and self-confident scientist with excellent technical, analytical and communicational skills.

The position

We offer you an appointment at Leiden University for a period of one year; after evaluation the appointment can be extended for another three years.

You do not need to pay a tuition fee. The gross monthly salary is 2000,- in the first year and increases progressively each year to 2558,- in the fourth year. The appointment includes pension build-up and facilitates other benefits in accordance to the Collective Labour Agreement for Dutch Universities (CAO Nederlandse Universiteiten).

The appointment must lead to the completion of a PhD thesis within four years. During your appointment you will be supervised by one of the staff members of the NHN or Hortus botanicus as your copromotor/co-advisor. Prof. Dr. Erik Smets is promotor/advisor. A PhD student at the NHN-L is imbedded in the Leiden University Graduate School of Science (www.graduateschools.leidenuniv.nl < http://www.graduateschools.leidenuniv.nl/ > ) and the Research School Biodiversity (www.science.uva.nl/ibed/biodiversity/). These schools offer PhD courses on general (e.g. effective time management, scientific writing, presentation skills, etc.) and specialist subjects (molecular phylogenetics, economic botany, web-based taxonomy, etc.); in coordination with their supervisors PhD candidates are allowed to compile their own course program. Additionally, PhD students participate in the teaching at the BSc level at Leiden University. In general ca. 80% of the time is spend on your PhD research and ca. 20% on teaching and following courses.

For further information please contact Dr. J.B. Mols, Mols@NHN.Leidenuniv.nl or visit http://www.nationaalherbarium.nl < http://www.nationaalherbarium.nl/ > and http://www.hortusleiden.nl < http://www.hortusleiden.nl/ > .

Applications using the vacancy number and including a complete CV with marks obtained, a research proposal of two pages, and the names, telephone numbers and email addresses of at least two referees (who have agreed to be contacted) should be submitted before February 16th 2009 and only to:

Leiden University / Faculty of Mathematics and Natural Sciences

Attn. Ms. M. van Schoonhoven, Human Resource Adviser

Human Resource department

P.O. Box 9504

2300 RA Leiden

The Netherlands

Or by mail to m.vanschoonhoven@science.leidenuniv.nl <mailto:m.vanschoonhoven@science.leidenuniv.nl>

More information on working for the University can be found on: www.medewerkers.leidenuniv.nl < http://www.medewerkers.leidenuniv.nl/ > (Dutch site only) and on www.leidenuniv.nl/en/staff (English site with information for international staff and PhD students).

Dr. J.B. Mols Instituutsmanager Nationaal Herbarium Nederland Universiteit Leiden vestiging P.O. Box 9514 2300 RA Leiden Nederland Tel: +31 (0) 71 5273527 Fax: + 31 (0) 71 5273522

"Mols, J.B. (Johan)" <Mols@nhn.leidenuniv.nl>

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## NorthCarolinaStateU EvolutionaryBiol

Dr. Marc Johnson's lab of Evolutionary Ecology (www.evoeco.org) at North Carolina State University is accepting applications for graduate school in the Department of Plant Biology. North Carolina State University offers broad training in ecology and evolution and is ideally suited for students interested in interdisciplinary research that incorporates both lab and field components. Students will have the opportunity to interact with colleagues across multiple departments including Biology, Entomology, Genetics, and Statistics. Research in the lab focuses on the molecular and phenotypic evolution of plant defenses, the ecological effects of genetic variation and evolution on communities, and the coevolution between plant hosts and their insect parasites. Students are free to work on any topic related to the lab's foci. For more information on this research please visit www.evoeco.org . There are presently two positions open in the lab that will be funded by a combination of research assistantship (50%) and teaching assistantship (50%) support. Students can expect to earn ca. 20K (USD) per year, and tuition and health insurance will be covered on top of this. Students entering the graduate program in plant biology are required to have a bachelor's degree in plant biology or a related undergraduate program that includes biological, physical and mathematical science training. Students will be considered regardless of race, gender, religion, nationality, or physical ability.

Interested students are encouraged to send a covering letter and CV/resume to marc_johnson@ncsu.edu by January 25, 2009. The cover letter should outline the applicant's research interests as they relate to evolution or ecology, past research experience, and why the student would like to do graduate work at NCSU.

Marc Johnson, Ph.D. Assistant Professor Department of Plant Biology North Carolina State University Campus Box 7612, Gardner Hall Raleigh NC, 27695 Office: 919-515-0478, Lab: 919-515-0479 Web: www.evoeco.org marc_johnson@ncsu.edu marc_johnson@ncsu.edu

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## StonyBrookU EvolutionaryBiol

GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Ecology and Evolution at Stony Brook University is recruiting graduate students for Fall 2009. Our graduate program trains students in Ecology, Evolution and Biometry. The following faculty are seeking graduate students for their labs:

H. Resit Akcakaya http://life.bio.sunysb.edu/ee/akcakayalab/ Stephen B. Baines http://life.bio.sunysb.edu/~sbaines/ Michael A. Bell http://life.bio.sunysb.edu/ee/belllab/ David O. Conover http://www.msrc.sunysb.edu/~conover Liliana M. Dávalos http://life.bio.sunysb.edu/ee/davaloslab/Welcome.html Daneil Dykhuizen http://life.bio.sunysb.edu/dykhuizenlab/ Walter F. Eanes http://life.bio.sunysb.edu/ee/eaneslab/ John G. Fleagle http://gibbon.anat.sunysb.edu/Department/jfleagle.html Lev Ginzburg http://life.bio.sunysb.edu/ee/people/ginzbgindex.html Jessica Gurevitch http://life.bio.sunysb.edu/gurevitchlab/ Jeffrey Levinton http://life.bio.sunysb.edu/marinebio/levinton.main.html Steve Munch http://msrc.sunysb.edu/people/munch.htm Dianna K Padilla http://life.bio.sunysb.edu/ee/padillalab/padilla/index.htm Massimo Pigliucci http://www.genotypebyenvironment.org Joshua Rest http://life.bio.sunysb.edu/ee/restlab/ F. James Rohlf http://life.bio.sunysb.edu/morph John J. Wiens http://life.bio.sunysb.edu/ee/wienslab/homepage.html Pat C. Wright http://icte.bio.sunysb.edu For more information regarding the Graduate Program in Ecology and Evolution see: http://life.bio.sunysb.edu/ee and http://life.bio.sunysb.edu/ee/programs.htm The deadline for receipt of all application materials is January 18. For additional assistance, e-mail our Graduate Program Coordinator, Iris Roth, iroth@notes.cc.sunysb.edu

lmdavalos@gmail.com

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## UAntwerp DamselflyEvolution

PhD POSITION - UNIVERSITY OF ANTWERP (BELGIUM)

PhD position at the Department of Biology - Evolutionary Ecology group http://www.ua.ac.be/hans.vangossum Duties and research:

Preference goes to a candidate with a keen interest for evolution, behaviour and ecology. Research topic is the study of the causes and consequences of coexistence of multiple discrete female damselfly (Insecta: Odonata) morphs (with genetic base). Intriguingly, one female morph much resembles the conspecific male's phenotype to such extent that intraspecific mimicry in the context of sexual conflict has been suggested. Several studies indicate frequency-and density-dependent selection. Broad aim of the PhD research is study of causes and consequences of variation in social environments (densities and frequencies of males and female morphs) on the success, behaviour and phenotype of males and females. Fieldwork is planned at several locations in Europe (such as Belgium, Netherlands, Spain). It also is expected for the candidate to take part in a limited amount of teaching assistance.

Requirements:

* Degree in Biology (also students that finish later this term are encouraged to apply).

* Preparing a PhD. The job offer is for two years, while typically 4 years are required to complete a PhD in Belgium. Therefore, the candidate will need to apply for additional funding for which several possibilities are available (e.g.; www.fwo.be < http://www.fwo.be/ > , www.iwt.be < http://www.iwt.be/ > ).

* Owner of a driver's license.

* Preferentially the candidate also is used to advances statistical methods. The field work requires independence, flexibility and a taste for adventure.

Offer and further information:

Full time job from March 1 2009 or later (as agreed) for a period of two years. For further please contact me at: email hans.vangossum@ua.ac.be or phone ++ 32 3 265 32 82

Procedure?

CV and motivation letter are awaited before 15 February 2009 and can be send to Hans Van Gossum, by email (hans.vangossum@ua.ac.be), or post: Hans Van Gossum, Universiteit Antwerpen, Departement Biologie, Onderzoeksgroep Evolutionaire Ecologie, Groenenborgerlaan 171, 2020 Antwerpen, Belgium, Europe. Please also provide the contact details for two persons willing to write a letter of recommendation. On Monday 16 July 2009 you will be informed whether you have been selected for further interview and how selection will be continued.

Van Gossum Hans <hans.vangossum@ua.ac.be>

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## UBern 2 EvolutionaryEcol

VACANCY FOR 2 PhD-STUDENTSHIPS

two PhD positions are available in our group. We work on bird-parasite interactions using wild populations of great tits around Bern, Switzerland. Current projects include the genetics of local adaptation, the interaction between predation and parasitism, parasites and oxidative stress, parasite-induced developmental effects on song, and effects of oxidative stress on sperm traits. For information on previous projects please go to (http:// evolution.unibe.ch). PhD-students are in general expected to define their own topics within this framework. If a student has substantial interests in another theme, however, it is also possible to develop it into a PhD-project. PhD-students are well supported during all processes of identifying interesting questions, experimental design, field- and labwork, analysis and writing. The PhD-dissertation usually consists of 3-5 papers published in the top ecological and evolutionary journals. The positions are available immediately, for a period of 3 years with a possible extension of an additional year if needed. Salary is in the range of 39k sFr per annuum. Given equal qualification preference will be given to women in order promote women in academic careers. The positions ara available until filled by suitable candidates.

The University of Bern is located in the town of Bern, which is a world heritage site. It is close to several lakes, the Jura mountains and the alps.

Please send a CV and statement of interests by e-mail to:

Heinz RICHNER, Prof Dept of Biology Evolutionary Ecology Lab University of Bern, Baltzerstr.6 CH-3012 Bern, Switzerland Tel 0041 31 631 3009 (S.Maurer, secretary) e-mail: richner@esh.unibe.ch

heinz richner <heinz.richner@esh.unibe.ch>

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## UBern PlantEvolution

We are seeking a PhD student highly motivated to work on determinants of the invasiveness of clonal plants. The work will be part of a Sino-Swiss collaborative research project, which will involve field work in Europe and China, and experimentation on multiple clonal plant species in greenhouse and garden. Ideally, the candidate for this position should have a background in experimental ecology and basic knowledge of statistical methods (including generalized linear models).

The positions will be with Dr Mark van Kleunen and Prof. Dr Markus Fischer in the Plant Ecology group at the Institute of Plant Sciences of the University of Bern (http://www.botany.unibe.ch/planteco/index.php), Switzerland. Our collaborators in China are Dr Fei-Hai Yu, Prof. Dr. Ming Dong and a Chinese

PhD student (position not filled yet) in the State Key Lab of Vegetation and Environmental Change, Institute of Botany, Chinese Academy of Sciences, Beijing.

We offer a stimulating research environment in a beautiful city close to the Alps. In addition to projects on invasive plants, our group is involved in projects on evolutionary and molecular plant ecology, plant population biology and community ecology. The position is funded by the Swiss Science Foundation for a period of three years starting on February 1, 2009. Salaries (before taxes) rise from CHF 37 200 in the first year to CHF 43 200 in the third year.

Requirements for the positions include a Masters degree (or equivalent) in biology, a drivers license, fluency in German and English and good collaboration skills.

Applicants should e-mail a letter of application, a curriculum vitae and contact details of two references to Mark van Kleunen at vkleunen@ips.unibe.ch. In the letter of application, the applicant should motivate why she or he wants to do a PhD and why she or he wants to work on plant invasions. The applicant should also present details on her or his experimental and statistical skills. The application deadline is January 15, 2009.

For more information on this position, the project and research in our lab contact Mark van Kleunen at vkleunen@ips.unibe.ch.

Mark van Kleunen

Institute of Plant Sciences University of Bern Altenbergrain 21 3013 Bern Switzerland

Phone Tel. +41 31 631 49 23 Fax +41 31 631 49 42 e-mail vkleunen@ips.unibe.ch http://www.staff.unibe.ch/vkleunen/ van Kleunen Mark <mark.vankleunen@ips.unibe.ch>

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## UCollegeLondon SoftTissueEvolution

Title:

The evolution of soft tissues characters and hard tissue corollaries across the order Primates.

Supervisors:

Dr Helen Chatterjee (UCL Research Department of Genetics, Evolution and Environment). Primary Supervisor

Dr Margaret Clegg (Department of Palaeontology, Natural History Museum) CASE partner. Secondary Supervisor

Deadline for applications: 1st February 2009. To apply please send an email to Dr Helen Chatterjee outlining your interest and experience, along with a CV to h.chatterjee@ucl.ac.uk Only applicants with previous experience of anatomical dissection and/or a relevant MSc will be selected. This position is open to UK citizens only.

Outline:

The primate phylogeny is one of the best studied parts of the tree of life, with numerous molecular phylogenies having been proposed for most primate families and genera. Despite this persistent interest there is still surprising little known about the evolution of non-molecular phylogenetic characters such as hard and soft tissue morphology; this is in spite of the diverse range of fossils representing numerous stages of primate evolution dating as far back as 55 million years ago. Given the extensive and continually growing, if incomplete, fossil record for primates it is crucial we gain a better understanding of the evolution of morphological characters.

The aim of this PhD is to define a broad set of hard and soft tissues characters with a view to creating a cross-taxic database covering a wide range of primates, including all of the major groups (lemurs, lorises, tarsiers, new and old world monkeys and apes). Previous research (Gibbs et al., 2000) has shown that soft tissue characters are informative in phylogenetic analyses across higher primates and this PhD seeks to expand and build upon these initial findings. Data will be acquired through extensive dissections using wet collections housed at the Royal College of Surgeons of England Museums (principally the Osman Hill Primate Collection) and the Natural History Museum. Data will include: muscle fibre function and type, muscle attachment sites, visceral dimensions and shape, and function-specific innervations.

These data will then be mapped onto an existing molecular phylogeny recently produced by Chatterjee et al. (In review) using the phylogenetic comparative method (e.g. Independent Contrast) in order to investigate the timing and mode of character acquisition, implemented via programs such as CAIC and Mesquite. This method will allow predictions about the timing of particular morphological adaptations (such as arboreality, bipedalism) and through analogy and comparison, the likely functional specialisations of extinct primates. The research will afford a better understanding of the relationship between soft tissue characters and their hard tissue corollaries (such as muscle attachment sites on bones). Furthermore, it will provide methodological support for the value of character mapping using PCM which allows analysis of trait coevolution and, through comparison with socio-ecological parameters, the identification of ecophysiological and ecomorphological traits.

Chatterjee, H.J., Ho, S.Y.W., Barnes, I., & Groves, C. (In review). A New Combined Molecular Phylogeny for the Order Primates, with Relaxed-Clock Estimates of Divergence Times using Multiple Fossil Calibrations. Molecular Biology and Evolution.

Gibbs, S, Collard, M. & Wood, B. (2000). Soft-tissue characters in higher primate phylogenetics. Proc. Natl. Acad. Sci. USA. 97 (20), 11130-11132

To apply please send an email to Dr Helen Chatterjee outlining your interest and experience, along with a CV to h.chatterjee@ucl.ac.uk Only applicants with previous experience of anatomical dissection and/or a relevant MSc will be selected. This position is open to UK citizens only.

Dr Helen Chatterjee Deputy Director and Lecturer in Biology UCL Museums & Collections and Research Department of Genetics, Evolution and Environment.

Darwin Building University College London Gower Street London WC1E 6BT

Tel: 020 76794113 (Internal ext. 34113) Fax: 020 76797096 Email: h.chatterjee@ucl.ac.uk http://www.ucl.ac.uk/museums http://www.ucl.ac.uk/museums/learning/touch_research http://www.ucl.ac.uk/biology

Helen Chatterjee <h.chatterjee@ucl.ac.uk>

## UCork Ireland ArabidopsisReproductionGenetics

UniCork(Ireland).ArabidopsisReproductionGenetics

3 PhD Positions (Arabidopsis Reproductive Genetics)

The Genetics & Biotechnology lab of Dr. Charles Spillane at University College Cork, Ireland is seeking applicants for 3 PhD positions within the lab to work on genomic imprinting, dosage effects and apomixis technology development in Arabidopsis thaliana. The Science Foundation Ireland (SFI) funded research will involve work on genetics, epigenetics, molecular biology, microscopy and genomics techniques, and significant exposure to bioinformatics. The successful applicants will work closely with postdocs and other research team members working on these areas within the lab. We are seeking highly motivated applicants who are eager to develop a long-term career in plant research. In particular, we encourage applicants who have prior practical experience of Arabidopsis and/or molecular genetics or genomics research (e.g. as RAs, interns, etc) in research lab/institute settings. Applicants should send an e-mail outlining research interest and motivations, including; (a) your C.V. (list grades, interests and experimental skills) & (b) contact details and e-mail addresses for 3 referees to:

Dr. Charlie Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, LM 2.10, Cork, Ireland. E-mail: c.spillane@ucc.ie

The deadline for applications is Wednesday 18th February 2009.

Dr. Charlie SPILLANE, SFI Investigator & Senior Lecturer, Genetics & Biotechnology Lab, Dept of Biochemistry & Biosciences Institute, University College Cork (UCC), 2.10, Lee Maltings, Cork, IRELAND

[T] 00-353-21-4904124 (office) [E] c.spillane@ucc.ie [W] www.ucc.ie/spillane "Spillane, Charles" <C.Spillane@ucc.ie>

## UEastAnglia FlyReproduction

PhD: School of Biological Sciences, University of East Anglia, Norwich, UK

Applicants are invited for a PhD studentship to start October 2009.

Title: Is it all in the nose? The role of odorants in reproduction Synopsis: Recent research, particularly in the model organism Drosophila melanogaster, has highlighted roles for odorants (smells) in the perception of the external and internal reproductive environment. For example, many odorant receptors and their binding proteins are highly expressed in the male and female reproductive systems. This project aims to test the role of odorants in reproduction, both in the detection of, and response to, mating rivals and to reveal the role of odorants in determining fertility. The role of external odorants: male D. melanogaster respond adaptively to variation in the average level of sperm competition in a population by increasing mating duration and ultimately their reproductive success. How males perceive the presence of rivals is not yet known, although the detection of pheromones is a possibility. The role of internal odorants: the presence of odorant binding proteins and receptors in the reproductive system suggests novel roles for odorants in determining fertility. The aim of this project is to test, using mutants, the hypothesis that males and females that are mutant for odorant receptors and binding proteins in the reproductive system have lowered fertility.

Eligibility for funding: full fees and stipend are available for students satisfying UK residence requirements; fees only are available for students satisfying EU residence requirements. Funding for this award will be determined as a result of a competition within the School.

To apply, complete an application form to be found at:

http://www.uea.ac.uk/bio/courses/bioresdegrees Informal enquiries, please contact tracey.chapman@uea.ac.uk

– – Tracey Chapman School of Biological Sciences University of East Anglia Norwich Norfolk NR4 7TJ UK

Phone: + 44 (0)1603 593210 FAX: + 44 (0)1603 592250 Web: http://biobis.bio.uea.ac.uk/-biosql/fac_show.aspx?ID=365 Tracey Chapman <Tracey.Chapman@uea.ac.uk>

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## UFribourg EvolutionaryGenetics

PhD position in evolutionary biology

Project: Evolutionary genetic consequences of small vs. large population size in Daphnia

A PhD position is available at the University of Fribourg, Switzerland, in the research group of Christoph Haag. We are looking for a highly motivated candidate with interests and a solid background in the fields of evolutionary biology, population genetics, and / or molecular evolution. The PhD project is concerned with the evolutionary genetic consequences of small vs. large population size in Daphnia and will involve experimental work on Daphnia, analyses of sequences, genotyping, and, potentially, field work. Details of the project will be worked out with the candidate, to accommodate interests and strength.

The starting date is negotiable (any time from April 2009 onwards). Funding from the University of Fribourg is for three years (annual salary is ca. CHF 35,000). Some knowledge of French or German is helpful in every day life, but the working language in the group is English. A Diploma or Masters degree (or equivalent) in biology or related subject is necessary for admission. Fribourg is a lively town with over a quarter of the population being students.

To apply, please send an e-mail with the application materials in a single pdf file to Christoph Haag. Application materials should include a CV, a list of publications, and a short (less than one page) statement of research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 6 February 2009 will be given full consideration. Interviews will take place in late February / early March.

Further information and address for application: Dr. Christoph Haag E-mail: christoph.haag@unifr.ch, Tel: +41 26 300 88 71 Web: http://www.haagliautard.net/-christoph_haag.htm For more information about the Ecology and Evolution in Fribourg see http://-www.unifr.ch/biol/ecology/ christoph.haag@unifr.ch christoph.haag@unifr.ch

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## UGlasgow IntrogressionDiseaseMammals

Funded PhD position available

Project: Disease and genetic introgression from domestic species as global risk factors in mammalian conservation Supervisors: Dr R Biek & Dr S Cleaveland - University of Glasgow

Around the world, natural habitat is rapidly being converted into landscapes dominated by humans and human-associated species. Thus, wildlife populations everywhere are increasingly likely to live in direct or potential contact with domesticated species. This provides opportunities for disease spread and in some cases even genetic exchange between domestics and wildlife, often resulting in significant conservation challenges. Among wild mammals, disease is considered an important threat for a large proportion of endangered carnivores and artiodactyls (IUCN Red Data Book). Curiously, this proportion is much higher for these two groups, possibly because they also contain our most ubiquitous domesticated mammals (Pedersen 2007).

While the problems of disease transfer and introgression are well documented for certain species and locations, there has been little attempt to examine these phenomena systematically and on a global scale. This PhD project would attempt to fill this knowledge gap, primarily through statistical analysis of existing data as well as spatial and mathematical modelling. Using these tools, the student would aim to identify risk factors (e.g. behavioural, socio-economic, taxonomic, geographic, etc) associated with the transfer of domestic mammal diseases or genes into wildlife populations and develop and test conservation strategies to minimise these risks. There would also be potential opportunities to integrate the developed approaches with ongoing research at Serengeti National Park, where domestic/ wildlife interactions are a major management issue.

The student would join two lab groups with a common research focus on disease dynamics in wild and domestic animal populations. We are part of the Boyd Orr Centre for Population and Ecosystem Health (http://www.gla.ac.uk/departments/boydorr/) which constitutes a multi- disciplinary and vibrant community of researchers at Glasgow University whose expertise ranges from veterinary sciences and behavioural ecology to epidemiological modelling and geographical information systems.

Project starts October 2009, funding is guaranteed for 3 years (annual stipend of £13,290, tuition fees are paid). Candidates must either hold, or expect to obtain, a First or Upper Second class Honours degree, a Masters, or an equivalent degree in a relevant subject and must be eligible by residence for a UK research council studentship. Candidates from EU countries outside the UK are eligible for award subject to particular conditions (http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp); candidates from outside the EU are not eligible. Background in veterinary sciences and previous experience with statistics, modelling, population genetics or databases would be advantageous.

Please send a copy of your CV, together with a cover letter describing your interest in this project, your suitability for it, and the names and contact details of at least two academic referees to Dr. Roman Biek (from whom further details may be obtained): r.biek@bio.gla.ac.uk

Review of applications will start immediately and will continue until the position is filled.

References:

Cleaveland S, Laurenson MK and Taylor LH 2001 Diseases of humans and their domestic mammals: pathogen characteristics, host range and the risk of emergence. Phil Trans Roy Soc B 356: 991-999

Pedersen, AB, KE Jones, CL Nunn, S Altizer. Infectious diseases and extinction risk in wild mammals. 2007. Cons Biol 21(5): 1269-1279

r.biek@bio.gla.ac.uk r.biek@bio.gla.ac.uk

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## UGuelph MarineTemperatureAdaptation

Graduate Position (MSc or PhD) in Marine Ecological Genetics: Global warming may allow predators from the subtropics to extend their geographical range into Canada. Range expansions into Canadian waters occurred during the 1997/1998 El Niño event when the entire West Coast experienced abnormally warm sea surface temperatures. This provided an excellent preview of what effects global warming might have on coastal ecosystems because several predator species more typical of California, including the Pacific mackerel and the lined shore crab, became temporarily common in Barkley Sound, Vancouver Island and impacted the distribution of native prey species. Prey species from Canada have not co-evolved with these specialized subtropical predators and consequently may go extinct unless they can quickly adapt.

I suspect that non-indigenous intertidal invertebrate species with free-swimming larval stages are more likely to extend their range into Canada if average sea surface temperatures permanently increase than species with direct development. Additionally, I am curious whether temperate prey species are more vulnerable to invading tropical predators than the temperate ones they have coevolved with.

We are doing experiments to predict what ecological and evolutionary effects these invading species may have on native Canadian species. We have transplanted small predatory crabs to wave-exposed shores by building them concrete shelters near Bamfield Marine Sciences Centre. We have tethered gastropods differ at different distances from the shelters and find that they were most likely to be preyed upon if they were within 2 metres of the shelters and if they have thin shells. We have used microsatellites to estimate the population boundaries (demes) of the snails so we could see how this compared with the selection gradient created by the predators. This work is funded by my NSERC Discovery grants.

Requirements: Grade average of A- (3.7 or 80%) or better for the last two years of undergraduate studies. Canadian citizen or permanent resident B.Sc. in biology, ecology or zoology Interest in conservation biology, molecular ecology, near shore oceanography. Experience with marine intertidal field work or with molecular ecological lab work an asset. Should be available to start graduate work by September 2009.

Contact Information: Dr. Elizabeth Boulding Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 Email: boulding@uoguelph.ca Home page: http://www.uoguelph.ca/ ~ bouldlab/ Elizabeth Grace Boulding Associate Professor and Academic Advisor MFWB Office: room 1464 New Science Complex Department of Integrative Biology 50 Stone Road East University of Guelph Guelph, Ontario N1G 2W1 Canada office phone: (519) 824-4120 x54961 lab phone: (519) 824-4120 x58156 fax: (519) 767-1656 Email: boulding@uoguelph.ca webpage: http://www.uoguelph.ca/~bouldlab/ boulding@uoguelph.ca

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## UHawaiiHilo EvolutionaryDivergences

Graduate Student Positions in the Tropical Conservation Biology and Environmental Sciences (TCBES) M.S. Program at UH Hilo

< http://www2.hawaii.edu/ ~ tcbes/ > http://www2.hawaii.edu/~tcbes/

Priority deadline for applications to TCBES is 1 February 2009

- to study local adaptation and evolutionary divergence of native Hawaiian species - Hawaiian Picture-winged Flies and Ohia lehua (Metrosideros polymorpha).

We are looking for several students to work with Dr. Donald Price, Dr. Elizabeth Stacy and Dr. Cam Muir in the TCBES M.S. Program at the University of Hawaii at Hilo.

Students selected for these positions will receive $22,000 annual salary and will enroll in the TCBES Program in August 2009. These students will join a vibrant research community in evolutionary genetics at UH Hilo, comprising faculty, postdocs, and graduate and undergraduate students.

Students working with Dr. Donald Price ( <mailto:donaldp@hawaii.edu> donaldp@hawaii.edu < http://www2.hawaii.edu/ ~ donaldp/ > www2.hawaii.edu/~donaldp/) will investigate the Hawaiian Picture-winged Drosophila, a remarkably diverse group of insects endemic to Hawaii. We are investigating the biological diversity of these species and adaptation of several species to elevation and temperature gradients. We will investigate the process of local adaptation along multiple elevation and temperature gradients by examining variation in behavior and morphology, reproductive barriers through behavioral observations, neutral genetic variation using DNA sequencing and genotyping, and gene expression among populations.

Students working with Dr. Elizabeth Stacy (estacy@hawaii.edu www2.hawaii.edu/~estacy/) will join a team that examines the mechanisms of speciation using multiple varieties of Ohia lehua (Metrosideros polymorpha) a common, endemic tree species that appears to be in the early stages of diversification. This project will use molecular, field, and greenhouse methods to contrast patterns of neutral and expressed genetic variation among habitat-associated varieties and to quantify the fitness of intra-specific hybrids. Together, these studies will allow estimation of the strength of isolation of the gene pools of varieties on the same and different islands, insight into the molecular genetic changes that accompany divergence into multiple varieties, and determination of the stage and strength of reproductive barriers between varieties.

Students working with Dr. Cam Muir ( <mailto:cmuir@hawaii.edu> cmuir@hawaii.edu < http://www2.hawaii.edu/ ~ cmuir > www2.hawaii.edu/~cmuir) will join a program that uses genetic techniques to address evolutionary questions on inbreeding and declining populations, adaptation to novel environments, speciation, and hybridization. A variety of organisms and topics have been studied in the Muir lab including population structure of anchialine shrimp and amphidromous fish, genetic diversity of Picture-winged Drosophila, gene expression of two species of Picture-winged Drosophila differently adapted to temperature extremes, and divergence rates in several species of Drosophila and endemic crickets.

We encourage students of Native Hawaiian, Pacific Islander, or other under-represented ancestries to apply to the Tropical Conservation Biology and Environmental Science Master's program at the University of Hawaii at Hilo and join our research teams. For information on the TCBES Program and application procedures, visit: < http://www2.hawaii.edu/ ~ tcbes/ > http://www2.hawaii.edu/~tcbes/. A Bachelor's degree in biology is preferred with courses or experience in ecology and evolutionary biology. Priority application deadline for the TCBES Program is 1 February 2009 with applications accepted after that time, if positions are available. To discuss these positions further, please contact the individual faculty above.

Elizabeth Stacy Assistant Professor Department of Biology TCBES Graduate Program University of Hawaii at Hilo 200 West Kawili Street Hilo, HI 96720 Phone: 808-933-3153 Fax: 808-974-7693

estacy@hawaii.edu estacy@hawaii.edu

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## UInnsbruck IntegrativeBiodiversityResearch Ants

MOLECULAR ECOLOGY, INSTITUTE OF ECOLOGY, UNIVERSITY OF INNSBRUCK

PhD position

The University of Innsbruck, Austria, seeks to hire at the PhD student level in the area of molecular ecology. The position is a 4-years position at the Molecular Ecology group of the Institute of Ecology, starting from 1 April 2009.

The recently founded Molecular Ecology group uses the exciting opportunities offered by the advance in molecular biology, to study ecology as a snap-shot in the spatiotemporal continuum of evolving biodiversity. Data from multiple sources are integrated to enhance the success of biodiversity research. The research focuses on terrestrial animals. The group's mission is to centre on the Alpine Space, by interdisciplinary means, and in international collaboration networks.

***Responsibilities***

1. participation in an interdisciplinary and integrative biodiversity research project on ants (see Project description), i.e., addressing of population genetic, phylogeographic, phylogenetic and taxonomic questions relating to the delimitation of cryptic species, and the evolution and evolutionary ecology of cryptic diversity

2. application of molecular genetic lab techniques (mtDNA, microsatellites, possibly AFLP) and associated inference methods (gene flow analysis, phylogenetic reconstruction, phylogeographic analysis coupled with ecological niche modelling), morphometry and statistical methods related to discriminant analysis as well as elaboration of formal taxonomic consequences (analysis of type specimens, descriptions under the ICZN)

3. fieldwork

4. contact and collaboration with a range of scientists at the Faculty of Biology in Innsbruck, at other Austrian research facilities and internationally

5. preparation of manuscripts

6. participation in the PhD program of Innsbruck University; see <http://www.uibk.ac.at/-fakultaeten-servicestelle/pruefungsreferate/studien/c091_2001w.html>

***Selection criteria***

A. completed study of biology, MSc level

B. demonstrated research experience in population genetics, phylogeography, phylogenetics or taxonomy of arthropods

C. keen interest in evolution and ecology

D. ability to work effectively as part of a multidisciplinary team

E. flexibility in the course of progressing research

F. ability to work independently

G. ability to work under pressure

H. good knowledge of oral and written English

***PhD supervisor***

Birgit C. Schlick-Steiner

***Salary***

The annual gross salary is Euro 21,932.40; should at some stage teaching possibilities arise and the successful candidate opts for at least 2 hours of teaching per week, the salary would be increased accordingly

***Project description***

An outstanding number of cryptic species was discovered in the European Tetramorium caespitum/impurum ant complex but very recent, unpublished evidence suggests that intermediate forms between two of the cryptic species may occur, necessitating to revisit the present species delimitations, also through additional molecular markers.

Central hypotheses to be tested for the whole complex hence include whether observed genetic and phenetic variation is intraspecific vs. interspecific and whether or not gene flow occurs among species, recently and/or in the evolution of the complex. Via an interdisciplinary, integrative approach the project aims at (i) definitive species delimitations including taxonomic acts, and (ii) elucidation of the evolutionary patterns that shaped the cryptic diversity (e.g., parallel evolution? convergence? plesiomorphy? introgression?) and how they were mediated (e.g., palaeoclimatic dynamics? ecological niche shifts? interspecific competition?).

Collaborators include Birgit Schlick-Steiner (University of Innsbruck; PhD supervision), Bernhard Seifert (Senckenberg Museum of Natural History Goerlitz; morphometry and taxonomy), Lacey Knowles (University of Michigan; coupled phylogeographic and ecological niche modelling), Karl Moder (University of Applied Life Sciences and Natural Resources Vienna; statistics), Florian Steiner (University of Innsbruck; project coordination).

Further reading:

Schlick-Steiner et al 2006 Molecular Phylogenetics and Evolution 40:259-273

Schlick-Steiner et al 2007 Trends in Ecology and Evolution 22: 391-392

Moder et al 2007 Journal of Zoological Systematics and Evolutionary Research 45: 82-87

Steiner et al 2006 Myrmecologische Nachrichten 8: 175-180

Steiner et al 2008 Conservation Genetics 9: 757-759

Schlick-Steiner et al 2007 Biological Journal of the Linnean Society 91: 247-255

Steiner et al 2008 Diversity and Distributions 14: 538-545

***How to apply***

To apply, please submit, by E-mail to <fss-technik@uibk.ac.at>, with cc to <birgit.schlick-steiner@uibk.ac.at>, and with the subject line “Chiffre: BIO-5459 - Bewerbung um ein wissenschaftliche Stelle”: a cover letter

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## UKiel FishStressEvolution

The Leibniz Institute of Marine Sciences (IFM-GEOMAR) at the University of Kiel is one of the leading institutes in marine research in Germany. Its major goal is fundamental research in all areas of marine sciences. For more information please visit www.ifm-geomar.de. The Leibniz Institute of Marine Sciences at the University of Kiel (IFM-GEOMAR), is offering a

PhD position in fish stress evolution and trancriptomics

in the newly founded research unit Evolutionary Ecology of Marine Fishes

Job Description The PhD project is one of 8 interrelated projects within the project cluster NEMO (=âNachhaltige Ernaehrung mit Marinen Organismenâ - sustainable use of aquatic organisms). We are seeking a highly motivated and enthusiastic candidate who is expected to pursue a doctoral thesis aside from working within the project. The holder of the position should perform transcription analysis using state-of-the art tools (Q-PCR, 454 transcription profiling, array technology) in cod and turbot. Behavioral and physiological assays will partly be provided by other projects within the cluster. Our goal is to identify in controlled experiments the impact of stressors such as crowding, food types and temperature on fish behavior and welfare, and its interaction with population origin. Another focus will be the genetic effects of domestication on transcription patterns. Through the cluster of excellence âThe Future Oceanâ access to high throughput genomic facilities is provided. Candidates with a freshwater background are also encouraged to apply, provided they commit to entering the marine world.

Qualification We request a Msc or Diploma degree in Biology, Evolution, Ecology, Genetics or a related subject.

This is a half time position is available for a period of 3 years. The salary depends on qualification up to the class 13 TV-L of the German tariffs for public employees. Working language in the group is English. The Leibniz-Institute of Marine Sciences is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply.

Please send your applications for this post not later than 27 February 2009 by normal mail using the keyword “fish gene expression” to the following address:

Leibniz-Institut für Meereswissenschaften an der Universität Kiel Personalbüro Wischhofstraße 1-3 D-24148 Kiel GERMANY

Please give name and address of two references and mention the keyword on the envelope and on the application. A re-addressed envelope is greatly appreciated.

Questions are answered by Prof. Reinhold Hanel (rhanel@ifm-geomar.de) or Prof. Thorsten Reusch (treusch@ifm-geomar.de).

Prof. Dr. Reinhold Hanel Leibniz-Institut für Meereswissenschaften IFM - GEOMAR Dienstgebäude Westufer Düsternbrooker Weg 20 D-24105 Kiel Germany ><((((Â> <Â))))>< Tel: +49 431 600 4556 Fax: +49 431 600 4553 e-mail: rhanel@ifm-geomar.de www.ifm-geomar.de Reinhold Hanel <rhanel@ifm-geomar.de>

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## ULausanne Evolution of InvasiveSpecies

We have an open position for a Ph.D. student to study the evolutionary history of the environmental niche in invasive species in Europe.

Evolutionary Niche dyNamics of Invasive Species (ENNIS)

The project seeks to understand the relationship between the evolutionary history, niche variation and accompanying variation in the distribution of species. The project will focus on plant clades that have naturalized and invasive member species in Switzerland and central Europe. We will use an interdisciplinary approach that includes activities in niche modeling, phylogenetic reconstruction and modeling trait evolution. The research includes characterization of the environmental niches and distribution of clade members using multivariate statistics and niche-based species distribution modeling, sequencing DNA, use of sequence and phylogenetic databases, and use of other databases on the distribution of invasive species. Collection of material for sequencing, and additional data on species global distributions may involve visiting national herbaria, botanical gardens, individual researchers, and doing fieldwork throughout the sum distribution of the species in the focal clades. Phylogenetic reconstruction of evolutionary relationships will be undertaken using likelihood and Bayesian methods. Modeling of evolutionary processes of ecological diversification will be approached through the use of experimental software and the development of original algorithms.

This is a fully-funded 3-year Ph.D. with stipend, travel money, etc. You would be associated with both the Department of Ecology and Evolution at the University of Lausanne and the Swiss Federal Research Institute WSL near Zurich. (Knowledge of French or German is not required)

< http://www.unil.ch/dee > < http://www.wsl.ch >

See the following websites for info: http://www2.unil.ch/phylo http://www.wsl.ch/personal_homepages/pearman Application deadline is 15 February 2009

For more information, feel free to contact either:

Peter B. Pearman Pearman@wsl.ch Or Nicolas Salamin Nicolas.Salamin@unil.ch

"Peter B. Pearman" <pearman@wsl.ch>

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## ULondon BatMateChoice

Funded PhD position (start Oct 09) - MATE CHOICE IN HORSESHOE BATS Supervisor: Dr S Rossiter - Queen Mary, University of London, UK

The genetic basis of mate choice might rely on overall relatedness between partners, or on specific genetic profiles. For example, recent studies of a range of taxa show that gamete interaction, storage and fertilisation can be controlled by genes expressed on the surface of sperm and eggs as well as in semen and the female reproductive tract.

The students will study behaviour in a wild population of horseshoe bats in the UK. Specifically, he or she will combine parentage and pedigree analyses based on neutral and functional genetic markers to test for the determinants of mate choice. This project will also involve collaboration with colleagues from the University of Bristol.

Training will be provided in molecular methods (DNA isolation, PCR, sequencing, microsatellite genotyping) and statistical analyses (pedigree construction, modeling). The student will be expected to undertake a limited amount of fieldwork. A driving license, a background in genetics and an enthusiasm for quantitative approaches will be advantageous.

Questions or applications are invited from candidates with, or expecting to obtain, at least an upper-second class honours degree in an area relevant to the project. Send your CV, the names and contact details of two academic referees, a covering letter and a note of where you saw the studentship advertised, to Dr. S. Rossiter (s.j.rossiter@qmul.ac.uk).

Deadline - 2nd February 2009

REFERENCES Swanson & Vacquier (2002) Nature

Genetics 3: 137-144 Rossiter et al. (2005) Nature, 437: 408-411 Rossiter et al. (2006) Molecular, Ecology 15: 3035-3043

- Please pass on to applicants who you think might be interested -

IMPORTANT NOTE ON FUNDING A successful candidate would receive funding (covering fees and stipend) via the Natural Environment Research Council. This funding is ONLY possible for candidates who meet the residence criteria described here: http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp Stephen Rossiter <s.j.rossiter@qmul.ac.uk>

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## ULouisiana EvolutionaryBiol

Doctoral Fellowships and other assistantships are available for students joining the program in Environmental and Evolutionary Biology at the University of Louisiana.

We will be awarding six fellowships to Ph.D. students entering Fall 2009. University Fellows are funded for 3-4 years at $15,750 per 9 months (with tuition waiver), and have limited teaching responsibilities. BoR Fellows are funded for 4 years at $25,000 per year (with tuition waiver) and have no formal teaching duties. Eligibility requirements include US citizenship (or permanent residency) or degree from a US institution. We will also have teaching and research assistantships available for incoming Ph.D. students. Rather than replying to this message, potential applicants are strongly encouraged to directly contact prospective advisors at the University of Louisiana. Their contact information and research interests can be found at our departmental web site (http://biology.louisiana.edu/). More information is also available at our graduate program web site (http://www.ucs.louisiana.edu/~pll6743/biogradstudies.htm). The department of Biology has approximately 25 faculty members and 70 graduate students. Areas of strength include ecology, conservation biology, evolution, and marine/coastal biology.

– Paul Leberg Professor and Graduate Coordinator Department of Biology University of Louisiana Lafayette

For more information on my research please visit: http://www.ucs.louisiana.edu/ ~ pll6743/ For more information about the graduate program please visit: http://www.ucs.louisiana.edu/~pll6743/biogradstudies.htm and http://biology.louisiana.edu/ PO Box 42451 Lafayette, LA 70504 Leberg@Louisiana.edu 337-482-6637 337-482-5660 (Fax)

Paul Leberg <leberg@louisiana.edu>

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## ULouvain TetrahymenaBiodiversity

Ph.D. position, Louvain-la-Neuve, Belgium

Experimental study of metapopulation dynamics and viability with microcosms of a unicellular microorganism, Tetrahymena thermophila

Efficient biodiversity conservation requires a clear understanding of factors affecting (meta)population viability. Our research team studies the impact of major perturbations (habitat fragmentation, climate change...) on determinants of (meta)population viability (like habitat quality, demography, dispersal, metapopulation dynamics...).

We are currently looking for a highly motivated student to start a Ph.D. within the framework of a new and stimulating project focusing on the experimental study of metapopulation dynamics and viability with microcosms of a unicellular microorganism, Tetrahymena thermophila. Such microcosms are simplified versions of real world systems, with a level of control and replication impossible to achieve on real populations. We intend to use such microcosms to unravel the complex links between life history traits, population structure and viability. More information on the project is available on http://www.uclouvain.be/en-81937.html (see also BMC Evol. Biol. 7, 133 for our previous work). This project nicely complements our ongoing research on threatened butterfly metapopulations.

Candidates should have excellent CV, with a background in ecology, conservation biology or evolutionary biology. Some research experience, and/or publications, in these fields are an asset.

You will work within a young research team at the Biodiversity Research Centre of the Université catholique de Louvain (UCL) in Belgium: the Quantitative Conservation Biology Group (5 researchers) headed by Prof. Nicolas Schtickzelle (www.uclouvain.be/quant-cons-biol). Our university is in the French-speaking part of Belgium (Louvain-la-Neuve, close to Brussels). Lab meetings and other scientific activities are in English. The project will involve close collaboration with the French CNRS lab "Station d'Ecologie expérimentale de Moulis" (Dr. Jean Clobert), including stays there (near the Pyrenees mountains). Dr. Clobert is a leading expert in ecology and is using Tetrahymena systems to study questions related, among others, to dispersal, cooperation and their evolution.

This Ph.D. position is for 12 months. Once in Belgium, you are expected to apply for a grant to continue and finish your Ph.D. (4 years on average in Belgium). Several options are available, and our past record of success rate is high. The starting date is negotiable from March to July.

If you are interested, please send an e-mail message to nicolas.schtickzelle@uclouvain.be in which you explain why you would like to join us on this project, attach your CV as a separate document, and arrange for one reference letter to be sent separately to support your application.

Please submit your file no later than March 1st 2009.

Prof. Nicolas Schtickzelle Research Associate (FNRS) & Lecturer

Quantitative Conservation Biology Biodiversity Research Centre Universite catholique de Louvain Croix du Sud 4 B-1348 Louvain-la-Neuve Belgium

phone : +32 10 47 20 52 fax : +32 10 47 34 90 office: building Carnoy, room C.157

nicolas.schtickzelle@uclouvain.be http://-www.uclouvain.be/quant-cons-biol

## UNorthCarolina Wilmington ConservationGenetics

Graduate M.S. Positions in Conservation Genetics, in the lab of Dr. Brian Arbogast, University of North Carolina, Wilmington. I am anticipating accepting two M.S. students into my lab for Fall 2009. The broad focus of research will be conservation genetics and statistical phylogeography. Potential projects include conservation genetics of isolated populations of the northern flying squirrel in the Appalachian Mountains and comparative phylogeographic studies of mammals. Conservation genetic projects on other taxonomic groups are also possible depending on funding and student interest. Students will be housed in a newly outfitted genetics laboratory on UNCW's main campus and have access to an extensive molecular genetics core facility at UNCW's Center for Marine Science. Successful applicants should have some background in population genetics or phylogenetics, modern molecular skills (PCR etc.) and an interest in fieldwork. Applicants with experience using microsatellites are especially encouraged to apply. Stipends for these positions are approximately $14,000 per year and include an out-of state tuition waiver and research funds. Additional funds to cover In-State tuition may also be available.

Please Visit the Arbogast Lab Page at: http://-people.uncw.edu/arbogastb/ Information on the graduate program at UNCW can be found at http://-www.uncw.edu/bio/grad-ms.html Interested parties should contact Dr. Arbogast at: arbogastb@uncw.edu

Brian Arbogast, Ph. D. Department of Biology and Marine Biology University of North Carolina Wilmington, NC 28403

Phone: (910) 962-2644 Fax: (910) 962-4066 Email: arbogastb@uncw.edu

Arbogastb@uncw.edu Arbogastb@uncw.edu

## UNorthernColorado PlantPhylogeography

Graduate positions (MS or PhD) in Plant Phylogeography in the lab of Dr. Mitchell McGlaughlin, School of Biological Sciences, University of Northern Colorado.

I am seeking a MS student for an NSF funded project examining phylogeography in Lotus (Fabaceae) from the California Channel Islands. This project is examining the phylogeographic relationship of two species of Lotus found on the Channel Islands, with particular interest in rates of gene flow and isolation by distance. The selected student will collect low copy nuclear sequence data from all sampled taxa. I am looking for a student with DNA sequence experience or extensive experience with PCR methods, an understanding of coalescence and incomplete lineage sorting, and a willingness to carry out computer based data analysis. This project has two years of RA support with an anticipated start date of August 2009.

Additionally, I am recruiting MS or PhD students interested in the population genetics, conservation, speciation, and phylogeography of plant species. Doctoral students are encouraged to develop projects within the scope of research in my lab and masters students can develop their own projects or work on research already initiated in the lab. Funding is available to support graduate students through teaching and research assistantships, scholarships, and grants.

For more information please visit my lab website: http://www.unco.edu/mcglaughlinlab/ or the department website: http://www.unco.edu/nhs/biology/index.htm The University of Northern Colorado is a public institution with about 11,000 undergraduate and 1,500 graduate students, located in Greeley, Colorado. Greeley is situated 50 miles northeast of Denver and 20 miles east of the rockies, with easy access to Rocky Mountain National Park and other outdoor activities.

Interested applicants should send a letter of interest and CV to Dr. Mitchell McGlaughlin (Mitchell.mcglaughlin@unco.edu). To apply, students will need to submit a complete application to the UNC School of Biology (http://www.unco.edu/nhs/biology/students/gradapp-instructions.html) and Graduate School (http://www.unco.edu/grad/index.html). There is no fixed application deadline, but applications are reviewed when they are received.

– Mitchell McGlaughlin, Ph.D. Assistant Professor 501 20th Street, Ross Hall 1560 University of Northern Colorado Greeley, CO 80639 970-351-2139 Mitchell.McGlaughlin@unco.edu http://www.unco.edu/mcglaughlinlab Mitchell.McGlaughlin@unco.edu Mitchell.McGlaughlin@unco.edu

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## UNottingham AdaptiveRadiation

Graduate position: Adaptive radiation and host-parasite interactions in three-spined sticklebacks

An enthusiastic student is sought to do a PhD on the ecological causes of evolutionary diversification in the adaptive radiation of three-spined sticklebacks, Gasterosteus aculeatus. The successful student will contribute to shaping their own project, but possible themes include:

(1) The geographic mosaic of coevolution between sticklebacks and their parasites. This project would use artificial infection experiments and immunological assays to explore inter-population variation in host resistance and parasite virulence, their quantitative genetic basis and their contribution to the evolution of reproductive isolation. (see e.g. Brodie, Ridenhour & Brodie, 2002; Thompson, 2005). (2) The role of parasites in the evolution of senescence. You would explore variation in rates of (actuarial and immune function) senescence between stickleback populations to see whether these are associated with variation in parasite burdens or virulence (see e.g. Reznick et al., 2004; Williams et al., 2006). (3) Phenotypic plasticity and speciation in sticklebacks. This project would investigate the contribution of plasticity in ecologically relevant traits (including immune function) to facilitating the invasion of novel environments and the accumulation of reproductive isolation (see e.g. Price, Qvarnstrom & Irwin, 2003; Pigliucci, Murren & Schlichting, 2006).

Any project is likely to combine aquarium based work with lab-reared sticklebacks, immunological assays and molecular or quantitative genetics to explore natural variation among populations in the adaptive radiation of sticklebacks on the island of North Uist in the Scottish Outer Hebrides. Populations of three-spined sticklebacks on this island are very numerous and diverse, occurring as isolated freshwater populations, freshwater populations that hybridise with marine three spined sticklebacks in defined hybrid zones, and sympatric, isolated population pairs of marine and freshwater 'species'.

Applicants should have a good degree in a relevant subject, and an interest and enthusiasm for evolutionary biology. Previous field work experience and a full driving licence would be beneficial but are not required.

The School of Biology, University of Nottingham has at least 5 PhD studentships to begin in October 2009. These will be awarded, on a competitive basis, to the best applicants across the School.

Prospective students should send a CV and a one page outline of how they would tackle the project to Andrew MacColl (andrew.maccoll@nottingham.ac.uk) before 30 January 2009.

Andrew MacColl School of Biology, University of Nottingham, University Park, Nottingham, NG7 2RD, U.K.

References Brodie, E.D., et al. (2002) Evolution, 56, 2067-2082. Pigliucci, M., et al. (2006) J. Exp. Biol., 209, 2362-2367. Price, T.D., et al. (2003) PRSB., 270, 1433-1440. Reznick, D.N., et al. (2004) Nature, 431, 1095-1099. Thompson, J.N. (2005) The Geographic Mosaic of Coevolution University of Chicago Press, Chicago. Williams, P.D., et al. (2006) Trends Ecol. Evol., 21, 458-463.

you are advised to perform your own checks. Email communications with the University of Nottingham may be monitored as permitted by UK legislation.

Andrew.Maccoll@nottingham.ac.uk

## UOttawa CarletonU Bioinformatics

GRADUATE OPPORTUNITIES IN BIOINFORMATICS

Multiple graduate positions in bioinformatics are available for Fall 2009 at the University of Ottawa and at Carleton University. The following faculties are seeking graduate students for their labs:

- Stephane Aris-Brosou (BIO/MAT): computational molecular evolution, http://aix1.uottawa.ca/~sarisbro/ - David Bickel (BCH/MAT): statistical genomics and systems biology, http://www.statomics.com/ - Frank Dehne (CS), protein interaction prediction, RNA aptamer design, http://lab.dehne.net - James Green (CS): pattern classification and multicore acceleration, http://www.sce.carleton.ca/faculty/green - Evangelos Kranakis (CS): computational molecular biology, http://www.scs.carleton.ca/~kranakis/ - David Sankoff (MAT/BIO/CS): mathematical genomics, evolution, http://albuquerque.bioinformatics.uottawa.ca/ - Xuhua Xia (BIO): bioinformatics and molecular evolution, http://dambe.bio.uottawa.ca Besides intramural collaborations and cosupervision, the program benefits from tight collaborations with the Ottawa Institute of Systems Biology (http://www.oisb.ca/), a strong medical campus (http://www.ohri.ca/ and http://www.cheo.on.ca/) and from the presence of federal Research Centres such as the National Research Council (http://www.nrc-cnrc.gc.ca/), Agriculture Canada (http://www.agr.gc.ca/), Health Canada (http://www.hc-sc.gc.ca/), the Canadian Food Inspection Agency (http://www.inspection.gc.ca/), or Statistics Canada (http://www.statcan.ca/). These Institutes and research Centres offer both training and job opportunities to our students.

For more details on the Bioinformatics program, please see:

http://www.grad.uottawa.ca/Default.aspx?tabid=1727&monControl=Profs&ProgId=826 Additional information can be obtained from the program coordinators: Drs. Stephane Aris-Brosou (sarisbro@uottawa.ca) and Michel Dumontier (Michel_Dumontier@carleton.ca).

Stephane Aris-Brosou, PhD Assistant Professor Department of Biology, Department of Mathematics & Statistics University of Ottawa 30 Marie Curie Pr. Ottawa, ON, K1N 6N5 CANADA

Stephane Aris-Brosou <sarisbro@uottawa.ca>

## UPF Barcelona EvolutionaryGenomics

Funded PhD scholarship in evolutionary genomics and Systems Biology in Pompeu Fabra University (Barcelona).

The group of Evolutionary Biology in the Experimental Sciences and Health Department of the Pompeu Fabra University offers one PhD scholarship in the field of Evolutionary Genomics. Selected candidate will have the opportunity to develop novel research lines that will contribute to the understanding of the biology of genomes at evolutionary, molecular and biomedical level. The successful candidate would work on integrating different bioinformatics tools for the identification of network structures of genes and metabolic pathways under selective forces.

Our group offers an unusual and highly formative research frame, in which leading edge computational resources and experimental laboratory facilities are combined to achieve our research goals.

Particular priority will be given to candidates with background on bioinformatics. Programming and general computational skills are desirable, but all candidates will be considered.

If you are interested, please send your CV to Jaume.bertranpetit@upf.edu <mailto:Jaume.bertranpetit@upf.edu> or Hafid.laayouni@upf.edu <mailto:Hafid.laayouni@upf.edu>

– Hafid Laayouni Centro de Investigación Biomédica en red Epidemiología y Salud Pública (CIBERESP) IBE, Institut de Biologia Evolutiva (UPF-CSIC) Parc de Recerca Biomèdica de Barcelona (PRBB) Dr. Aiguader, 88. 08003 Barcelona Tel. (34) 93-316-0845 Fax: (34) 93-316-0901 Spain

Hafid Laayouni <hafid.laayouni@upf.edu>

## URhodeIsland ComparativeGenomics

There will be an opening for a Ph.D. student in the Lane lab (http://cels.uri.edu/bio/lanelab/) at the University of Rhode Island for the fall semester (2009) to work on comparative genomics of red algal parasites. I am looking for a motivated and organized student to help explore this unusual and exciting system. The ideal candidate would already have a Master's degree and have experience with molecular techniques (DNA/RNA extraction, PCR, cloning and sequencing) and bioinformatic/phylogenetic analyses. Some programming knowledge would be an asset, but a willingness to learn is essential. As part of their fellowship, the student would be expected to TA during the academic year.

The Lane lab is well equipped to carry out molecular investigations in a variety algal taxa and will be moving within the month to the newly built Center for Biotechnology and Life Sciences on the URI Kingston campus, which will house much of the university's substantial genomics infrastructure. Additionally, there are ongoing opportunities for collaboration with the labs of Drs. Goldsmith, Jenkins, Rynearson and Udwary. The university has a strong tradition of marine research and the Lane lab is part of a growing multi- departmental concentration in marine genomics.

Rhode Island offers numerous opportunities for outdoor activities and hundreds of miles of sandy beaches. The Kingston campus is located 20 minutes from Newport and 30 minutes from Providence, each offering a unique culture, including live entertainment and dozens of restaurants.

Interested individuals should send a CV, letter of interest and contact information for three references as a single PDF to me at clane@mail.uri.edu by January 23rd. Please indicate in your letter 1) previous relevant experience, 2) why you are interested in pursuing a Ph.D., and 3) your interest in comparative genomics.

For further details about the position, project and lab, feel free to contact me

Chris Lane Assistant Professor Department of Biological Sciences University of Rhode Island 100 Flagg Road Kingston, RI., 02881 ph (401) 874-2683 fax (401) 874-4256 http://cels.uri.edu/bio/lanelab/ clane@mail.uri.edu

## UWyoming MolEvolution

Ph.D. Positions in Evolutionary Biology at University of Wyoming

Several positions are currently available for Ph.D. students in the Liberles Research Group at University of Wyoming. Applicants should have skills in programming, some knowledge of statistics, protein structure, and molecular biology, as well as an interest in evolution. Research projects include several areas in phylogenetics and/or the evolution of protein structure. For more details on research in the Liberles Research Group, please see

http://www.wyomingbioinformatics.org/-LiberlesGroup.

University of Wyoming is located in Laramie, WY, 2 hours north of Denver in the rocky mountains. It is an ideal location for those with interests in skiing (both downhill and cross country), rock climbing, hiking, ....

To apply, please send a CV, statement of research interests, and contact information for three references, to liberles@uwyo.edu. Informal inquiries before application are welcome.

"David A. Liberles" <liberles@uwyo.edu>

# Jobs

## Avian FieldAssistants

FIELD ASSISTANTS needed, 15 April - 15 August (flexible) to aid DR. ELLEN KETTERSON in a study of the breeding biology of Dark-eyed Juncos. At least one position is available at each of two locations: Mountain Lake Biological Station in SW Virginia and the Black Hills National Forest of South Dakota. Responsibilities may include mist netting, blood sampling, nest finding, behavioral observation, GPS, and data entry. Applicants must be able to distinguish colored leg bands in the field, enjoy working outdoors (even in bad weather), be self-motivated and demonstrate a willingness to learn new skills, be able to work well with others, and be willing to do minor manipulative research with animals. Experience strongly preferred but not absolutely necessary. However, motivation is a primary consideration: the work is sometimes hard and demanding and can require long hours. Transportation allowance, room, board, and stipend (amount dependent upon experience and level of funding for project) provided. The work is very rewarding if you are interested in animal behavior and like to be outdoors. Write to Amy Dapper, Field Assistant Position, Department of Biology, Indiana University, 1001 E. 3rd St., Bloomington, IN 47405 or email (preferred) adapper@indiana.edu. Please include a summary of your background, your reasons for applying for this position, your site preference (VA or SD) and the names and email addresses of 3 people who might evaluate your work or potential. REVIEW OF APPLICATIONS WILL BEGIN 1 FEB 2009, but applications will be accepted until positions are filled. Please contact Amy Dapper ( adapper@indiana.edu) with any questions regarding these positions.

amy.dapper@gmail.com

## ChicagoBotanicGarden SummerResearch PlantEvolution

Summer field research experience for undergrads and recent graduates

Are you interested in gaining field research experience and learning about the ecology and evolution of plants and plant-animal interactions in fragmented prairie? We are looking for 3-5 summer field researchers for an NSF-funded project on habitat fragmentation of the tallgrass prairie. We are investigating how small plant population size influences inbreeding, demography, pollination, and herbivory in the purple coneflower, Echinacea angustifolia. This is a great summer internship or co-op for those interested in field biology or conservation research.

No experience is necessary, but you must be enthusiastic and hard-working. You will survey natural plant populations, measure plant traits in experimental plots, hand-pollinate plants, observe & collect insects, and assist in all aspects of research. Housing is provided and there is a stipend. Undergraduate students have the opportunity to do an independent project as an REU participant.

If you want more information or wish to apply, please visit this website http://echinacea.umn.edu/ or contact Stuart Wagenius. Applications due 6 March 2009.

Stuart Wagenius, Ph.D. Conservation Scientist Division of Plant Science and Conservation Chicago Botanic Garden 1000 Lake Cook Road Glencoe, IL 60022 phone: 847 835 6978 fax: 847 835 5484

email: stuart09@echinaceaproject.org web: http://echinacea.umn.edu SWagenius@chicagobotanic.org

## CornellU OysterAdaptation

Date: 23 December 2008

Department of Natural Resources Cornell University

Position: FIELD RESEARCH ASSISTANT

Description: Help perform an NSF-funded field experiment designed to examine differential oyster adaptation to warm-temperate and subtropical estuaries in eastern Florida. Field work is based out of Fort Pierce, Florida and the Harbor Branch Oceanographic Institution.

Duties: The successful applicant will gain experience conducting field and laboratory research. Major field objectives will be to measure oyster growth, health, disease resistance, and reproductive development. Specifically, the assistant will help with oyster spawning and larval culture, photograph juvenile oysters over a time series at multiple field sites, help deploy, monitor and retrieve field equipment, sample water for phytoplankton and oyster tissue for DNA analyses, and retrieve data from remote data loggers.

Requirements: The ideal applicant will be available to work in Florida from Mid-March through August 2009. Must be able to lift 50 lbs. Extensive driving will be necessary ' a clean driving record is desirable and the candidate must have held a U.S. driver[1]s license for at least three years. Some field and/or laboratory experience is desired. Please note that fieldwork can be strenuous and that much of the outdoor work will be performed in hot and sometimes rainy conditions. No scuba diving is required but regular entry into shallow water is necessary. This is a paid position and costs for travel to Florida and housing (but not food) will be provided.

Instructions: Please submit an application through the Cornell Human Resources site at http://www.ohr.cornell.edu/jobs/. Under [3]Staff (non-academic)and Librarian positions[2] search for job 10261. Applications will be accepted at least until January 10 and then until the position is filled. Informal inquires can be made with Martha Burford (mob8@cornell.edu)

Payment: $9/hour for 40hours/week for 22 weeks.

Background information on the project: http://www.dnr.cornell.edu/HareLab/harelab.html#divzoo

CORNELL CONTACT INFORMATION: Martha O. Burford, Ph.D. Postdoctoral Associate Department of Natural Resources 208 Fernow Hall Cornell University Ithaca, NY 14853 Phone: 607.255.5685 Fax: 607.255.0349 mobile:831.419.7586 E-mail: mob8@cornell.edu

FLORIDA CONTACT INFORMATION: Martha O. Burford, Ph.D. NSF Oyster Project Harbor Branch Oceanographic Institute C/O Dr. John Scarpa 5600 U.S. 1 North Fort Pierce, FL 34946 Phone: 772.465.2400, ext. 402 Fax: 772.466.6590

mob8@cornell.edu mob8@cornell.edu

## FHCRC UWashington DiseaseDynamics

Associate or Assistant Member KW - 22181

Faculty Position in Mathematical Modeling of Immune responses and Within-host Dynamics of Infectious Diseases

The Vaccine and Infectious Disease Institute of the Fred Hutchinson Cancer Research Center (FHCRC) and the University of Washington (UW) are jointly recruiting a full-time faculty position at the Assistant or Associate Member level in the Public Health Sciences Division of the FHCRC with a joint appointment as an Assistant or Associate Professor without tenure in the Department of Global Health at the UW. Preference is given to those with a professional expertise in mathematical, statistical and computational methods for understanding the dynamics of immune responses and pathogens. Ph.D. qualification is required in one of the following areas: evolutionary biology, evolutionary ecology, mathematics and biology, population biology, or related field. The applicant should have a strong track record in basic immunology, the biology of infectious diseases, the use of deterministic and stochastic modeling, analytic and computational approaches, and statistical analysis. Expertise the area of HIV, influenza, TB, malaria, HSV2, dengue, cholera, or other important infectious diseases in the developing and developed world will be particularly welcomed. This individual will be expected to develop an independent research program. A vital role of this position will be to forge collaborations between colleagues at FHCRC and UW; the successful candidate should have a proven ability to establish productive collaborations with both theorists and experimental immunologists. Salary DOE + excellent benefits. Interested candidates may submit a CV, a concise statement of their research plan, and three (3) letters of reference to:

Helen Pagal Vaccine and Infectious Disease Institute Public Health Sciences Division Fred Hutchinson Cancer Research Center 1100 Fairview Ave. N., LE-400 P.O. Box 19024 Seattle, WA 98109

The University of Washington and the Fred Hutchinson Cancer Research Center are affirmative action, equal opportunity employers. We are dedicated to the goal of building a culturally diverse and pluralistic faculty and staff committed to teaching and working in a multicultural environment and strongly encourage applications from women, minorities, individuals with disabilities and covered veterans. The University of Washington, a recipient of the 2006 Alfred P. Sloan award for Faculty Career Flexibility, is committed to supporting the work-life balance of its faculty.

"Otis, Stephanie" <sotis@fhcrc.org>

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## KansasStateU LabTech PlantGeneticVariation

POSITION - Research Assistant

JOB RESPONSIBILITIES The Toomajian laboratory in the Department of Plant Pathology at Kansas State University seeks applications for a full time laboratory research technician. The RA will join a new laboratory investigating patterns of genetic variation in natural populations of plants and fungi with the aim of understanding the genetics of adaptation and processes involved in genome evolution. The lab spans the intersection of computational biology, evolution, and functional genomics. The RA will be expected to participate in research projects in the field of molecular population genetics/genomics. Techniques used will include: plant growth and care, genetic crosses, nucleic acid isolation, PCR, DNA genotyping and sequencing, and related sample preparation. The RA will also assist in supervision and training of laboratory personnel, maintain records, manage biological materials, oversee laboratory compliance issues and contribute to the maintenance and running of the laboratory. For questions and informal inquiries, please contact Chris Toomajian, Department of Plant Pathology, Kansas State University, toomajia@ksu.edu.

For a full description, including required and preferred qualifications, and more information about the lab, see https://sites.google.com/site/toomajianlab The appointee is expected to contribute towards the research effort of the laboratory and department, and to develop his/her research expertise through the pursuit of defined projects. The appointee will be expected to work both as a member of a team and independently under limited supervision and will have the opportunity to contribute to research publications (including co-authorship).

TO APPLY Please submit by email or hard copy: (1) a cover letter, including your anticipated start date, (2) a curriculum vitae, (3) a statement describing your research experiences and interests, and (4) names, addresses, telephone numbers and email addresses of at least three referees to: Dr Chris Toomajian, Department of Plant Pathology, 4024 Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506-5502, email: toomajia@ksu.edu; Tel: 785-532-0879. Please address in your application how you meet the required and preferred qualifications. Review of applications will begin January 27, 2009; screening will continue until the position is filled.

Kansas State University is an equal opportunity, affirmative action employer and actively seeks diversity among its employees. Background checks required.

chris.toomajian@gmail.com

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## London Biodiversity 2ProjectManagers

Associate Project Managers in Biodiversity

2 POSTS AVAILABLE

Hours of work: 36 per week (excluding lunch breaks)

Job status: Casual Contract ending 26 November 2009 or 1 January 2010 (depending of the post)

Salary per annum: GBP 20,972

Department and location: Jodrell Laboratory RBG Kew and Imperial College London (Silwood Park)

Job Details

To assist Dr Vincent Savolainen, a dual appointee between RBG Kew ands Imperial College in the management, day-to-day research and student teaching and training of the following 2 Projects:

- HOTSPOTS 'Understanding and Conserving the Earth's Biodiversity Hotspots'

- 'BRIDGE - 'Bridging Information on Tree Diversity in French Guiana and a Test of Ecological Theories' -

To produce molecular phylogenetic data sets for the project including DNA barcodes for tree species of biodiversity hotspots in French Guyana and South Africa.

Essentials: University degree (eg BSc) in relevant subject.?Basic knowledge of molecular techniques (PCR and DNA sequencing) ?Experience of working as part of a team. ?Familiarity with Microsoft Office packages. ?Ability to use own judgement and make independent decisions on molecular work.?Be highly self motivated and understand when to refer project problems to others.

Desirable: An MSc and fluency in Molecular Biology (DNA extraction, PCR and sequencing) ?Computing skills in phylogenetic and genetic softwares, eg: PAUP, MacClade and BEAST?Phylogenetics and Project Management

CLOSING DATE: 9am, Friday 30 January 2009

INTERVIEW DATE: Friday 6 February 2009

FURTHER DETAILS AND APPLICATION PACKS AT http://www.kew.org/aboutus/jobs/ Dr Vincent Savolainen Reader in Ecology and Evolutionary Biology Imperial College London, and Royal Botanic Gardens, Kew Silwood Park Campus Buckhurst Road, Ascot, Berkshire, SL5 7PY, UK Tel +44 (0)20 7594 2374 Fax +44 (0)20 7594 2339 v.savolainen@imperial.ac.uk http://www3.imperial.ac.uk/people/v.savolainen "Savolainen, Vincent" <v.savolainen@imperial.ac.uk>

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## MBL WoodsHole ResAssistant BacterialEndosym

~~~ Research Assistant, Bacterial endosymbionts, Woods Hole, Mass. ~~~

We are looking for a highly motivated research assistant to contribute to our studies of bacterial endosymbionts at the Marine Biological Lab in Woods Hole. We are exploring gene expression patterns, population dynamics, and genome evolution among endosymbionts that live within ant hosts. We're also using pyrosequencing and computational approaches to examine genome variation across diverse host-associated bacteria. This position is ideal for someone interested in functional and comparative genomics, molecular biology, nutritional physiology, evolution, bioinformatics, and/or microbiology.

Responsibilities will include high-throughput sequencing, DNA and RNA extractions, real-time quantitative PCR, microscopy, rearing of ants in the lab, and general lab maintenance and organization. Data analysis will include DNA sequence alignment, genome comparisons, phylogenetic analysis, and use of molecular databases in a UNIX/LINUX environment. Experience with any or all of the above is ideal.

Requirements include a Bachelor's or Master's degree in biology or a related field, as well as previous molecular biology experience in a research setting. Exceptional organizational and record-keeping skills are essential. The position is available immediately, although it may be possible to start in early summer if you're completing an academic program.

For additional information and application instructions, please see:

mbl.simplehire.com/applicants/Central?quickFindP611

or go to: https://mbl.simplehire.com/ >> Research >> "Research Assistant I or II, Molecular analysis of bacterial endosymbionts"

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

-Jen

Jennifer Wernegreen Associate Scientist Josephine Bay Paul Center for Comparative Molecular Biology and Evolution Marine Biological Lab 7 MBL Street Woods Hole, MA 02543

jwernegreen@mbl.edu http://jbpc.mbl.edu/labs-wernegreen.html Jennifer Wernegreen <jwernegreen@mbl.edu>

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## NorthCarolinaStateU LabTech EvolutionaryBiol

Research Assistant Department of Plant Biology North Carolina State University, Raleigh NC

Dr. Marc Johnson's lab (www.evoeco.org) in Plant Biology at North Carolina State University invites applications for a Research Assistant seeking a career in ecology and evolutionary biology focusing on plant-insect interactions. The Research Assistant will serve as the technician for the lab and will assist with multiple aspects of research investigating the molecular and phenotypic evolution of plant defenses, the ecological effects
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of genetic variation and evolution on communities, and the coevolution between plant hosts and their insect parasites.

Applicants are expected to have a B.Sc. degree or higher in biology and a minimum of two years experience conducting research in a related field. The principle duties of the research associate pertain to the design and implementation of experiments, the collection of data, and lab management. Experiments will be conducted in the laboratory, greenhouse, and in the field, and applicants should be proficient with basic molecular procedures (DNA/RNA extraction, PCR, electrophoresis, molecular cloning, sequencing), and willing to learn how to grow and maintain plants, maintain insect colonies, and assist with large field experiments. Duties will also include contributing to lab management like safety awareness, ordering, chemical inventories and the repairs of minor equipment. Computer literacy is expected.

The starting salary will be commensurate with education and qualifications ($32,000-40,000 plus benefits). The successful candidate is expected to start on approximately March 1, 2009.

To apply, please send a CV/resume, cover letter, as well as the names and addresses of at least three references by February 1 to marc_johnson@ncsu.edu.

Marc Johnson, Ph.D. Assistant Professor Department of Plant Biology North Carolina State University Campus Box 7612, Gardner Hall Raleigh NC, 27695 Office: 919-515-0478, Lab: 919-515-0479 Web: www.evoeco.org marc_johnson@ncsu.edu marc_johnson@ncsu.edu

## NorthDakotaStateU EvoDevo

North NorthDakotaStateUniv.EvoDevo

The Department of Biological Sciences at North Dakota State University has a 9-month, tenure-track faculty position in evolutionary developmental biology at the rank of Assistant Professor, available fall 2009 (16 August 2009). The position is 40% teaching, 50% research, and 10% service. The successful candidate is expected to develop an externally-funded dynamic research program that complements existing strengths in the department. Teaching duties include 1 course per semester and advisement of undergraduate and graduate students. The position will be highly competitive with regard to start-up funds, space, and salary.

Candidates must have 1) a Ph.D. degree from an accredited institution in a discipline appropriate to evolutionary/developmental biology; 2) relevant postdoctoral experience, (3) demonstrated research experience in evolutionary/developmental biology that complements existing strengths in the department and evidence of peer-reviewed publication; 4) evidence of ability to develop an externally-funded research program; 5) evidence of ability to teach at the undergraduate and graduate levels; 6) strong oral, written, and interpersonal communication skills, including demonstrated ability to work/collaborate with others. Preference will be given to candidates with 1) an application of their research program to evolutionary aspects of developmental biology 2) background in studying genetic and developmental bases to evolutionarily and ecologically important traits; 3) experience with non-model systems.

Apply for this position through NDSU's online application system at:

jobs.ndsu.edu/applicants/Central?quickFindP727

Applicants should complete an online application and submit the following items 1) a letter of application, 2) a curriculum vitae, 3) a description of research interests (2 pages maximum), 4) a statement of teaching interests and philosophy (1 page maximum), and 5) reprints of a maximum of three representative publications. Only online applications will be accepted.

For questions regarding this position, feel free to contact the Evolutionary Developmental Biologist* *Search Committee at ndsu.biological.sciences@ndsu.edu <mailto:ndsu.biological.sciences@ndsu.edu>.

Review of applications will begin February 15, 2009, and continue until a suitable applicant pool has been established.

Steve Travers <Steven.Travers@ndsu.edu>

## UBasel FieldAssist BirdMigrationEvolution

Field assistants and bird ringers in evolution of bird migration

Eight field assistant positions are available in an international research project on the evolution of migration patterns and communication in nightingales (Luscinia megarhynchos).

The project is run by the Swiss Ornithological Institute (www.vogelwarte.ch , Dr. Steffen Hahn), the Research Station Petite Camargue Alsacienne, University of Basel (www.camargue.unibas.ch, Dr. Valentin Amrhein), and the Netherlands Institute of Ecology, NIOO-KNAW (www.nioo.knaw.nl, Prof. Dr. Marc Naguib).

Fieldwork will be done from April to June 2009, at the Research Station Petite Camargue Alsacienne in France (www.camargue.unibas.ch), and at a study site near Bologna, Italy.

We are looking for two qualified bird ringers and for six field assistants. Field assistants will participate in systematic surveys of territory settlement and assist bird ringers in capturing and banding the birds. To investigate vocal communication in nightingales, we will record songs and conduct playback experiments. Field work will include nocturnal bicycle trips, and field assistants are expected to work on their own at night and in the early morning.

Field assistants will receive 1000 euros per month, and qualified bird ringers will receive 1500 euros per month. Applicants are expected to stay for the entire field season from the beginning of April to the beginning of June 2009. The language at the study sites will be English.

The positions will be filled as soon as possible. Applications should be in English and should include, in one single pdf or word file, a curriculum vitae and a letter of motivation. Bird ringers should indicate their level of experience and include their ringing licences into the application. Please provide names and email addresses of two persons who are willing to write a letter of recommendation, and send applications by email to the following addresses:

Valentin Amrhein, pca.recherche@orange.fr Steffen Hahn, steffen.hahn [at] vogelwarte.ch

valentin amrhein <pca.recherche@orange.fr>

## UEdinburgh FieldAssist SoaySheep

SOAY SHEEP RESEARCH - ST KILDA SPRING 2009

FIELDWORK ASSISTANTS

We are currently looking for volunteers for this year's Soay sheep Spring expedition to St. Kilda, a group of islands 180 km off the coast of north-west Scotland. The expedition runs for two time periods of mid February until the beginning of April, and mid March until early May.

Activities: - Population census of sheep using telescopes and hand-held computers - Mortality searches - Systematic daily searches to record the birth of lambs - Catching lambs for tagging and identification purposes

Requirements: . Must be available for the full period of one of the time periods stated . Must be fit, St Kilda has a very demanding terrain; ability to run essential . A background in Biological Sciences

Travel to the island will be by helicopter from Benbecula (Outer Hebrides) and the team will stay in cottages built by the original inhabitants of St Kilda (since restored by the National Trust for Scotland). Expenses incurred whilst travelling in Scotland will be reimbursed and food/accommodation on island are provided. This is an ideal opportunity to gain field experience in large mammal research and to visit St Kilda, the remotest of British islands.

If you wish to apply for this work please send: a CV with covering letter, contact phone number and details of two referees that can be contacted immediately by email.

CONTACT: Jill Pilkington EMAIL: j.pilkington@ed.ac.uk

## UNSW Sydney GenomeSequencingManager

Genome Sequencing Manager (Research Fellow) Faculty of Science SCHOOL OF BIOTECHNOLOGY & BIOMOLECULAR SCIENCES REF. 6340NET A full-time position is available for a period of one year commencing early 2009. The successful applicant will be responsible for the operation of the Next-Generation Sequencing Facility in the Ramaciotti Centre for Gene Function Analysis within the School of Biotechnology & Biomolecular Sciences. The position will work with a group of highly dedicated individuals to provide genomic sequencing, methylation analysis, ChIP-Seq and RNA-Seq services for research institutions in the Sydney/Newcastle area. This is a one year fixed term position with a possibility of renewal. Salary range for Research Fellow is A$75,413- A$88,902 per year (plus 9% employer superannuation plus leave loading). Applicants should systematically address the selection criteria in their applications. Women and people from EEO groups are encouraged to apply. Please direct any enquiries to Prof. Ian Dawes on telephone (61 2) 9385 2089 or email i.dawes@unsw.edu.au Information Package: www.hr.unsw.edu.au//services/-recruitment/jobs/ info/pd16010907.pdf School Web site: www.babs.unsw.edu.au Job Advertisement: http://www.hr.unsw.edu.au/services/recruitment/ jobs/16010907.html

Applications close : 13 February 2009

a.wilton@unsw.edu.au a.wilton@unsw.edu.au

## UppsalaU EvoDevo Research and PhD

>From Graham Budd : graham.budd@pal.uu.se

We are happy to announce two positions in the Palaeobiology Programme of the Dept of Earth Sciences, Uppsala University, Sweden. The first is a four year research position (Forskarassistenttjänst) and the second is a PhD position on the origin of insects. Both palaeontological and evo-devo applicants are warmly welcomed for both positions. Details follow for both.

Graham Budd

graham.budd@pal.uu.se Uppsala University hereby declares the following position to be open for application:

Assistant Professor/Research Associate in Palaeobiology

at the Department of Earth Sciences.

Current research in the department includes Proterozoic biodiversity and ecology; the Cambrian Explosion and exceptionally preserved biotas, with particular expertise in arthropods, mollusks, brachiopods; Early organic-walled microbiota (prokaryotes and eukaryotes); and evo-devo.

Appointment period: The position can be held for a maximum of 4 years.

Nature of duties: The position is oriented towards research in Palaeobiology. It is principally a research appointment but will also involve teaching at basic, advanced and postgraduate level and supervision of students at postgraduate level.

Qualifications required: To qualify for appointment as Assistant Professor/Research Associate you must have a PhD or an equivalent foreign degree. Priority is given to applicants who have completed their PhD within 5 years of the application deadline. Furthermore, according to Uppsala University's general employment regulations, it is also a requirement that teachers possess the necessary skills and qualifications to carry out their duties proficiently.

The ability to teach in Swedish or English is a requirement.

Criteria for ranking: In ranking qualified applicants particular importance will be attached to scientific excellence in palaeobiology. The teaching competence including the planning, carrying out and evaluation of teaching and examinations, as well as the supervision of students, will also be evaluated.

A documented ability to initiate/lead and organise research project(s) is highly desirable. The ability to cooperate and good communication skills are required. The candidate's aptitude in interacting with the surrounding community, informing people about research and development work are also important.

Ability to inform people about research and development work is demonstrated by popular scientific activities, for example participating in extramural education, publishing popular scientific papers and participating in public discussions on topics of education and research.

In filling this position, the university aims to recruit the person who, in a combined evaluation of competence, skills and documented qualifications, is judged most suitable to carry out and develop the work-in-hand and to contribute to a positive development of the department and programme.

Personal circumstances that may be of positive relevance to the application, for example parental leave, should be mentioned in the list of qualifications (CV).

Uppsala University is striving to achieve a more even gender balance in its research and teaching staff and women are especially invited to apply for this position.

How to apply: The application must be written in English and the applicant is required to submit two copies of documents and one copy of publications according to instructions found on the web site < http://www.teknat.uu.se/english/instructions.php >http://www.teknat.uu.se/english/instructions.php or available from Jenny Lundström, phone+46 18 471 1798, e-mail Jenny.Lundstrom@uadm.uu.se . For further information about the position, please contact Professor Lars Holmer, phone +46 18 4712761, e-mail Lars.Holmer@pal.uu.se. The trade union representatives are Anders Grundström, SACO (the Swedish Confederation of Professional Associations), phone +46 18 471 5380, Carin Söderhäll, TCO/ST (the Swedish Confederation of Professional Employees), phone +46 18 471 1996 and Stefan Djurström, SEKO (the Union of Service and Communication Employees), phone +46 18 471 3315.

Applications should be directed to the Vice-chancellor and mailed so as to arrive at Uppsala University, RegistrarZs Office UFV-PA 2008/3116, Box 256, S-751 05 Uppsala, Sweden or fax +46 18 471 2000, no later than February 28, 2009. E-mail applications may be sent to registrator@uu.se. An application sent by fax or e-mail must be followed by a signed original of the application sent within a week of the deadline.

This advertisment is also available on the web at

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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

## USFWS NewMexico ConservationGenetics

Position is located in Southeastern New Mexico with the US Fish and Wildlife Service. Dexter's website can be viewed at http://www.fws.gov/southwest/fisheries/dexter/index.html. This vacancy will soon be open to the general public.

To apply, go to Http://usajobs.gov, search with the Vacancy Id number FWS2-09-001

INTERDISCIPLINARY (Fish & Wildlife Biologist OR Fish Biologist)

SALARY RANGE:46,625.00 - 73,329.00 USD per year OPEN PERIOD:Monday, January 26, 2009 to Friday, February 13, 2009 SERIES & GRADE:GS-0482,0401-09/11 POSITION INFORMATION:Full-Time Permanent PROMOTION POTENTIAL:11 DUTY LOCATIONS: 1 vacancy - DEXTER, NM WHO MAY BE CONSIDERED: Applications will be accepted from current and former competitive service Federal employees, and people eligible under special hiring authorities.

MAJOR DUTIES:

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Employee will conduct applied research projects for the Dexter NFHTC as directed by supervisor. This includes the application of advanced molecular tools to solve genetic management problems, using appropriate molecular techniques and knowledge of conservation biology to assist regional partners in endangered species management.

Employee uses subject matter expertise to enhance and facilitate applied research conducted at the Center. This may include expertise in physiology, nutrition, conservation genetics, herpetology, or pathogens. Incumbent is responsible for participating in multi-agency stakeholder meetings related to new and ongoing research. Provides subject matter expertise for diverse, complex, and multi-disciplinary planning efforts with public and private groups of state, local, and Federal agencies to achieve Service policies, objectives, and goals.

Prepares objective and complete written reports and other documents and delivers oral presentations based on investigations conducted. Prepares written correspondence, reports, and papers for publication, based on peer reviewed literature, observations made, and investigations conducted. Advanced expertise is used to analyze current conditions and assess implications of management actions on threatened and endangered species.

Connie Keeler-Foster, Ph.D. Research Leader Dexter National Fish Hatchery and Technology Center 7116 Hatchery Road, P. O. Box 219 Dexter, NM 88230 Phone 575.734.5910 ext 16, Fax 575.734.6130

Connie_KeelerFoster@fws.gov

## UTexas LabTech MarinePhylogeography

Laboratory Technician, Marine Science Institute, University of Texas at Austin

I am looking for a highly motivated and organized scientist to help manage a new lab at the Marine Science Institute, University of Texas. Laboratory work will include DNA extraction, PCR, gel quantification, genotyping, cloning and analysis of genotypic and sequence data. The work also will include maintaining a laboratory database, general laboratory tasks, and supervising students working in the lab. Fieldwork will involve scuba diving from research vessels or small boats, and will include collecting samples and population surveys.

The ideal applicant would have a bachelor's or master$^1$s degree in biology or related field. Applicants must have the appropriate citizenship/visa status to work in the U.S. and should have experience with population genetic and molecular systematic techniques. The laboratory is located at Port Aransas, coastal Texas.

Questions regarding the position should be directed to Dr. Luiz A. Rocha (rocha@mail.utexas.edu - 361-749-6845)

Additional information about the department and lab can be found at http://www.utmsi.utexas.edu/ Applications materials consist of (1) a brief cover letter; (2) CV, (3) PDF files of up to three representative publications, (4) names of scientists who can be contacted for letters of reference. Materials should be submitted through the University$^1$s website (posting # 09-01-23-01-4222). Direct link:

http://utdirect.utexas.edu/pnjobs/-pnjobsvw.WBX?comp=3D0&job_nbr=-3D090123014222 The University of Texas at Austin is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment.

rocha@mail.utexas.edu

## UVictoria PopulationBiology

Department of Biology University of Victoria Assistant Professor Position in Population Biology

The Department of Biology at the University of Victoria invites applications for a tenure-track assistant professor position in POPULATION BIOLOGY. We seek individuals who are strongly quantitative and whose research addresses fundamental population-level questions in evolution, ecology and/or genetics. Applicants whose research complements strengths in the department, particularly in the areas of marine and freshwater biology, and plant or microbial ecology and evolution, are especially encouraged. Information about our department can be found at http://web.uvic.ca/biology/ To apply, please arrange to have a curriculum vitae, statement of teaching interests (graduate and undergraduate) and research interests and plans, copies of three publications, and contact information for three references sent to: biochair@uvic.ca or Population Biology Search Committee, Department of Biology, University of Victoria, PO Box 3020, STN CSC, Victoria, British Columbia, Canada. Review of applications will begin on February 28, 2009 and continue until a suitable candidate is identified.

The University of Victoria is an equity employer and encourages applications from women, persons with disabilities, visible minorities, Aboriginal Peoples, people of all sexual orientations and genders, and others who may contribute to the further diversification of the University.

All qualified candidates are encouraged to apply; however, in accordance with Canadian Immigration requirements, Canadians and permanent residents will be given priority.

Steve Perlman

## UWyoming Bioinformatics

Research Scientist in Bioinformatics

(Position #4939)

The University of Wyoming Bioinformatics Core is seeking to hire a Research Scientist to be located in the Department of Molecular Biology. The position will involve leadership of both the collaborative service and research elements of the Bioinformatics Core. The service component of the position will consist of collaborating with biological researchers on bioinformatics problems, resulting in co-publication and novel uses of bioinformatics on campus. A candidate with a history of interdisciplinary collaboration would be preferred. Common research topics for collaboration in this position will include phylogenetics, microarray statistics, and protein homology modeling, among other areas. The research component will involve developing an independent bioinformatics or computational biology research program. The successful candidate will submit grants and research papers. Research in any area of bioinformatics or computational biology will be considered. The successful candidate will have the opportunity to supervise graduate students in the Molecular Biology and/or MCLS (Molecular and Cellular Life Sciences) Ph.D. programs depending upon qualifications. Funding for one Ph.D. student will be provided with the position. The anticipated start date of the position will be June 1, 2009, although alternative start dates may be negotiated. The successful candidate should have a Ph.D. in a relevant area, proficiency in statistics and programming, and knowledge of molecular biology. To apply, send your CV and a statement of research accomplishments, future research interests, and interdisciplinary background by email to liberles@uwyo.edu. In addition, arrange to have three letters of recommendation sent directly by the letter writer by email to the same email address. Review of applications will begin on March 9, 2009 and continue until the position is filled. Inquiries about details of the position may be directed to Dr. David Liberles (liberles@uwyo.edu).

The main campus is in Laramie, a safe, vibrant, small city ina scenic valley between the Laramie and Medicine Bow Ranges of the Rocky Mountains. Laramie is a two-hour drive north of Denver, Colorado.Located at 7200 feet, Laramie and its surrounding areas offer abundant outdoor recreational opportunities. The university and the region provide a rich array of cultural activities. More information about the university and its geographic setting is available on the university's web site, http://www.uwyo.edu . The University of Wyoming is an EO/AA employer.

"David A. Liberles" <liberles@uwyo.edu>

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# Other

## Astrobiology Summer Program

2009 Astrobiology Summer Program for undergraduates

Penn State will once again host the Astrobiology Summer Program (ASP), supported by the National Science Foundation and NASA Astrobiology Institute. Undergraduates with an interest in astrobiology and contemplating a career in the sciences are encouraged to apply. Participants receive a stipend, travel, and living expenses, and conduct research for ten weeks at Pennsylvania State University under the guidance of astrobiology faculty mentors. Research topics are diverse and include (among others) the early evolution of life on Earth, the early Earth environment, and search for life elsewhere. Among the summer activities is a field trip to NASA Headquarters, NASA-Goddard Space Flight Center, the Smithsonian's Air and Space Museum and Udvar-Hazy Center. The application deadline is February 15th, 2009.

For more information, visit http://evo.bio.psu.edu/asp/ or contact Blair Hedges, sbh1@psu.edu.

sbh1@psu.edu sbh1@psu.edu

## Austria SummerFellowship EvolutionaryModeling

Summer Fellowships for Young Scientists at the International Institute for Applied Systems Analysis

Funding is available for PhD students interested in three months of collaborative research on

Evolutionary and Ecological Modeling

in population ecology, evolutionary ecology, community ecology, spatial ecology, and fishery ecology.

Young scientists from all countries are eligible for stipends, provided by IIASA's Evolution and Ecology Program, contributing to travel and accommodation costs. Students from Austria, China, Egypt, Estonia, Finland, Germany, India, Japan, Korea, the Netherlands, Norway, Pakistan, Poland, Russia, South Africa, Sweden, and the USA are eligible for fellowships providing travel, accommodation, and living expenses.

Summer research projects are invited in any of the following areas

Fisheries-induced Evolution Adaptive Speciation Adaptive Dynamics Food Web Evolution Evolution of Cooperation Evolutionary Conservation Biology Spatially Explicit Evolutionary Models Moment-based Spatial Models

Previous experience with implementing and studying evolutionary or ecological models will be an important asset. Potential applicants are welcome to send informal inquiries about specific research interests and plans to Ulf Dieckmann (dieckmann@iiasa.ac.at).

Online applications have to be submitted before January 19, 2009.

Since 1977, the annual Young Scientists Summer Program (YSSP) of the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria, has attracted 1400+ students from 70+ countries. The YSSP 2009 will take place from June1 to August 31, 2009. IIASA is located in the former summer palace of Austria's royal family, ca. 15 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on regular personal interaction with advising scientists, and typically leads to a publication in an international journal (as well as to a chapter in a candidate's PhD thesis).

Some useful links:

+ http://www.iiasa.ac.at/Admin/YSP/reg-info/more_about_the_program.html Details about the summer program, and online application

+ www.iiasa.ac.at/Research/EEP Information about IIASA's Evolution and Ecology Program

+ www.iiasa.ac.at/Research/EEP/Students.html Examples of successful YSSP projects

+ www.iiasa.ac.at/docs/IIASA_Info.html General information about IIASA

Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web http://www.iiasa.ac.at/Research/EEP Online reprints http://www.iiasa.ac.at/~dieckman FishACE Network http://www.iiasa.ac.at/Research/EEP/FishACE FinE Network http://www.iiasa.ac.at/Research/EEP/FinE

dieckmann@iiasa.ac.at dieckmann@iiasa.ac.at

## Brazilian mouse samples

Dear EvolDir members,

I'm a PhD student at the University of York and I'm looking for house mouse (Mus musculus) samples from

Brazil for a phylogeography study. If you're interested in a collaboration please e-mail me at sg542@yotk.ac.uk and I'll be happy to further discuss that with you.

Even if you don't work with rodents but have access to little tail tips or any other tissue samples, it would be very much appreciated.

Even if your cat brings you mice from the barn it's just fine!

Looking forward to hear from you!

Thanks in advance,

Sofia Gabriel

P.S. If you're Brazilian you're very welcome to reply in Portuguese.

sg542@york.ac.uk sg542@york.ac.uk

## Bryophyte phylogeny genes

Dear all,

I am doing a molecular phylogeny of a bryophyte genus and for that purpose I'm looking for informative nuclear regions expect ITS region. GapC/Cp as well as GapA/B seem to be promissing regions regarding the few litterature (e.g. Stone, 2006).

But primers and sequences on NCBI are rare and PCR do not amplify well !

Do you have any advices using theses genes for phylogeny purpose ? Do you know other nuclear regions that can fit ?

Thanks in advance, and best whishes for this new year,

Amélie

Amélie PICHONET

PhD Student, Teaching Assistant National Museum of Natural History Departement of Systematique and Evolution, Bryology Team Case 39, 57 rue Cuvier 75005 Paris - France Tel : 00 33 1 40 79 31 88 Fax : 00 33 1 40 79 35 94 Email : pichonet@mnhn.fr

pichonet@mnhn.fr

## Coauthor missing

Hi,

I'm desparately trying to find out the whereabouts of the co-author of a paper that I have just submitted: Dr Kelley Whitaker. She has done genetic work on corals and a few years ago, she was based in Pretoria, South Africa. She may presently be in Australia.

Anyone who knows her contact details should please get in touch with me asap.

Thanks, Peter Teske (Peter.Teske@bio.mq.edu.au)

Dr Peter R. Teske Postdoctoral Researcher Molecular Ecology Lab Dept. of Biological Sciences, E8C Macquarie University Sydney, NSW 2109 Australia Phone: +61 2 9850 8190 Fax: +61 2 9850 8245 E-mail: Peter.Teske@bio.mq.edu.au Website: http://www.bio.mq.edu.au/molecularecology/-people.htm Publications: http://www.ru.ac.za/-academic/departments/botany_research/peter/ Peter.Teske@bio.mq.edu.au Peter.Teske@bio.mq.edu.au

## Darwin year stuff

A friend and I have put together a series of Darwin Year items for sale, with 50% of the profits donated to conservation charities and 50% used in developing online evolution resources.

http://www.darwinyear2009.com Have a look and let me know if you think it would be ok to write a message on this.

- R

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

http://www.genomesize.com/gregorylab/

## Distance software question

Dear all.

Does anybody out there know a software that will build a genetic distance dendogram for POPULATIONS with bootstrap values based on individual RAPD/RFLP/ISSR/AFLP profiles?

I would greatly appreciate your help.

Walter A Boeger UFPR-Brazil

wboeger@ufpr.br

## DNA from ETA cards

Our lab has a collection of dried avian blood (nucleated red blood cells) samples on Whatman FTA cards. Some samples consist of only a small spot of blood, while others contain several drops of blood with the sample soaking through and visible on the back of the card.

Rather than using a sample disk directly in a PCR, we are interested in extracting total genomic DNA to be used as a stock solution in downstream sequencing. I'm wondering if anyone has experience with this, and might be able to provide advice on types of kits/protocols used. Also, any input on DNA quality/yield, sample variation, punch tools, and sample disk diameter would be appreciated.

Thanks in advance, Jeff DaCosta Boston University

dacostaj@bu.edu dacostaj@bu.edu

## DNA from ETA cards answers

Thanks for all that responded to my query about the extraction of total gDNA from avian blood samples on FTA cards. Below is the original post followed by many useful replies.

*****Original post***** Our lab has a collection of dried avian blood (nucleated red blood cells) samples on Whatman FTA cards. Some samples consist of only a small spot of blood, while others contain several drops of blood with the sample soaking through and visible on the back of the card.

Rather than using a sample disk directly in a PCR, we are interested in extracting total genomic DNA to be used as a stock solution in downstream sequencing. I'm wondering if anyone has experience with this, and might be able to provide advice on types of kits/protocols used. Also, any input on DNA quality/yield, sample variation, punch tools, and sample disk diameter would be appreciated.

*****Papers***** Smith lm & LA Burgoyne. 2004. Collecting archiving and processing DNA from wildlife samples using FTA databasing paper. BMC Ecology. 4:4.

Borisenko AV et al. 2008. DNA barcoding in surveys of small mammal communities: a field study in Suriname. Mol. Ecol. Res. 8: 471-479.

McClure Mc et al. In press. Extraction of DNA from FTA cards for use on the Illumina iSelect BeadChip. Animal Genetics. (Whatman GenSolve Kit vs Phenol:Chloroform:Isoamyl alcohol extraction)

Barbanera, F et al. In press. Human-mediated introgression of exotic chukar (Alectoris chukar, Galliformes) genes from East Asian into native Mediterranean partridges. Biol. Invasions.

*****FTA Elute***** The new product from Whatman - 'FTA elute cards' - requires only water both for purification and elution, and is much more efficient. If you plan to sample avian blood later on, I would recommend switching to FTA elute.

*****Hole punches***** In terms of punches - the Harris Micro-Punch lasts forever and is a good investment: http://www.sigmaaldrich.com/labware/labware-products.html?TablePage=3D17216376 http://www.whatman.com/PRODFTAPurificationReagentandAccessories.aspx My preference is a 1.2 mm punch - if I need more DNA, I punch a card several times. This is also the optimal size to use the disk directly in PCR in a 12.5 or 25 ul reaction.

Don't get Harris Unicore punches, they don't last!

To ensure that your punch lasts, get self-healing Harris cutting mat: http://www.sigmaaldrich.com/catalog/ProductDetail.do?N4=3DZ708755|SIGMA&N5=Product%20No.|BRAND_KEY&F=SPEC *****Hole punches 2***** Oh, and for the punches, I simply bought the smallest available punch-out tool in the scrapbook department at Michael's (the craft store).

*****Taq for PCR***** Regarding PCR... Platinum Taq from Invitrogen is one of the best enzymes to deal with samples from FTA cards.

*****Qiagen DNeasy Kit***** We do this kind of work regularly. We have tried a number of extraction kits and organic extraction methods and now use only the Qiagen DNAeasy Tissue Kit. We use a small pair of dissecting scissors to cut out a small piece of the paper (and usually cut it up into pretty small pieces) because they can be cleaned between samples. The final step in the Qiagen kit is an elution in AE (or you can use TE or TLE depending on what you want the DNA stored in). This is one thing that can help control the DNA yield. We use 2 elutions, 100 ul of AE twice but you can change that to a 100 and a 50 ul elution to get higher concentrations. I suggest playing around a little with how much paper to use depending on the blood spot - our experience has been that even a very small spot works just fine - and so for very heavily soaked paper you may want to use less and/or elute with a higher volume of TLE, TE or AE buffer.

We get consistently excellent yield (anywhere from 10 or 20 to >100 ng/ul) and the DNA is very good quality. We have used it primarily for microsatellite work but also for sequencing (mostly mtDNA) and for AFLPs.

This is our working protocol for gauze and for paper (we tend to use filter paper - and have used other kinds of unlikely things - depends on the people in the field!) Everything not listed follows the manufacturer protocol for "Purification of Genomic DNA from Whole Nucleated or Non-nucleated Animal Blood,"

DNA was extracted from the blood on the gauze using a DNeasy Tissue kit (Qiagen) following the manufacturer's protocol, "Purification of Genomic DNA from Whole Nucleated or Non-nucleated Animal Blood," with modifications. Rather than adding 5-10 $\mu$L anticoagulated blood to 20 $\mu$L proteinase K in the bottom of a 1.5 mL microcentrifuge tube, a sample

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## DNA preservation liquids answers

G'day folks

My original post is followed by the various suggestions I got for alternative methods for preserving DNA. Thank you very much to all the people who sent me messages. I tried to incorporate most of the emails I received, but some were a little redundant.

Cheers Peter

G'day folks

I was wondering if folks have any experience with preserving DNA in the field in liquids other than ethanol? My target organisms are fishes, but I'm sure different liquids work on most groups just fine. It some parts of the world ethanol can be very difficult and/or expensive to obtain. Are there any good viable alternatives that can be obtained in third world countries that should be ok that people have experience with? Isopropanol is often available it seems, but I've only seen one report that suggested it should be ok. Also, I guess the isopropanol one would buy in a pharmacy varies depending on who makes it and the country (wikipedia says that in the USA and the UK Isopropyl Rubbing Alcohol is made of ethanol, not isoproyl).

One paper looked at preservation of spiders, and found RNAlater and propylene glycol worked well. Another paper on aphids found acetone was good, as was diethyl ether, and ethyl acetate. I'm not sure though how easy these are to obtain, or safely these can be transported though (RNAlater is too expensive to consider).

I also searched the archives, but suprisingly this doesn't seem to be a topic that has come up before.

Thanks Peter Unmack

Details of the different things people suggested are given below. It seems like laundry detergent and salt may be the best options, while silica gel is good for small tissue samples. I'm rather leary of DMSO as that stuff has the potential to be dangerous (it makes your skin highly permeable to everything), and as noted by one respondant, some tubes tend to leak. I'd be really interested to hear anything further from folks who have used detergent or salt for preservation.

Here are the responses.

You can also consider dry storage of DNA, as implemented in FTA cards: http://www.whatman.com/FTAandFTAElute.aspx At our lab we work almost exclusively with fish tissue, from both marine and freshwater species, and our preferred method of preserving DNA in the samples prior to extraction is air-drying in blotter paper, with each sample in a separate coin envelope. I am not sure if this would work for you in a humid location, as the key to high quality DNA seems to be rapid drying of the tissue, but barring access to a dessicator, a sunny windowsill works just fine. This method also makes storage and transport of tissues a breeze.

DMSO

20% DMSO saturated with NaCl for a variety of species, including fish - easier to transport on planes than alcohols, and preserves well at RT for extended periods (see Amos, W. & Hoelzel, A.R. 1991. Long-term preservation of cetacean tissue at ambient temperature for molecular genetic analysis. IWC Special Issue 13:99-104).

DMSO is typically available as 'horse liniment' or veterinary rubbing compound in country stores in the US, or from local vets. Pour in NaCl or table salt to saturation, collect the supernatant fluid. DMSO tends to leak from regular eppendorf tubes, you'll want to use gasketed tubes or parafilm.

NaCl

I used 5M NaCl solution to preserve bat wing membrane in the field, prior to extraction. For memory, I think it also worked well for Quokka ear tissue.

Saturated table salt (NaCl) in clean water works well for small arthropods.

silica gel

When ethanol is not available then the best alternative is dessication with silica gel. I know of a few studies that used acetone successfully, but in my experience isopropanol and rnalater are not reliable.

Laundry detergent.

Someone once told me that they used washing powder to preserve specimen when they go sampling in muslim countries where it is rather hard to get alcohol. There is actually a protocol for extracting DNA with laundry detergent - I attach the pdf!

However, since it is tricky to do all the extraction steps "in the wild" preserving your samples in detergent is also an option. I have tried to preserve freshwater snails when I had no access to alcohol and it seems to have worked ok. I haven't "properly" tested the quality of the DNA but I got quite a lot of DNA out of those animals using commercial kits and a chelex extraction protocol. In the field I just put the snails as they were into the powder, hoping that their excess water would mix with the detergent powder which would then seep into the cavities preserving the tissues. However, I also prepared some snails out of their shells before I stored them in the powder and they gave much better results. Perhaps it would be even better to dissolve the washing powder first and then store the tissue in the liquid.

I DID put the snails straight into the powder, but I think it would be

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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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## Dobzhansky and Fisher Prize nominations

Final reminder from the Society for the Study of Evolution Nomination/application deadlines: Fisher Prize - January 31st, 2009 Dobzhansky Prize - February 15th, 2009

For further details see this month's issue of Evolution, or http://www.evolutionsociety.org Dale H. Clayton, Ph.D. (outgoing secretary) Professor, Dept. of Biology 257 South 1400 East Univ. of Utah Salt Lake City, Utah 84112-0840 Phone: 801-581-6482 FAX: 801-581-4668 http://darwin.biology.utah.edu Dale Clayton <clayton@biology.utah.edu>

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## Dublin MuseumSummerResearch

Dear all,

This summer programme offers research projects and activities for students in organismal biology using biological collections, combining resources from University College Dublin, the National Museum of Ireland, and the National Botanic Gardens. Students must apply to work with a specific research group.

Please circulate this notice to undergraduate students and other colleagues who may be in contact with potential summer students. Note the closing date for applications is March 29 2008.

Collections-Based Biology in Dublin Undergraduate Research Experience & Knowledge Award (CoBiD-UREKA)

Full funding for the 10-week programme will be provided for 10 successful candidates, including assistance with air transportation to and from Dublin, accommodation in Dublin, and a small weekly living allowance, as well as research project expenses. The programme is open to students of all nationalities.

Term dates: June 15 to August 21 2008

Students must submit an application form (available online) and arrange for a letter of support to be sent to <UREKA@ucd.ie> For application instructions, research group descriptions, and more information: http://www.ucd.ie/ureka/ Applications must be received by 29 March 2009

Kind regards,

The UREKA Team

Collections-based Biology in Dublin Undergraduate Research Experience & Knowledge Award www.ucd.ie/ureka ureka@ucd.ie

## Ecuador VolunteerFieldAssist

VOLUNTEER FIELD ASSISTANT POSITION, RAINFOREST FROG BEHAVIOR AND SPECIATION

We have two positions for field assistants to help with research on mate choice and the selective forces driving speciation in rainforest frogs. This work will focus on video monitoring and field observation of frog predators. Assistants will work directly with two PIs, Kim Hoke and Chris Funk at Colorado State University.

TIME PERIOD: Three months, starting early February 2009. Some flexibility on dates possible.

LOCATION: Amazonian Ecuador near the Napo River.

FUNDING: All travel and lodging expenses will be covered, including plane tickets and food.

QUALIFICATIONS: Applicant must have a BS in Biology or a related field and experience in field ecology or behavioral ecology. Past experience in the tropics is desirable. Applicants must have a yellow-fever vaccination, passport, and minimal international traveler?s insurance (as included with an International Student Identity Card).

TO APPLY: Send a CV, names of 3 references, and a cover letter explaining why you are interested in helping with this research to kimhoke@colostate.edu.

Chris

W. Chris Funk, Assistant Professor Department of Biology Colorado State University Fort Collins, CO 80523-1878 Tel: 970-491-5947 Fax: 970-491-0649 E-mail: Chris.Funk at colostate.edu URL: http://rydberg.biology.colostate.edu/funklab/ "Funk,Chris" <Chris.Funk@colostate.edu>

## Edinburgh FieldVolunteers BlueTits

NEEDED: FIELD ASSISTANTS

BLUE TITS in EDINBURGH April-June 2009

We are looking for 2 volunteers to assist with fieldwork from April to June. The project will focus on the evolutionary ecology of blue tits with all fieldwork carried out on a population near Edinburgh, Scotland, UK. The fieldwork will involve nest monitoring and measuring of chick and adult birds. Candidates should have an interest in ecology and evolutionary biology, and preferably have experience in handling birds. A high level of fitness is necessary.

Accommodation costs are covered and will be in private accommodation in the city. The field site is about 15 minutes from the city centre and transport will be provided.

If you wish to apply for a post then please send a CV with a covering letter and details of two referees (academic or field biology related - with e-mail address) to Jarrod Hadfield, indicating dates you are available. E-mail applications are preferred and are to be received by Tuesday 10th March.

Contact: Dr Jarrod Hadfield

E-mail: j.hadfield@ed.ac.uk Institute of Evolutionary Biology Kings Buildings University of Edinburgh Edinburgh EH9 3JT

– The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Jarrod Hadfield <j.hadfield@ed.ac.uk>

## EvolDir on Twitter

With the aim of liberating EvolDir posts from my cluttered email inbox I've created a Twitter feed for EvolDir. See http://bioguid.info/services/evoldir/ for details, or go straight to http://twitter.com/evoldir to follow.

Regards

Rod

Roderic Page Professor of Taxonomy DEEB, FBLS Graham Kerr Building University of Glasgow Glasgow G12 8QQ, UK

Email: r.page@bio.gla.ac.uk Tel: +44 141 330 4778 Fax: +44 141 330 2792 AIM: rodpage1962@aim.com Facebook: http://www.facebook.com/profile.php?id=1112517192 Twitter: http://twitter.com/rdmpage Blog: http://iphylo.blogspot.com Home page: http://taxonomy.zoology.gla.ac.uk/rod/rod.html r.page@bio.gla.ac.uk r.page@bio.gla.ac.uk

## GalapagosIslands VolunteerFieldAssist

Voluntary Field Assistants Required

Galapagos Islands, 17th Feb - 13th May 2009

The Galapagos sea lion project is an investigation into immune system ontogeny and the differential ability of the sexes to respond to infection in the Galapagos sea lion (Zalophus wollebaeki). Sea lions are well suited to studies of sexual selection because they are sexually dimorphic and live in crowded conditions that can lead to high levels of pathogen-driven mortality. I'm using a combination of field challenge experiments and laboratory techniques to characterise how males and females combat infection. This research will contribute to my PhD < http://www.zoo.cam.ac.uk/ioz/people/brock.htm > and follows on from previous work carried out by my supervisor.

Two field assistants are sought to help with the sampling of sea lion pups on the Galapagos Islands of San Cristobal and Santa Fe between 17th February and 13th May 2009. We will tag as many pups as possible and recapture them as frequently as is feasible to examine body condition, carry out an eye exam and take a blood sample. This process requires three people as the pups need to be restrained, data needs to be recorded and samples need to be processed on site. Blood samples and data will be further processed in the Galapagos Genetics Epidemiology and Pathology Laboratory in the evenings. Some camping may be involved, so applicants must be comfortable working in remote environments with minimum conveniences.

While food and accommodation are provided, volunteers will have to cover the cost of their flights. Ideal candidates will have a good degree in biological sciences, field experience in remote locations, an interest in evolutionary biology and functional Spanish. Veterinary field and lab experience would be useful but are not required. Priority will be given to Ecuadorian applicants.

Please get in touch if you would like more information and to apply please include a CV and covering letter (paddy.brock@ioz.ac.uk). The deadline for applications is Thursday 22nd January.

Paddy Brock Institute of Zoology Zoological Society of London Regent's Park London NW1 4RY Tel: 00 44 (0) 20 7449 6496 Email: paddy.brock@ioz.ac.uk http://www.zoo.cam.ac.uk/ioz/people/brock.htm

Paddy Brock <Paddy.Brock@ioz.ac.uk>

## Genome Biology Evolution

Dear all,

The Society for Molecular Biology and Evolution (SMBE) has launched a new online journal named Genome Biology and Evolution (GBE) [http://www.oxfordjournals.org/page/3423/1], which has an editorial board [http://www.oxfordjournals.org/page/3423/4] that brings together top expertise from the full breadth of evolutionary and population genomics.

The scope [http://www.oxfordjournals.org/page/3423/5] of GBE is focused on genome evolution and it will report the most significant advances as genomic technology continues to enrich our understanding of the evolutionary process. Like its established sister journal, MBE [http://www.oxfordjournals.org/page/3423/6], GBE is built to be the leading journal in its field. The journal is an open access publication and, thanks to SMBE, publication will be free for all accepted papers that are submitted during 2009 (starting in 2010, open access fees will be charged). Color figures are free, there are no page charges, and accepted papers are published within days to meet the demands of a rapidly developing field.

In 2007 more than 2,000 scientists in the field participated in our survey in which we at SMBE sought to find out what the field needs and wants. The result of that survey is GBE, which is designed to serve a significant and growing discipline at the interface between molecular evolution and genomics.

To submit an article to GBE, consult the Instructions to authors (http://www.oxfordjournals.org/page/3423/3) and submit your paper at http://mc.manuscriptcentral.com/gbe Sign up here - http://www.oxfordjournals.org/page/3423/2 to receive table of contents alerts.

We hope that you are as excited about the journal as we are, and hope that you will keep GBE keenly in mind for the publication of your best genome evolutionary work.

With best wishes,

Takashi Gojobori, Founding Editor William Martin, Editor-in-Chief Michael Lynch, President of SMBE

"Jianzhi Zhang" <jianzhi@umich.edu> "Jianzhi Zhang" <jianzhi@umich.edu>

## HIV sequence database tool

HIV evolution colleagues,

After a good start, the webtool for Los Alamos HIV sequence database queries at http://fortinbras.us/hivq has run afoul of internet issues. These are being resolved, with invaluable help from LANL. In the meantime, I have made a Perl program available that provides a command-line interface to the LANL DB, allowing you to make the same kind of queries directly on and from your own machine. Please see the distribution at http://fortinbras.us/hivqpl . You need to be able to run Perl, but do not need any Perl programming skills to run this script. Internet tests are included in the distribution, so that you can tell immediately upon installation whether it will run on your setup.

If you have any difficulties, questions or comments, please email me directly. This will both help you and improve the software.

Thanks, Mark Jensen

maj@fortinbras.us

## J Bioinformatics Seq Analysis

From jbsa@acadjourn.org Thu Jan 22 06:13:46 2009

Journal of Bioinformatics and Sequence Analysis www.academicjournals.org/JBSA Introducing "Journal of Bioinformatics and Sequence Analysis" * *

Dear Colleague,

The *Journal of Bioinformatics and Sequence Analysis (JBSA)* is a multidisciplinary peer-reviewed journal published that will be monthly by Academic Journals (http://www.academicjournals.org/JBSA). JBSA is dedicated to increasing the depth of the subject across disciplines with the ultimate aim of expanding knowledge of the subject.

*Editors and reviewers*

JBSA* *is seeking qualified researchers to join its editorial team as editors, subeditors or reviewers. Kindly send your resume to JBSA@acadjourn.org

*Call for Papers*

JBSA will cover all areas of the subject. The journal welcomes the submission of manuscripts that meet the general criteria of significance and scientific excellence, and will publish:

Original articles in basic and applied research

Case studies

Critical reviews, surveys, opinions, commentaries and essays

We invite you to submit your manuscript(s) to JBSA@acadjourn.org for publication in the Maiden Issue (April 2009). Our objective is to inform authors of the decision on their manuscript(s) within four weeks of submission. Following acceptance, a paper will normally be published in the next issue. Instruction for authors and other details are available on our website; http://www.academicjournals.org/JBSA/Instruction.htm JBSA is an Open Access Journal

One key request of researchers across the world is unrestricted access to research publications. Open access gives a worldwide audience larger than that of any subscription-based journal and thus increases the visibility and impact of published works. It also enhances indexing, retrieval power and eliminates the need for permissions to reproduce and distribute content.JBSA is fully committed to the Open Access Initiative and will provide free access to all articles as soon as they are published.

Best regards,

*Precious Ejegi* Editorial Assistant Journal of Bioinformatics and Sequence Analysis (JBSA) E-mail: JBSA@acadjourn.org www.academicjournals.org/-JBSA jbsa@acadjourn.org jbsa@acadjourn.org

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## Journal ContributionsToZoology

Other: Old journal has new focus

Contributions to Zoology The journal Contributions to Zoology '..since 1848..' solicits high-quality papers in all systematics-related branches of Zoology and Paleontology. Preference will be given to manuscripts dealing with conceptual issues and to integrative papers. Reviews and alpha-taxonomic contributions may be considered for publication, but acceptance will depend on their high quality and exceptional nature. The journal is published by the National Museum of Natural History Naturalis, Leiden and the Zoological Museum Amsterdam and is freely available online since 1997 at www.ctoz.nl . Editor-in-Chief: J.W. Arntzen - Leiden

Advisory Editorial Board: N.H. Barton - Klosterneuburg, Austria B. David - Dijon, France C. Groves - Canberra, Australia D.A.T. Harper - Copenhagen, Denmark G.M. Hewitt - Norwich, UK M. Laurin - Paris, France A. Minelli - Padova, Italy C. Nielsen - Copenhagen, Denmark H. Philippe - Montréal, Canada G. Vermeij - Davis, California, USA

Associate Editors: L.W. van den Hoek Ostende - Leiden J. Miller - Leiden V. Nijman - Oxford, UK M. Schilthuizen - Leiden R.W.M. van Soest - Amsterdam R. Vonk - Amsterdam

For manuscript preparation and submission see www.ctoz.nl

CTOZ <CTOZ@naturalis.nl>

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## MarieCurie candidates

Dear all, In the context of the next Marie Curie's call we are looking for higly motivated candidates in order to prepare together a research project and send an application in our lab in Marseille (http://www.com.univ-mrs.fr/DIMAR/).

The main research topics would be: - Molecular evolution of bindin _ a prezygotic isolation molecule_ in Spatangoid sea urchins: sexual conflict or speciation reinforcement ? - Gene expression analyses and stress response in Mediterranean invertebrates: plasticity and natural selection in a context of environmental change.

The candidates must have a PhD with enough publications and experience in the corresponding themes (experienced researchers). They should not have resided or carried out their main activity (work , studies, etc) in France for more than 12 months in the 3 years immediately prior to the reference date. According to the situation, this could be an Intra-European Fellowship, or a Reintegration Grant. Please e-mail your CV and your motivations to didier.aurelle@univmed.fr and anne.chenuil@univmed.fr Best Regards Didier and Anne

– Didier AURELLE

Courriel: didier.aurelle@univmed.fr / aurelle.didier@gmail.com

Maître de Conférences UMR 6540 DIMAR Université de la Méditerranée / Centre d'Océanologie de Marseille Station Marine d'Endoume Rue de la batterie des Lions 13007 Marseille FRANCE Tel: + 33 4 91 04 16 18 Fax: + 33 4 91 04 16 35

didier.aurelle@univmed.fr

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## Micro software TETRA

Dear Evoldir members

Does anyone know more about TETRA software? I ve read the Mol. Ecol Res article (TETRA: an improved program for population genetic analysis of allotetraploid microsatellite data Wan-Jin Liao, Bi-Ru Zhu, Yan-Fei Zeng, Da-Yong Zhang, Journal: Molecular Ecology Resources,ISSN: 1755-098X, Vol: 8, Issue: 6,Date: 2008, 1260)

TETRA is a improvement of a previous program TETRASAT by S. Markwith that only allowed 15 partial heterozygote samples in microsatellite data.

about it and became enthusiastic however the site indicated to download the software (http://ecology.bnu.edu.cn/zhangdy/TETRA/TETRA.htm) gave me a file that when executed looks like a suspicious file (with questions marks in the window, wrong words on buttons like CANCLE instead of CANCEL) I can not get other download. Does any one know about it, where to download or how to install it properly?

Thank you very much Helena

Helena Cotrim, PhD Jardim Botânico da Universidade de Lisboa, Museu Nacional de História Natural. Rua Escola Politecnica 58 1250-102 Lisboa Tel: +351-213 921 882 Fax: +351-213 921841

Helena Cotrim <hmcotrim@fc.ul.pt>

## mtDNA inheritance mussels

Dear Evoldir members,

has anyone looked for the presence of DUI (doubly uniparental inheritance of mitochondrial DNA) in the invasive freshwater mussel Dreissena polymorpha or in other dreissenids?Or is anyone planning to do that? I have been looking in the literature but it seems that nobody has payed attention to it.

Thanks

Carlos Saavedra

Dr. Carlos Saavedra Instituto de Acuicultura de Torre de la Sal Consejo Superior de Investigaciones Científicas 12595 Ribera de Cabanes (Castellón), SPAIN Phone +34 964 319 500 Ext 48 FAX +34 964 319 509 E-mail: saavedra@iats.csic.es

Carlos Saavedra <saavedra@iats.csic.es>

## NatlCenterScienceEdu WhyEvolution

The National Center for Science Education has joined with the Coalition on Public Understanding of Science to help put together content for their Year of Science website http://www.yearofscience2009.org/home/ .One part of the website for February (which focuses on Evolution) will highlight scientists and their research, and specifically why evolution is important to their work.

We are asking for interested researchers to submit the information below. We will then incorporate their information into the website.

Responses can be sent to Louise Mead at mead@ncseweb.org

Thank you.

1. Name and institution

2. BRIEFLY describe your research focus, in language that the general public would understand.

3. Why is evolution important to your research?

Unfortunately, we are fast approaching February, so responses must be submitted by January 30th.

Sincerely, Louise S. Mead, Ph.D. Education Project Director National Center for Science Education 420 40th Street Suite 2 Oakland, CA 94609 510-601-7203

Louise Mead <mead@ncseweb.org>

## NESCent USouthDakota SummerTraining ComparativeOntology

Summer Training Opportunities for Graduate Students and Postdocs Phenoscape (http://phenoscape.org) is a pioneering effort to apply ontologies to comparative biology. The project aims to relate traditional character descriptions from fish evolutionary studies to zebrafish genetics and mutant phenotypes. This is being achieved by a large-scale data curation effort, as well as the development of new software and database technologies.

We are offering summer traineeships for graduate students and postdocs interested in gaining expertise in informatics and the application of ontologies to evolutionary, anatomical, developmental, and genetic data. Opportunities are available to work as part of the Phenoscape team on data curation or open source software/database development. Participants would be located at the National Evolutionary Synthesis Center, http://nescent.org or the University of South Dakota. Stipends of $5,000 will be given to participants to cover travel, room and board for 10-12 weeks.

To apply, please provide the following: 1. A cover letter of no more than 2 pages with > 1. your name >

2. your current status (grad or postdoc) > 3. your institutional affiliation and research supervisor > 4. the dates of the proposed exchange, and your preferred location (Durham, > North Carolina or Vermillion, South Dakota) > 5. your current research goals, and an indication of where you are in your > research timeline > 6. the relevance of the internship opportunity to your research and/or career > goals. > 7. the extent of your background training in, e.g., morphology, paleontology, > molecular/developmental biology, programming, computer or information science. 2. A curriculum vitae (max. 2 pages) listing educational history (including relevant coursework), work experience, publications, and presentations. 3. A letter of recommendation from your advisor/supervisor, and the names and contact information for two other references.

Applications should be sent via email (in Word or PDF format) to Dr. Paula Mabee (pmabee@usd.edu) before March 15, 2009. Funding decisions will be made by April 1, 2009. Further inquiries about the position may be directed to Dr. Mabee by email, or by phone at (605) 677-6171.

Reporting Requirement: Recipients will be expected to submit a 1-page report describing the accomplishments and value of the training within one month after the end of the internship.

NESCent and the University of South Dakota are equal opportunity employers. Applications from women and underrepresented minorities are specifically encouraged. Phenoscape is funded by NSF grant BDI-0641025 from the National Science Foundation.

Paula Mabee <paula.mabee@usd.edu>

## Next-Gen Sequencing Survey

Dear Evoldir members,

Please take the time to fill out a very short next-gen implementation survey posted at:

https://www.surveymonkey.com/s.aspx?sm=-oHz60bWePPN_2fPgcDFk0BeQ_3d_3d It should not take more than 5 minutes to complete. All participants will receive the stats from the survey including service pricing, demand for the technology and the level of subsidy labs are receiving for NGS.

The intent of the survey is to gather data for the upcoming ABRF meeting (http://www.abrf2009.org), to be presented in the Monday, Feb. 9th afternoon Concurrent Workshop. It complements data from some recent surveys that will also be presented at that session.

Thank you in advance for your time!!

Helaman Escobar DNA Sequencing and Genomics Cores University of Utah dna@cores.utah.edu

## Oomycete Diatom Genomes

Genome Project Solutions announces the release of version 2 of our evolutionary analysis of the complete genomes of four oomycetes and their diatom outgroups.

Results can be seen at http://-oomycetes.genomeprojectsolutions-databases.com/ .

At this release, we are analyzing approximately 100,000 total genes. We use a unique, graph-based method to cluster genes into families while considering the evolutionary relationships among the organisms, and then perform a maximum likelihood phylogenetic analysis on each set of genes. We assign all orthologous and paralogous relationships and determine when each gene duplication or loss occurred.

Users can see the multiple sequence alignments and phylogenetic trees of all genes, compare intron-exon structures, and see maps of the relative arrangements of homologous genes across all genomes.

Learn more about this project and see our analysis of the oomycete and diatom genomes at http://-oomycetes.genomeprojectsolutions- databases.com/.

Learn more about our method at http://-genomeprojectsolutions.com/PHRINGE_project.html Learn more about our organization at http://-genomeprojectsolutions.com/ . Jeffrey L. Boore, Ph.D. Chief Executive Officer Genome Project Solutions 1024 Promenade Street Hercules, CA 94547

http://GenomeProjectSolutions.com 1 (877) 867-0146 (toll free)

Associate Adjunct Professor, University of California Berkeley Guest Researcher, Joint Genome Institute and Berkeley National Lab

jlboore@GenomeProjectSolutions.com Fri Jan 9 21:21:01 2009 jlboore@GenomeProjectSolutions.com Fri Jan 9 21:21:01 2009

## Petition for Evolutionary Biology in the Netherlands

Dear Evoldir members,

I would like yo bring to your attention the following situation. Because of reorganization in some Dutch Universities and money cutting in research, several colleagues from Leiden University will be fired by the end of the year if we do not react. They might be fired anyway, but I think that we should at least do our best for this not to happen.

The following evolutionary biologists will be fired or will not be able to continue their research: Jacques van Alphen (Marie Curie professor of Excellence), Tom Van Dooren, Frietson Galis (president of the European Society for Evolutionary Developmental Biology), Sacha Gultyaev, Patsy Haccou (Executive vice-president of the European Society of Evolutionary Biology), Ken Kraaijeveld, Femmie Kraaijeveld, Hans Metz (retired, but still very active) Rino Zandee.

People in Leiden have just set up a petition, which you will find here : < http://evodevo.eu/petition/ > http://evodevo.eu/petition/

I strongly encourage you to sign this petition, which will be sent to every person in the Netherland government who might be able to do something.

I think it is quite incredible that Darwins'year will see an entire and excellent department of evolutionary ecology close down and leave people without a job (even those with a "permanent" job!) because of budget restrictions. As written in the petition, although evolutionary biology will be heavily cut, molecular biology will be spared. This is part of an alarming national trend. Unfortunately, with growing creationism in Europe, and budget cuttings elsewhere (including, alas! France) I am afraid the Dutch trend will soon become international.

Please react ASAP !

Isabelle Olivieri President of the European Society for Evolutionary Biology 2007-2009

Université Montpellier 2, cc 65 Institut des Sciences de l'Evolution (ISEM, UMR 5554) Place Eugène Bataillon 34095 Montpellier cedex 05 Tel. 33 (0)4 67 14 37 50 Fax 33 (0)4 67 14 36 22 Portable 33 (0)6 86 43 19 45

Isabelle Olivieri <Isabelle.Olivieri@univ-montp2.fr>

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## Question on Kingroup Software

Dear all,

I am having problems since last Monday for accessing the Kingroup software webpage at www.kingroup.org. Does anyone knows if has it been moving to another address?

Thank you very much, Sincerely

Carolina I. Miño, MSc. Doctoral Student Laboratório de Genética de Aves Departamento de Genética e Evolução Universidade Federal de São Carlos Rodovia Washington Luis km 235 SP-310 CEP: 13565-905 Monjolinho. São Carlos,SP, Brazil. Phone number: +55 16 3351 8391 (Work) Fax: +55 16 3351 8377 Mobile: +55 16 91190380

Carolina Minio <carolinaianido@yahoo.com.ar>

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## Redimensioned BIOSYS-2 software

Hi All

Many thanks to the EvolDir community for providing me with the BIOSYS-2 software following my previous post. As it happens, my version was not corrupt and merely needed to be redimensioned and recompiled. However, not knowing the second thing about compiling, and unable to find the suggested compiler (Microsoft FORTRAN Compiler 5.1) or a living FORTRAN expert, I have spent two months struggling with it. Would anyone perhaps have a version of BIOSYS-2 that has already been redimensioned (essentially I need the number of alleles it can handle to be increased from 10 to 22)? Appreciate anyone's help (or a borrowed copy of the compiler).

Many thanks!

Gavin

South African Institute for Aquatic Biodiversity Private Bag 1015 Grahamstown 6140 South Africa

Tel: +27 (0)46 603 5843 Fax: +27 (0)46 622 2403

http://www.saiab.ac.za Alternative e-mail: gavingouws@gmail.com<mailto:gavingouws@gmail.com>

Gavin Gouws <g.gouws@saiab.ac.za>

## Samova question

Dear all,

I have a question about SAMOVA analysis. A reviewer worries about the use of SAMOVA that I have recently performed in a submitted paper. The classical phylogenetic analysis splits my dataset into well-supported distinct clades that are geographically strictly parapatric. In order to investigate whether each clade may be further subdivided into distinct geographical groups (that would not be well supported in the phylogenetic tree), I have conducted independant SAMOVAs within each clade.

Although this approach has been previously reported in the literature, it is inaccurate according to my reviewer. I can not follow his point, and wonder if I'm really wrong. Note that running a SAMOVA on the entire dataset only allows me to retrieve the groups already found with the phylogenetic analyses (i.e major clades), and so is of limited interest for my purpose. I would be very grateful for comments or suggestions about this question.

Many thanks for your attention,

Carine Brouat brouat@mpl.ird.fr

– Carine Brouat Centre de Biologie et Gestion des Populations Campus International de Baillarguet CS 30016 34988 Montferrier sur Lez Cedex Tel : (33) 4 99 62 33 09 (lab) / (33) 4 90 16 03 43 (pers.) Fax : (33) 4 99 62 33 45

Carine Brouat <brouat@mpl.ird.fr>

## Sequence alignment and translation answers

A number of people wanted to see the responses I got in looking for software that can translate an alignment into amino acids, align based on on amino acids, and back translate to the original DNA sequences. Two PC - only programs seems the most commonly used, MEGA and BioEdit but a number of other programs were also suggested. here they are....

MEGA - PC and linux BioEdit -PC RevTrans http://www.cbs.dtu.dk/services/RevTrans/ Genious - there is a freeware version, but I don't know yet whether the freeware version includes this function. DAMBE -PC and LInux PAL2NAL http://coot.embl.de/pal2nal/ Bioperl toolkit TransAlign http://www.biomedcentral.com/1471-2105/6/156 aa2dna http://www.bio.psu.edu/People/Faculty/Nei/Lab/software.htm Biopython MacClade DNAstar (not free) Prank/ Prankster: http://www.ebi.ac.uk/goldman-srv/prank SeaView http://pbil.univ-lyon1.fr/software/seaview.html Christopher Balakrishnan Institute for Genomic Biology University of Illinois phone: 617-905-2910 https://netfiles.uiuc.edu/cbala/www/ Christopher Balakrishnan <cbala@igb.uiuc.edu>

## Sequence alignment and translation question

Dear EvolDir Readers,

I am looking for something which I am sure must exist, but I am having trouble finding:

I am looking for software with which I can take DNA sequences (from multiple taxa), translate them to amino acids, conduct amino acid sequence alignment (using Clustal and/or other), and then back- translate to the original DNA sequences (while maintaining the alignment).

Ideally this software would run on a mac.... I am not working with particularly huge files (~1 to 5 kb per seq, ~10 - 20 taxa)

It seems to me that programs like CLC Sequence Viewer, and eBiox can translate into amino acid and do alignment, but they do not keep the underlying DNA sequences, so you cannot back translate to the original sequences (you can translate back to random or most frequent codons in CLC).

The ancient and beloved Se-Al allows you to toggle easily between DNA and amino acid, but doesn't have any alignment algorithms.

Any ideas for a good software package?

Thanks!

Chris

Christopher Balakrishnan Institute for Genomic Biology University of Illinois phone: 617-905-2910 cbala@igb.uiuc.edu https://netfiles.uiuc.edu/cbala/www/ Christopher Balakrishnan <cbala@igb.uiuc.edu>

## Software DAMBE on OSX

Dear All,

I have added instructions on how to install and run DAMBE on Macintosh/Linux computers. See instructions at

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

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

## Software GLMM R package

Dear Evoldir members,

I've written a GLMM package for R that is now downloadable (http://cran.r-project.org/web/packages/MCMCglmm/index.html ).

It fits standard mixed models to several types of distribution (Gaussian, Poisson, Exponential, Binary, Binomial, Multinomial, Zero- inflated Poisson) More than one response variable can be modeled at the same time and these can come from different distributions. Pedigrees and Phylogenies can be fitted as random effects as in "animal models" and the comparative method. Meta-analysis models can be fitted (even in conjunction with other terms, e.g. a phylogeny)

It uses MCMC, as REML/ML procedures are not very robust for fitting GLMM's. However, I've kept it simple to use and made it fast.

There are some other functions in the package for matrix comparisons, matrix visualisation, tensor analysis, random number generators on pedigrees/phylogenies + more.

Thanks,

Jarrod

Jarrod Hadfield <j.hadfield@ed.ac.uk>

## Software IDEA 2 4 4

Dear Evoldir members,

A new version of IDEA (Interactive Display for Evolutionary Analyses) has been released to sourceForge (http://ideanalyses.sourceforge.net/main.html)

IDEA (Interactive Display for Evolutionary Analyses) is a graphical interface for PAML (Yang, Z., 1997), a popular package for conducting molecular evolution analyses on phylogenies and associated sequences. IDEA$^1$s organized parameter-entry interface for codeml and baseml prevents common errors and adds options to reconstruct phylogenetic trees using PHYLIP (Felsenstein, J., 1989) and to combine the results of repeated analyses for increased accuracy. Many datasets may be analyzed in parallel. IDEA$^1$s output display for codeml analyses of sites-based evolutionary models features an interactive tabular summary of results, visualizations of selective pressure along genes, interactive histograms and depictions of phylogenetic trees with branch lengths proportional to the estimated number of nucleotide substitutions.

Release Name: IDEA 2.4.4

Updates in the new version: - support of PAML 4.1; - ability to browse for visualization errors within IDEA; - fixes a bug that prevented the visualization of selective constraints along a gene (sites-based analyses) when many omega values were excessively high; - fixes a bug that omitted the LRT results for single-dataset analyses.

IDEA has been published in BMC Bioinformatics http://www.biomedcentral.com/1471-2105/9/524 Best regards, Joana

Joana C. Silva, Ph.D. Assistant Professor

Institute for Genome Sciences & Dept Microbiology and Immunology University of Maryland School of Medicine BioPark II, Room 645 801 W. Baltimore St. Baltimore, MD 21201

jcsilva@som.umaryland.edu Ph:410.706.6721 Fax:410.706.6777

## Translation and alignment answers 2

Thanks again for all the responses!

A few more came in that I did not list on that previous message. Again, these are software that can translate DNA alignments to amino acids, conduct sequence alignments (Clustal or other), and then back- translate to the original DNA sequences while maintaining the alignment.

Matlab, MBEToolbox (Matlab toolbox for Molecular Biology & Evolution) http://www.bioinformatics.org/-mbetoolbox/ Hyphy http://www.hyphy.org/ Tranlator X http://homepage.mac.com/maxtelford/-FileSharing9.html Christopher Balakrishnan Institute for Genomic Biology University of Illinois phone: 617-905-2910 https://netfiles.uiuc.edu/cbala/www/ Christopher Balakrishnan <cbala@igb.uiuc.edu>

## UArkansas UndergradResearchExperience

REU Summer Research Program in the Arkansas Ozarks Assessment and Sustainable Management of Ecosystem Services

The University of Arkansas is conducting a Research Experience for Undergraduates (NSF/REU) during summer of 2009 for up to 15 undergraduates who have completed at least 3 semesters of coursework. The focus of this REU is on field-based research on ecological services, and each student will work with a faculty mentor on issues ranging from water quality to ecology of birds and black bears in the Ozarks. This program works primarily with federally recognized Native American tribes and Native American students. However, all other interested students are encouraged to apply. This 10-week program consists of a one-week immersion course on field methods, 8 weeks of intensive Research Experience and a one week Data Analysis and Symposia. Room and board are included at the University of Arkansas, as well as a $400 weekly stipend and a travel allowance.

University of Arkansas REU Program: 10-week summer program, 1 June to 7 August 2009 Stipend $4000, onsite room and board, round-trip travel costs Detailed Program Information: www.ecoreu.uark.edu/ Applications due: February 15, 2009

For applications and more information, contact:

Heather Sandefur 207 Engineering Hall University of Arkansas Fayetteville, AR 72701 ofc: 479.575.7585 email: hsandef@uark.edu

Questions about this program can also be directed to Dr. Marty Matlock (mmatlock@uark.edu) or Dr. Kimberly Smith (kgsmith@uark.edu).

wetges@uark.edu

## UK Systematics ResearchFunding

Collaborative Scheme for Systematics Research (CoSyst) Application deadline: 15 March 2009

A call for the third round of the BBSRC Collaborative Scheme for Systematics Research (CoSyst) is announced. The initiative is intended to support preliminary collaborative research that will form the basis of novel responsive mode proposals to UK Research Councils, with a substantial systematics component. The scheme is administered by The Linnean Society and the Systematics Association.

NOTE: Collaborations involving non-UK-based partners are not eligible for this scheme.

Further information and application forms are available from the websites of the Linnean Society : http:/-/www.linnean.org/index.php?id=335 and the Systematics Association http://www.systass.org/awards/-cosyst.shtml.

“Amanda Read (SO)” <Amanda.Read@bbsrc.ac.uk>

## UMinnesota Summer undergraduate research

Dear Undergraduate Student,

I write to invite you to apply for our summer undergraduate research program in Risk Analysis for Introduced

Species and Genotypes at the University of Minnesota. Please see our website at: isg-igert.umn.edu.

This program provides support and unique opportunities for undergraduate students. We strongly value a diverse learning environment and encourage applications from persons of color. Applicants must be US citizens or permanent residents.

Many pressing questions currently face the scientific and policy communities regarding introduced species and genotypes. I invite you to review some of the critical research projects that you could help with as a summer researcher at: isg-igert.umn.edu/faculty/full_faculty_info.htm.

This is a wonderful opportunity for you to prepare for graduate school or to polish your skills in preparation for a career in environmental science or policy. If you plan to graduate later than the summer of 2009 you are qualified to apply.

The program provides: * Summer stipend of $4500 for the 10-week program * Assistance for housing in the Twin Cities * Assistance for travel * Cutting-edge research experiences on invasive species and GMOs * An opportunity to present the results of your research to other scientists * Training in risk analysis * Collaborative research opportunities

To learn more about this summer opportunity and how to apply please visit our website at: isg-igert.umn.edu/summer_undergrads

Applications are due 15 February 2009. Apply to the Life Sciences Summer Undergraduate Research Programs directly at: http://www.cbs.umn.edu/main/-summer_research/ApplInstr.html Be sure to indicate you are applying to the IGERT: Risk analysis for introduced species and genotypes program.

If you have questions contact me (Dr. Ray Newman at RNewman@umn.edu) or Dr. Susan Solarz at the IGERT Program (isgigert@umn.edu).

Our program is sponsored by the National Science Foundation as a part of their Integrative Graduate Education and Research Traineeship (www.igert.org) program. IGERT trains scientists and policy workers to address the global questions of the future.

Please do not hesitate to contact me or Susan for further information or to chat about our summer program for undergraduate students.

All the best, Ray Newman –

Ray Newman, Prof. Fisheries Director of Graduate Studies, Fisheries, Wildlife & CB Water Resources Science 120 Hodson Hall Proj. Dir., ISG-IGERT University of Minnesota Internet: RNewman@umn.edu 1980 Folwell Ave. Phone: (612) 625-5704 St. Paul, MN 55108-6124 FAX: (612) 625-5299 http://-/fwcb.cfans.umn.edu/personnel/faculty/newman.php Le hasard ne favorise que les esprits prepares Chance favors only the prepared mind -Pasteur

Ruth Shaw <rshaw@superb.ecology.umn.edu>

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## Volunteer Tit Evolution

RESEARCH ASSISTANTS NEEDED SPRING/SUMMER 2009

We are currently looking to recruit enthusiastic volunteers to work on a research project investigating individual variation in steroid hormones and fitness in a population of blue tits. Research will be conducted in stunning oak woodland on the banks of Loch Lomond, Scotland, UK.

Positions are available between April-June 2009. Although starting and ending dates are flexible, you must be available to work for at least 2 weeks. You will be working as part of a team with Dr Kathryn Arnold and Dr Britt Heidinger of the University of Glasgow (www.gla.ac.uk:443//ibls/staff/-staff.php?who=PGe ~ Pn). This is a great opportunity to gain valuable experience in several field research techniques including: nest box monitoring, measuring eggs and nestlings, invertebrate sampling and behavioural observations. Basic living costs will be covered and accommodation during fieldwork will be provided at the University of Glasgow field station, SCENE, within Loch Lomond National Park (http://-/www.gla.ac.uk/departments/scene/).

Requirements: A strong interest in animal ecology and behaviour. Applicants must be reasonably fit and able to climb ladders (for fieldwork). Preference will be given to candidates with a background in biological sciences and experience handling birds but this is not essential.

General inquires and formal applications should be sent to: Lindsay Henderson (E-mail: l.henderson.1@research.gla.ac.uk). Applications must include: a CV, cover letter and two referees (academic or field biology related V with e-mail addresses). Be sure to indicate the dates that you are available. If it is not possible to send applications via email, please send them by post to: Lindsay Henderson, Division of Environmental and Evolutionary Biology, Graham Kerr Building, University of Glasgow, G12 8QQ Scotland, UK

Closing date: Friday 20th March.

Lindsay Henderson Division of Ecology and Evolutionary Biology, Faculty of Biomedical and Life Sciences, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ, UK

Lindsay Hendenson <9904916h@student.gla.ac.uk>

# PostDocs

## ARS Delaware HostRangeEvolution

POST-DOCTORAL RESEARCH ON DYNAMIC HOST RANGE IN PARASITOIDS

As part of a project on the evolution of host range in parasitic Hymenoptera, we are studying the behavioral plasticity of host range in generalists versus specialists that are quite closely related (Heraty et al. 2007. Mol Biol Evol 45: 480-493). In this research, we plan to determine whether parasitoids with different host ranges are more likely to accept low-quality species of hosts when their physiological state (i.e., age, egg load, and nutritional status) would suggest that they are unlikely to be able to lay all of their eggs.

QUALIFICATIONS: Ph.D. in evolutionary ecology or related subject. Experience with insect parasitoids desirable. LOCATION: USDA-ARS, Newark, Delaware SALARY: $47,810 per year plus benefits DURATION: 1 year with possibility of extension CONTACT: Dr. Keith Hopper; 302-731-7330 ext 238; Keith.Hopper@ars.usda.gov ARS is an equal opportunity employer.

Keith R. Hopper, PhD USDA-ARS-BIIR, 501 South Chapel St., Newark, DE 19713; phone 302-731-7330 x238; fax 302-737-6780; keith.hopper@ars.usda.gov

khopper@udel.edu

## CalTech SelfishGeneticElements

Mosquitoes are essential vectors for major human diseases such as dengue, yellow fever and malaria. An attractive approach to suppressing these diseases involves replacing the wild pest population with modified counterparts unable to transmit disease (population replacement). An essential component of such a strategy involves the use of a genetic drive mechanism able to promote the spread of genes conferring disease resistance, even if their presence carries a fitness cost. We have developed a synthetic selfish genetic element (Medea) that is able to drive population replacement in Drosophila [Chen et al., (2007) A synthetic maternal-effect selfish genetic element drives population replacement in Drosophila. Science. 316: 597-600].

Postdoctoral positions are available to study the basic biology of microRNAs, cell death, spermatogenesis and other developmental pathways in Drosophila and mosquitoes, which are tools necessary for the development of Medea and other selfish genetic elements. We are also interested in the development of novel selfish genetic elements able to bring about local population elimination, as well as methods for engineering reproductive isolation. Population genetic engineering is an exciting new research area with many opportunities. Postdoctoral candidates should hold recent Ph.D. and/or M.D. degrees.

We (http://www.its.caltech.edu/~haylab/) are an energetic and well- funded team with modern lab space located in sunny Pasadena. We seek to expand our group with the addition of highly motivated candidates with experience in molecular and population genetics, cell biology, developmental biology and modeling. Close interactions with other labs at Caltech and in the Southern California area (UCLA, UC Irvine, UC Riverside and USC) make the environment collegial and stimulating.

Contact:

Bruce A. Hay Professor Division of Biology, MC 156-29 California Institute of Technology 1200 East California Boulevard Pasadena, CA 91125

haybruce@caltech.edu haybruce@caltech.edu

## ColoradoStateU PlantEvolution and Genomics

Postdoctoral Associate in Rice Evolution and Genomics, Fort Collins, Colorado

A postdoctoral position is available at Colorado State University. The successful applicant will work in the Plant Evolutionary Genetics Lab of Dr. John McKay (www.mckaylab.colostate.edu). We are looking for a highly motivated individual with a PhD in Evolution, Plant Physiology or Molecular Genomics and with the demonstrated ability to carry out outstanding research in Plant Genetics and Physiology. Preference will be given to candidates with experience with training and experience in Statistical Genomics/Bioinformatics and Quantitative Genetics. The successful applicant will interact and work collaboratively with others including Drs. Jan Leach and Dan Bush and their labs at Colorado State and Dr. Hei Leung and our collaborators at IRRI.

This Postdoctoral position is part of a collaboration to explore the evolution and genetic basis plant growth and physiology in rice. The goal of the project is to identify and physiologically characterize genes underlying naturally-occurring variation in growth rates and biomass production in rice using genome-wide molecular techniques and whole-plant physiology.

The position is available summer 2009, but the start is flexible to some degree. Salary and benefits are competitive, and CSU is an excellent academic environment for the study of plant biology. Our lab group has excellent interactions with colleagues in bioinformatics, plant physiology, ecology, evolutionary genetics and molecular biology. Fort Collins is located on the Front Range of the Rockies and is ranked highly among great places to live.

If you are interested in this position, please send a letter of interest and a C.V. in pdf format via e-mail to jkmckay@colostate.edu

"McKay,John" <John.McKay@ColoState.EDU>

## CornellU CanineEvolutionaryGenomics

Postdoctoral position in canine evolutionary genomics at Cornell University

Seeking qualified applicants for a post-doctoral position with Nate Sutter in the College of Veterinary Medicine at Cornell University (Ithaca, New York). The research focuses on the evolution of the domestic dog genome, the dog's rapid acquisition of extreme phenotypic diversity, and the genetics of body size.

While the dog is our primary object of study due to the wealth of selected inbred lines that vary 50 fold in mass, we are also investigating morphologic diversity in the horse. In a related project, we are exploring the pattern of retrotransposon insertions in the dog genome and relating those insertion mutations to traits.

Candidates who wish to combine computational and bioinformatic approaches with experimental biology are highly encouraged to apply. The ideal candidate will hold a Ph.D. and have a record of productive research in molecular genetics or possibly statistical genetics, computational biology or a related field. Programming and database experience (perl, SQL, etc.) is desirable but not required.

Cornell's College of Veterinary Medicine is a highly stimulating research environment that features expert veterinary specialist colleagues, a busy vet hospital, and basic and clinically focused research labs. Ithaca is a small town situated in the heart of the "finger lakes" wine and tourism region of upstate New York. It has great schools and innumerable waterfalls and hiking trails within easy driving distances.

Interested applicants should submit an electronic version of their CV, the names and contact information for three references, and a brief cover letter describing their qualifications and relevant experience to nbs39@cornell.edu. The position is for two years and is available immediately.

Nate Sutter Assistant Professor of Medical Genetics Cornell University nbs39@cornell.edu

Nathan Sutter <nbs39@cornell.edu>

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## Duesseldorf 2 GenomeEvolutionaryNetworks

Duesseldorf.GenomeEvolutionaryNetworks.2postdocs

The Institute of Botany III, University of Düsseldorf, laboratory of Dr. William Martin, is currently seeking to fill two full-time postdoctoral positions to study the application of networks in genome evolution.

The Institute offers a modern and supportive working environment with solid funding and has recently received an Advanced Grant from the European Research Council to investigate the properties and utility of networks in genome evolution, specifically as it applies to non-treelike processes of microbial evolution, lateral gene transfer among prokaryotes and endosymbiosis among eukaryotes in particular. Information about our ongoing research activities can be found at http://www.molevol.de/lab/-publications.html . 1. Prokaryotes. Postdoctoral position (biologist/bioinformatician/computer scientist; three years with possibility of extension for additional two years). Candidates should have a PhD in Mathematics or Informatics with a good working knowledge of biology or a PhD in Biology with a good working knowledge of computer science (programming skills). Experience with networks, experience using MatLab or related tools and ideally a basic working knowledge of genome biology and will be advantageous. Salary is the standard for university postdoctoral researchers according to E14, the position can be filled immediately. The project aims to investigate modularity in prokaryote gene sharing patterns, hierarchical manifestations thereof, and network attributes of prokaryote genome evolution at various taxonomic levels (including strains). Candidates should be able to work independently and to should show an interest in co-supervision of PhD students.

2. Eukaryotes. Postdoctoral position (biologist/bioinformatician/computer scientist; three years with possibility of extension for additional two years). Candidates should have a PhD in Mathematics or Informatics with a good working knowledge of biology or a PhD in Biology with a good working knowledge of computer science (programming skills). Experience with networks, experience using MatLab or related tools and ideally a basic working knowledge of genome biology and will be advantageous, as will familiarity with genome sequences and the role of endosymbiosis in eukaryote evolution. Salary is the standard for university postdoctoral researchers according to E14, the position can be filled immediately. The project aims to identify and investigate the nature of gene sharing patterns between prokaryotes and eukaryotes using network approaches, and the network properties of the data. Candidates should be able to work independently and to should show an interest in co-supervision of PhD students.

Interested candidates should send their application as a single pdf file including c.v. with publication list and contact details of two potential references to Prof. William Martin (w.martin@uni-duesseldorf.de). Initial deadline for applications is March 31 but applications will be accepted until both positions are filled.

– Prof. Dr. William Martin Institut fuer Botanik III Heinrich-Heine Universitaet Duesseldorf Universitaetsstr. 1 40225 Duesseldorf

Germany

Tel : ++49-211-811-3011 Fax : ++49-211-811-3554 e-mail : w.martin@uni-duesseldorf.de web : http://www.molevol.de W.Martin@uni-duesseldorf.de W.Martin@uni-duesseldorf.de

## EmoryU HostParasite

Postdoc: Emory University, Host-parasite interactions

Post-Doctoral Position, Host-parasite interactions Emory University, Atlanta, GA USA Laboratories of Drs. Jacobus de Roode and Nicole Gerardo

A postdoctoral position is available for research on the coevolutionary interactions between monarch butterflies, their parasites and their larval host plants. The project would focus on identifying the molecular basis of host resistance to parasitism, and involve a combination of functional genomics, experiments and fieldwork. The postdoc would assemble sequences derived from 454 sequencing of cDNA, annotate genes using existing genome databases of insects and protozoan parasites, and implement statistical analyses to compare the transcriptome of infected and uninfected individuals. He/she would also carry out experiments to study the expression of candidate resistance genes in infected and uninfected monarchs, and in monarchs reared on different host plant species. Additional projects may focus on the population genetics and co-phylogenies of monarchs and their parasites in natural populations.

This is a joint project between the laboratories of Jacobus de Roode and Nicole Gerardo. Both labs combine field work, experimentation and molecular genetics to study host-parasite coevolution, and address questions related to virulence evolution, mutualism, and the molecular evolution of host resistance. The labs are part of Emory's Population Biology, Ecology and Evolution program, which has a strong focus on host-parasite interactions and molecular genetics. For more information on the labs and program, see: http://www.biology.emory.edu/research/deRoode/ http://www.biology.emory.edu/research/Gerardo/ www.biomed.emory.edu/PROGRAM_SITES/PBEE/ Candidates must have a strong background in bioinformatics, with emphasis in functional genomics and gene annotation, and should have an interest in evolutionary biology and host-parasite interactions. The postdoc is also expected to take part in the training of graduate and undergraduate students.

The position will be available for 1 year initially, with the possibility of a 1-2 year extension. Salary will be based on experience and will follow NIH guidelines; benefits will be provided. Applications should be sent by 6 February 2009 to jderood@emory.edu, and be accompanied by a short research statement, a CV and the names of 3 referees. The postdoc would ideally start no later than April 2009, but the starting date is negotiable.

***This job is a readvertisement to extend the application deadline; if you have already applied for it, there is no need to reapply; your application will be considered after the 6 Feb deadline.***

For more information, please contact Jacobus de Roode on jderood@emory.edu or 404 727 2340.

jderood@emory.edu jderood@emory.edu

## Frankfurt Biodiversity

The Biodiversity and Climate Research Centre (BiK-F) has recently been founded by the Senckenberg Gesellschaft für Naturforschung, the Goethe-Universität Frankfurt am Main, and additional partners. It is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The Project Area A "Evolution and Climate" invites applications for the position of a

PostDoc Position Model Selection PG A1 (Ref. #A21) BAT IIa

The applicant will be responsible to infer the relationship between major climatic events and cladogenesis of selected taxa. Phylogenetic hypotheses will be tested by model selection methods for a correlation between climatic changes and speciation/radiation events. Participation in university teaching is possible, while the acquisition of external research funding is highly desired. The applicant should hold an earned Ph.D. in biology, with a strong background in statistical phylogenetics. She or he should already have experience with phylogenetic inference and should be interested in linking evolutionary and climate change issues. Practical experience in molecular work is desired, but not mandatory. Applicants should have a strong publication record. Very good written and oral English language skills, willingness to learn at least basic German and interest in joining a multidisciplinary research team are required, as well as proven organizing abilities.

Salary and benefits are according to a public service position in Germany (BAT IIa).

The Research Centre BiK-F advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

The contract shall start as soon as possible and will be restricted to 24 months. Review of the application starts on February 1st 2009 and will continue until the position is filled. The duty station will be Frankfurt am Main, Germany.

Please send your application by mail or e-mail, including a detailed CV, 3 references, a list of publications and up to five selected re/e-prints to Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de. For enquiries about the position and the contract conditions please write to Prof. Dr. B. Stribrny (E-mail: bernhard.stribrny@senckenberg.de) and for scientific enquiries to Prof. Dr. Annette Klussmann-Kolb (E-mail: Klussmann-Kolb@bio.uni-frankfurt.de) or PD Dr. M. Pfenninger (E-mail: pfenninger@bio.uni-frankfurt.de).

Ursula Maurer M.A. Wissenschaftliches Koordinationsbüro LOEWE - Biodiversität und Klima Forschungszentrum BiK-F Besucheradresse: Georg-Voigt-Straße 16 Postadresse: Senckenberganlage 25 D-60325 Frankfurt am Main

Tel.: 069-7542-1819 Fax: 069-7542-7904 info-bik-f@senckenberg.de www.senckenberg.de/bik-f

Ursula Maurer <Ursula.Maurer@senckenberg.de>

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## IFREMER France TheoreticalGenetics

Postdoctoral position in theoretical genetics at the French Institute of Research for the Exploitation of the Sea (IFREMER), Port-en-Bessin, France

A postdoctoral position is available at the Fisheries Unit of the French Institute for the Exploitation of the Sea (IFREMER, Port-en-Bessin, France). The successful applicant will be expected to set up new methods to assess temporal quantitative genetic differentiation within wild exploited populations by: (i) developping statistical methods to estimate temporal quantitative genetic differentiation within natural populations (temporal Qst) based on regressing (generalized linear mixed models) temporal phenotypic differentiation on temporal differentiation at neutral markers (temporal Fst) according to the same principle as already existing methods for spatial differentiation (Ritland, 2000); (ii) extending this method to include environmental covariates as potentially responsible for a phenotypically plastic component in temporal phenotypic differentiation; and (iii) applying the developed methods to two case studies: growth and maturation of North sea and Channel cod and sole.

The position is co-funded by the European Research Network FinE, Fisheries-induced Evolution (http://www.iiasa.ac.at/Research/EEP/FinE/Home.html) and IFREMER. The FinE project is set up to investigate the prevalence of fisheries-induced evolutionary changes in life-history traits of exploited fish stocks in European and North American waters. The aims are to unravel the underlying mechanisms of changes ranging from the phenotypic to the genetic level, to evaluate their consequences on population and fisheries dynamics, and to provide recommendations for evolutionarily enlightened management. This objective necessitates the development and application of novel methodological tools for investigating field data both at phenotypic and genetic levels, together with the setup of relevant experiments on model species and the careful construction of theoretical models suitable for complementing field data analyses and for evaluating managerial options. More precisely, the present position is intimately related to Task 2.4 of WorkPackage 2 on Genetic analysis (http://www.iiasa.ac.at/Research/EEP/FinE/Tasks.html#wp2). The project is coordinated by the International Institute for Applied Systems Analysis (Laxenburg, Austria) and relies on 18 teams spread in 15 European countries and Canada.

Applicants should have a PhD in theoretical population/quantitative genetics or in theoretical evolutionary ecology with a strong background in modelling and/or theoretical statistics. Some knowledge in life history theory and/or fish ecology and/or fisheries would be an advantage. According to IFREMERs fellowship rules, applicants must be less than 35 years old on December the 31st, 2008, own their PhD since less than 36 months and should not have been employed as postdoctoral fellow by IFREMER before. The work will be conducted within the Fisheries Unit (IFREMER, Port-en-Bessin, France) in collaboration with the two teams involved in the molecular genetic work on the two case studies: the Laboratory of Aquatic Ecology (Prof. F. Volckaert and Dr. G. Maes, Catholic University of Leuven, Leuven, Belgium) for sole and the Population Genetic Group (Dr. E. E. Nielsen, National Institute of Aquatic Resources, Technical University of Denmark, Silkeborg, Denmark) (http://www.iiasa.ac.at/Research/EEP/FinE/Teams.html). The position is for a duration of 18 months with a monthly gross salary of around 2 600 .

IFREMER (www.ifremer.fr/anglais/) is a national research institute affiliated with the Ministry of Education, Research and Technologies, the Ministry of Agriculture and Fisheries, the Ministry of Environment and Sustainable Development, and the Ministry of Equipment, Transport, and Housing. The Institute conducts research in all fields of marine science among which fisheries and aquaculture sciences and the management of marine living resources. The Institute has about 1700 employees located in 24 marine stations distributed along the French coastline. The Fisheries Unit in Port-en-Bessin is part of a marine station located on the coast of the English Channel at 30 km from Caen, Normandy, France. It consists of about 35 persons among whom 15 senior researchers and 15 technicians in marine and fisheries science. Normandy is one of the most renowned regions in France for its food and its surroundings, which offers numerous opportunities for outdoor activities both on the seaside and inland. Caen is a lively town located only 2 hours away from Paris by train or car.

For more information please contact Bruno Ernande by email

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## ImperialCollege 3 Speciation

3 x Postdoc Research Associates in Speciation Genomics/Biology and Biodiversity

(Refs: NS2009006JT, NS2009007JT and NS2009008JT)

Imperial College London Division of Biology Department of Life Sciences Silwood Park Campus

Salary: GBP 26,580 - 38,730 p.a.

This is an exciting opportunity for three Research Associates with an interest in Speciation. The successful candidates will carry out cutting edge research investigating the mechanisms of speciation in - but not restricted to - plants on islands (e.g. Lord Howe Island, Australia, see Nature 441:210). You must have a PhD or equivalent qualification in biodiversity,evolution, ecology, genetics or a closely related discipline.

The successful candidates will have solid backgrounds in molecular evolution, population genetics and genomics, statistics and/or modelling with a strong interest in evolutionary biology and biodiversity. The posts are funded for 2-3 years by a European Research Council Advanced Grant and the Royal Society. The successful candidates will work closely with Dr Vincent Savolainen and his research group, see http://www3.imperial.ac.uk/people/v.savolainen Further details and an application form can be obtained from the College employment website: http://www3.imperial.ac.uk/employment see details at:

http://www3.imperial.ac.uk/employment/research/ns2009006jt http://www3.imperial.ac.uk/employment/research/ns2009007jt http://www3.imperial.ac.uk/employment/research/ns2009008jt Completed application forms accompanied by a cover letter, curriculum vitae and the name and contact details of two referees should be sent to: Mrs Diana Anderson, Imperial College London,Silwood Park Campus, Buckhurst Road, Ascot, Berkshire, SL5 7PY or - preferably by e-mail: to d.anderson@imperial.ac.uk

Closing date: 16 February 2009.

Dr Vincent Savolainen Reader in Ecology and Evolutionary Biology Imperial College London, and Royal Botanic Gardens, Kew Silwood Park Campus Buckhurst Road, Ascot, Berkshire, SL5 7PY, UK Tel +44 (0)20 7594 2374 Fax +44 (0)20 7594 2339 v.savolainen@imperial.ac.uk http://www3.imperial.ac.uk/people/v.savolainen v.savolainen@imperial.ac.uk

## ImperialCollegeLondon StatisticalPopGenetics

Postdoctoral position in human population genetics at EBI/Imperial College

The Vertebrate Genomics Team at the European Bioinformatics Institute (EBI) seeks a post-doctoral researcher to participate in the analysis of human genetic diversity. The post holder will have the opportunity to work with the dense genotyping data now being produced for large cohorts including those associated with diseases in the Wellcome Trust Case Control Consortium and world-wide population diversity as exemplified by the 1000 Genomes project and the Human Genome Diversity Panel. Genome-wide data generated by various high-throughput projects can be effectively combined. As a result, it is now possible to work on datasets including thousands of complete human genomes from a large number of populations.

The aim of the project is to exploit this extraordinary wealth of data to refine our understanding of past human demography and exploit novel approaches to detect regions of the human genome under natural selection. The analyses will take advantage of a new powerful geographically-explicit framework currently developed by Andrea Manica (Cambridge) and Francois Balloux (Imperial College). Some general background of the project can be found in the publications listed below.

* Handley LJL; Manica A; Goudet J; Balloux F. 2007. Going the distance: human population genetics in a clinal world. Trends in Genet. 23:432-439.

* Linz B; Balloux F; Moodley Y; Manica A; et al. 2007. An African origin for the intimate association between humans and Helicobacter pylori. Nature. 445:915-918.

* Manica A; Amos W; Balloux F; Hanihara T. 2007. The effect of ancient population bottlenecks on human phenotypic variation. Nature. 448:346-348.

* Liu H; Prugnolle F; Manica A; Balloux F. 2006. A geographically explicit genetic model of worldwide human-settlement history. Am J Hum Genet. 79:230-237.

The post-holder will be primarily based at the EBI but is expected to spend some of his/her time in Francois Balloux's group at Imperial College London. Further particulars of the post and information for interested applicants can be found at the following URL:

http://www-db.embl.de/jss/servlet/-de.embl.bk.emblGroups.JobsPage/08068EB I.html

f.balloux@imperial.ac.uk f.balloux@imperial.ac.uk

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## Marine DNA Barcodes

Institute: Centre for Microbial Diversity and Evolution, Departments of Zoology & Botany, University of British Columbia, Vancouver, BC, Canada.

Subject: Biodiversity, evolution and single cell barcoding of marine microeukaryotes.

Number of Postdoctoral Research Positions: Two positions are available.

Tasks: The post-doc candidates will examine the diversity of several groups of marine microeukaryotes (including excavates, chromalveolates, rhizarians and meiofaunal animals) from global marine samples using molecular markers. Selected markers (barcodes) will be developed from available culture collections and compared with sequence diversity from natural marine samples. The candidate will also participate in development of protocols for high throughput sequencing of barcode genes from single cells linked to microscopy. The candidates will be part of the Centre for Microbial Diversity and Evolution at UBC (www.cmde.science.ubc.ca/) as well as the International Barcode of Life initiative (www.dnabarcoding.org/). The following UBC laboratories will support and supervise one PDF each; however, collaborative work between the two labs is expected.

Laboratory webpages: The Leander Lab (www.botany.ubc.ca/bleander/) The Keeling Lab (www.botany.ubc.ca/keeling/)

Required skills: The successful candidates will have completed a PhD with a focus on barcoding, microbial biodiversity, protist molecular evolution/systematics, or a relevant field. The candidates must have a strong record of productivity, skills in molecular biology and analysis of sequence data. Skills in microscopy and background knowledge of marine biology and protist diversity are also highly desirable.

Starting date and duration: The appointments may begin as early as Sept. 2009. The appointments will be for one year initially, with continuation to four years depending on performance.

Application deadline: March 31, 2009.

Contact: Applicants should send a letter of application, current curriculm vitae, and contact information of two references to both Patrick Keeling and Brian Leander: bleander@interchange.ubc.ca and pkeeling@interchange.ubc.ca.

Brian S. Leander Associate Professor Departments of Zoology and Botany University of British Columbia #3529-6270 University Blvd. Vancouver, BC V6T 1Z4 CANADA

Web: http://www3.botany.ubc.ca/bleander/-index.html Email: bleander@interchange.ubc.ca Tel: 604 822-2474 (office), 604 822-4892 (lab) Fax: 604 822-6089

bleander@interchange.ubc.ca bleander@interchange.ubc.ca

## Muenster Germany HostParasiteCoevolution

Postdoc: Muenster (Germany) - Ecological Immunology and Host-Parasite Coevolution

A postdoctoral research associate position (for up to six years) is available in the group of Animal Evolutionary Ecology at the Institute for Evolution and Biodiversity, University of Muenster, Germany (http://ieb.uni-muenster.de/) from April 2009.

We invite applications for a research associate to establish a vigorous research group in the evolutionary ecology of immune defense and/or host-parasite coevolution. Requirement for the position is a PhD degree and research experience in a biological field. A background in evolutionary ecology and experience with molecular techniques are advantageous. We are particularly interested in candidates who want to work with the flour beetle Tribolium castaneum as a model organism. Current projects of the group focus on the evolution of specific memory and phenotypic plasticity in immune responses and the adaptation of host immune defenses to parasites and vice versa. Working language of the lab is English.

Successful candidates will develop externally funded research programs, direct graduate students and contribute to teaching in the fields of evolution, ecology and biodiversity of animals. The position will include some teaching and administrative duties. The position is paid according to TV-L 13.

The University of Muenster seeks to increase the proportion of female staff members and therefore strongly encourages interested female candidates to apply. In addition, preference will be given to qualified disabled applicants.

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

Interested candidates should send applications (preferentially as E- mail attachment) containing a CV, a list of publications, a research statement and the addresses of 3 potential referees to:

Prof. Joachim Kurtz

Institute for Evolution and Biodiversity, University of Muenster, Huefferstr. 1, DE-48149 Muenster, Tel. +49 251 83 24 661, joachim.kurtz@uni-muenster.de

Closing date is February 22nd, 2009.

Prof. Dr. Joachim Kurtz

University of Muenster Institute for Evolution and Biodiversity, Animal Evolutionary Ecology Group Huefferstr. 1, D-48149 Muenster, Germany Phone: + 49 251 83 24661 Fax: + 49 251 83 24668 joachim.kurtz@uni-muenster.de http://www.uni-muenster.de/Evolution/- joachim.kurtz@uni-muenster.de joachim.kurtz@uni-muenster.de

## Netherlands Bioinformatics

The Centraalbureau voor Schimmelcultures (CBS) is an independent research institute of the Royal Netherlands Academy of Arts and Sciences, situated on the campus of the largest university in the Netherlands (Utrecht). It studies fungal biodiversity in the widest sense, focusing on three priority areas, agriculture, human health, and industry (indoor air and food). Presently there are 5 research groups with a total of about 80 employees. The institute maintains a large culture collection of fungi and yeasts, and research groups such as those of Pedro Crous (Evolutionary Phytopathology), Robert Samson (Applied and Industrial Mycology), Sybren de Hoog (Origins of Pathogenicity in Clinical Fungi), Teun Boekhout (Yeast and Basidiomycete Research), and Vincent Robert (Bioinformatics). Additional information is available on our website: www.cbs.knaw.nl . The group of Dr. Vincent Robert currently has a vacancy for a

Postdoc full time (38 hours/week)

Description of the project: The CBS is looking for a post-doctoral candidate with a strong background in bioinformatics and/or informatics sensu stricto to form part of the newly established group on bioinformatics. Strong programming skills are required in one or several of the following languages: Visual Basic.Net, Visual C++.Net and Asp.Net. The successful applicant will be integrated within the existing team of developers and will work on a number of research subjects ranging from genome analyses, analyses of systematic data to the creation of databases and associated software and specialized bioinformatics tools. In agreement with the group leader, the candidate will also be able to develop his/her own research themes. There are ample opportunities to apply for additional grants. The institute supplies excellent resources and facilities; the language of internal communication is English.

Duration: The position is an appointment for five years.

Salary: According to [3] CAO-Nederlandse Universiteiten[2], ( CAO-NU), scale 10 or 11 depending on age and experience.

Location: Utrecht (The Netherlands)

Information: Applicants should send complete curriculum vitae with a list of publications and the names and contact information of at least three references. Further information can be obtained from and applications can be submitted to the bioinformatics group leader: Dr Vincent Robert, CBS Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, the Netherlands, stating vacancy CBS 2009-03 in the upper left corner or via e-mail (v.robert@cbs.knaw.nl or personeelszaken@niob.knaw.nl).

Sujeevan Ratnasingham <sratnasi@gmail.com>

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## UAntwerp damselflyEvolution

POSTDOC POSITION - UNIVERSITY OF ANTWERP (BELGIUM)

Postdoc position at the Department of Biology -Evolutionary Ecology group with Hans Van Gossum http://www.ua.ac.be/hans.vangossum Note that this same position was earlier announced as only available for graduate students (at: http://evol.mcmaster.ca/ ~ brian/evoldir/-GradStudentPositions/UAntwerp.DamselflyEvolution) but now is opened to also being available for postdoc applicants.

Duties and research:

Preference goes to a candidate with a keen interest for evolution, behaviour and ecology. Research topic is the study of the causes and consequences of coexistence of multiple discrete female damselfly (Insecta: Odonata) morphs (with genetic base). Intriguingly, one female morph much resembles the conspecific male's phenotype to such extent that intraspecific mimicry in the context of sexual conflict has been suggested. Several studies indicate frequency-and density-dependent selection. Broad aim of the research is study of causes and consequences of variation in social environments (densities and frequencies of males and female morphs) on the success, behaviour and phenotype of males and females. Fieldwork is planned at several locations in Europe (such as Belgium, Netherlands, Spain).

Requirements:

* PhD in Biology, keen interest for ecology and evolution and for behavioural work.

* Owner of a driver's license. * EU citizen, but not Belgian.

* Preferentially the candidate also is used to advances statistical methods. The field work requires independence, flexibility and a taste for adventure.

Offer and further information:

Full time job from March 1 2009 or later (as agreed) for a period of approximately 18 months. Salary ranges from 1650 to 2600 Euro monthly, tax free, but from which 14% goes to Social Security.

For further please contact me at: email hans.vangossum@ua.ac.be or phone ++ 32 3 265 32 82

Procedure?

CV and motivation letter are awaited before 15 February 2009 and can be send to Hans Van Gossum, by email (hans.vangossum@ua.ac.be), or post: Hans Van Gossum, Universiteit Antwerpen, Departement Biologie, Onderzoeksgroep Evolutionaire Ecologie, Groenenborgerlaan 171, 2020 Antwerpen, Belgium, Europe. Please also provide the contact details for two persons willing to write a letter of recommendation. On Monday 16 February 2009 you will be informed whether you have been selected for further interview and how selection will be continued.

Van Gossum Hans <hans.vangossum@ua.ac.be>

## UBasel EvoltuionaryGenomics EvoDevo

POSTDOCTORAL POSITION IN CICHLID EVOLUTIONARY GENOMICS/EVO-DEVO

A postdoctoral position in evolutionary genomics/evo-devo is available in the group of Dr. Walter Salzburger at the University of Basel, Switzerland (http://www.evolution.unibas.ch/salzburger/). The position is funded by a Starting Grant of the European Research Council (ERC), a new European funding body set up to support excellent investigator- driven research (http://erc.europa.eu).

The ERC Starting Grant 'INTERGENADAPT' runs for a period of five years. It will focus on the identification of the molecular basis of adaptation, evolutionary innovation and diversification in one of the most exciting model systems for evolutionary research, the adaptive radiations of cichlid fishes in the East African Great Lakes Tanganyika, Malawi and Victoria. These lakes harbor ecologically and morphologically highly diverse species flocks counting hundreds of endemic cichlid species each. We are interested in the genetic and developmental basis of the morphogenesis of sexually and naturally selected traits that might be crucial to the cichlid's evolutionary success (e.g. mouth morphology, pharyngeal jaw apparatus, color and pigmentation patterns; see Salzburger, 2009, Mol. Ecol.). To do so, we will apply cutting edge technologies. The forthcoming cichlid genome will certainly facilitate these efforts.

We are looking for a highly motivated, open-minded, creative and socially skilled young researcher that shares our enthusiasm in the study of evolution. Ideally, the candidate has some background in one or several of the following fields: bio-informatics, developmental biology, (cichlid) fish biology, evolutionary biology, evo-devo, evolutionary genomics, molecular evolution, and/or transcriptomics.

The initial appointment will be made for one year, with a possible extension to up to three years. The salary ranges between CHF 55'000 and CHF 70'000 (per year; after tax), depending on experience. The position is available right now, the starting date is negotiable though.

To apply, please send

(1) your CV, (2) a list of your publications, (3) a statement of your research interests, (4) a statement why you would like to join our team, and (5) the names of two persons who can be contacted for a reference letter

to the following email address:

salzburgerlab-dib@unibas.ch

Please also use this email address for informal enquiries.

Deadline for submission is January 30th, 2009.

With best Wishes,

Walter Salzburger

Dr. Walter Salzburger, Assistant Professor

Zoologisches Institut, Universität Basel Vesalgasse 1, 4051 Basel, Switzerland

tel. +41 (0) 61.267.0303; fax. +41 (0) 61.267.0301 iPhone: +41 (0) 78.888.1776 eMail: walter.salzburger@unibas.ch web: http://www.evolution.unibas.ch/salzburger/ ADDITIONAL INFORMATION:

The Salzburger Lab (http://www.evolution.unibas.ch/salzburger/) is a young, multinational, open-minded, enthusiastic and creative team. We are, at present, about twelve people. Our main model systems are East African cichlid fishes, although we also study the adaptive radiation of Antarctic notothenioid fishes and the diversification of Alpine taxa. We also develop our own software. Core of the Salzburger Lab is an excellently equipped molecular laboratory with an AB 3130xl genetic analyzer, an epMotion pipetting workstation, a StepOne Plus and Veriti gradient PCR machines, research microscopes, etc.

The Salzburger group is based within the evolutionary biology group of the University of Basel's Zoological Institute (http://www.evolution.unibas.ch ). The evolutionary biology group promotes higher education and up-to- date research in organismic and evolutionary biology, thereby complementing existing strengths in life-sciences at the University of Basel. The evolutionary biology group is located in the Vesalianum in the historical part of Basel, in close proximity to other University institutes, the University hospital and the Biozentrum of the University of Basel.

The University of Basel (http://www.unibas.ch/) is Switzerland's oldest University with a strong focus on "Culture" and "Life Sciences". About 9'000 undergraduates and 2'000 postgraduate and doctoral students are enrolled in Basel. The University is regularly ranked among the best 100 Universities worldwide and top-ten in the German speaking countries.

Basel (http://www.basel.ch) is located in north-western Switzerland on the river Rhine and borders Germany (Baden-Württemberg) and France

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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

## UBasel PopulationGenetics

Postdoc positions in microbial population genetics and evolutionary genomics

Universitat Basel, Switzerland Zoologisches Institut

A postdoc position is available at the Institute of Zoology at Basel University. I am looking for a highly motivated post-docs with interest in the evolutionary genetics of host-parasite interactions. The position is funded to work on the population genetics and evolutionary genomics of the microparasites (bacteria and microsporidians) of Daphnia. A background in evolutionary genetics, including knowledge of molecular methods is essential. Excellent written, verbal, and interpersonal skills, a superb work ethic, and the ability to think creatively and critically are desired. The starting date it is flexible. The positions are initially for 1 years, but can be extended to up to 4 years.

The post-docs will be part of Dieter Ebert's group working on the co-evolution of host-parasite interactions, focusing on the Daphnia system. Details about the group can be found under: http://evolution.unibas.ch/ Please send application by E-mail to Dieter Ebert (dieter.ebert@unibas.ch). Applications (1 pdf file, please) should include a CV, a list of publications and a 1 page description of your research interests and motivation. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 15. Feb. 2009 will be given full consideration. Interviews will be held soon after.

Contact information: Prof. Dr. Dieter Ebert, Universität Basel, Zoologisches Institut, Vesalgasse 1, 4051 Basel, Switzerland, Email: dieter.ebert@unibas.ch Tel.(Sekretariat) +41-(0)61-267 03 60; Fax +41-(0)61-267 03 62. http://evolution.unibas.ch/ dieter.ebert@unibas.ch dieter.ebert@unibas.ch

## UBritishColumbia Marine Protist Diversity

Institute: Centre for Microbial Diversity and Evolution, Departments of Zoology & Botany, University of British Columbia, Vancouver, BC, Canada.

Subject: Biodiversity, evolution and single cell barcoding of marine microeukaryotes.

Number of Postdoctoral Research Positions: Two positions are available.

Tasks: The research post-docs will examine the diversity of several groups of marine microeukaryotes (including excavates, chromalveolates, rhizarians and meiofaunal animals) from global marine samples using molecular markers. Selected markers (barcodes) will be developed from available culture collections and compared with sequence diversity from natural marine samples. The PDFs will also participate in development of protocols for high throughput sequencing of barcode genes from single cells linked to microscopy. The PDFs will be part of the Centre for Microbial Diversity and Evolution at UBC (www.cmde.science.ubc.ca/) as well as the International Barcode of Life initiative (www.dnabarcoding.org/). The following UBC laboratories will support and supervise one PDF each; however, collaborative work between the two labs is expected.

Laboratory webpages: The Leander Lab (www.botany.ubc.ca/bleander/) The Keeling Lab (www.botany.ubc.ca/keeling/)

Required skills: The successful candidates will have completed a PhD with a focus on barcoding, microbial biodiversity, protist molecular evolution/systematics, or a relevant field. The candidates must have a strong record of productivity, skills in molecular biology and analysis of sequence data. Skills in microscopy and background knowledge of marine biology and protist diversity are also highly desirable.

Starting date and duration: The appointments may begin as early as Sept. 2009. The appointments will be for one year initially, with continuation to four years depending on performance.

Application deadline: March 31, 2009.

Contact: Applicants should send a letter of application, current curriculm vitae, and contact information of two references to both Patrick Keeling and Brian Leander: bleander@interchange.ubc.ca and pkeeling@interchange.ubc.ca.

Brian S. Leander Associate Professor Departments of Zoology and Botany University of British Columbia #3529-6270 University Blvd. Vancouver, BC V6T 1Z4 CANADA

Web: http://www3.botany.ubc.ca/bleander/index.html Email: bleander@interchange.ubc.ca Tel: 604 822-2474 (office), 604 822-4892 (lab) Fax: 604 822-6089

bleander@interchange.ubc.ca bleander@interchange.ubc.ca

## UCaliforniaBerkeley SexChromosomes

UC Berkeley, Evolutionary genomics

A Postdoctoral position is available in the laboratory of Doris Bachtrog. Research in the lab combines comparative, computational and functional genomics approaches with evolutionary theory and modeling to study evolutionary and functional aspects of sex chromosome differentiation in Drosophila to address questions including: (1) How and why do Y chromosomes degenerate? (2) How does genetically inactive heterochromatin form on an evolving Y? (3) How does intragenomic conflict between the sexes shape the functional divergence of sex chromosomes? (4) How is dosage compensation acquired on an evolving X?

Funds are available to support this position for up to three years. The position is immediately available and the search continues until the position is filled.

To apply, please submit by email a CV, a brief description of research interests (no more than one page), and the names and contact information for two references to Doris Bachtrog (dbachtrog@berkeley.edu)

For further information about our research program, please visit our website and the departmental website:

http://ib.berkeley.edu/labs/bachtrog/ http://fisher.berkeley.edu/cteg/index.html http://ib.berkeley.edu/ Doris Bachtrog University of California, Berkeley Department of Integrative Biology Center for Theoretical Evolutionary Genomics Berkeley, CA 94720-3140 phone: (510)-325-9547

Doris Bachtrog <dbachtrog@ucsd.edu>

## UFrankfurt ModelSelection

The Biodiversity and Climate Research Centre (BiK-F) has recently been founded by the Senckenberg Gesellschaft für Naturforschung, the Goethe-Universität Frankfurt am Main, and additional partners. It is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The Project Area A “Evolution and Climate” invites applications for the position of a Post-Doc Position âModel Selectionâ PG A1 (Ref. #A21) BAT IIa

The applicant will be responsible to infer the relationship between major climatic events and cladogenesis of selected taxa. Phylogenetic hypotheses will be tested by model selection methods for a correlation between climatic changes and speciation/radiation events. Participation in university teaching is possible, while the acquisition of external research funding is highly desired.

The applicant should hold an earned Ph.D. in biology, with a strong background in statistical phylogenetics. She or he should already have experience with phylogenetic inference and should be interested in linking evolutionary and climate change issues. Practical experience in molecular work is desired, but not mandatory. Applicants should have a strong publication record. Very good written and oral English language skills, willingness to learn at least basic German and interest in joining a multidisciplinary research team are required, as well as proven organizing abilities. Salary and benefits are according to a public service position in Germany (BAT IIa).

The Research Centre BiK-F advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. The contract shall start as soon as possible and will be restricted to 24 months. Review of the application starts on February 1st 2009 and will continue until the position is filled. The duty station will be Frankfurt am Main, Germany.

Please send your application by mail or e-mail, including a detailed CV, 3 references, a list of publications and up to five selected re/e-prints to Prof. Dr. Dr.

h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de. For enquiries about the position and the contract conditions please write to Prof. Dr. B. Stribrny (E-mail: bernhard.stribrny@senckenberg.de) and for scientific enquiries to Prof. Dr. Annette Klussmann-Kolb (E-mail: Klussmann-Kolb@bio.uni-frankfurt.de) or PD Dr. M. Pfenninger (E-mail: pfenninger@bio.uni-frankfurt.de).

Markus Pfenninger <Pfenninger@bio.uni-frankfurt.de>

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## UGeneva PopulationGenomics

Post-doc positions on Population Genomics in Geneva

One or more post-doc positions are available starting October 2009 in the group of Manolis Dermitzakis. Prof. Dermitzakis (currently at the Sanger Institute in Cambridge) will be relocating and establishing a group at the Department of Genetic Medicine and Development at the University of Geneva Medical School in Switzerland. The main interests of the group are: (i) population genomics of human gene expression using both array and RNA sequence data in large samples (i) whole-genome and targeted resequencing of human population samples to study the effect of common and rare variants on complex traits and disease (i) quantitative genetics of cellular phenotypes. The Department is highly interactive with many groups working on human genomics. Tthe group will have close collaborations and links with the groups of Stylianos Antonarakis, Evgeny Zdobnov as well as colleagues from cell biology. Additional close collaborators are: Alexandre Reymond, Henrik Kaessmann, Sven Bergman and Jacqui Beckman in Lausanne and Laurent Excoffier in Bern.

The positions will be funded by an endowment from the Louis-Jeantet Foundation and/or pending grant applications.

Interested applicants should send their CV and statement of research interests to md4@sanger.ac.uk

Official announcement for the positions will follow later in the year.

Some recent work from our group is listed below:

Dimas, A., B.E. Stranger, C. Beazley, C. Ingle, R. Finn, M. Ritchie, M. Dunning, P. Deloukas, S. Tavare and E.T. Dermitzakis. 2008. Exploring epistatic effects between regulatory and protein-coding variation. PLoS Genetics e1000244

Dermitzakis, E.T. 2008. From gene expression to disease risk. Nature Genetics 40: 492-493

Stranger, B.E., A. Nica, A. Dimas, M.S. Forrest, C. Beazley, M. Dunning, C.P. Bird, C.E. Ingle, D. Koller, S. Tavaré, P. Deloukas and E.T. Dermitzakis. 2007. Population genomics of human gene expression. Nature Genetics 39: 1217-1224.

Stranger, B.E., M.S. Forrest, M. Dunning, C.E. Ingle, C. Beazley, N. Thorne, R. Redon, C. Lee, C. Tyler-Smith, N. Carter, S.W. Scherer, S. Tavaré, P. Deloukas, M.E. Hurles and E.T. Dermitzakis. 2007. Relative impact of nucleotide and copy number variation on gene expression phenotypes. Science 315: 848-853.

**PLEASE NOTE: TELEPHONE NUMBER CHANGE**

Emmanouil (Manolis) Dermitzakis, PhD Senior Investigator Population and Comparative Genomics The Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton, Cambridge CB10 1HH UK e-mail: md4@sanger.ac.uk Tel: +44 (0)1223 492322 Fax: +44 (0)1223 494919 URL: http://www.sanger.ac.uk/Teams/Team16/ < http://www.sanger.ac.uk/Teams/Team16/ >

md4@sanger.ac.uk md4@sanger.ac.uk

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## UJyvaskyla SpeciesInteractions PhDandPostdoc

We are welcoming applicants for the postdoctoral researcher to join our international Evolutionary ecology of the species interactions -group to work on the theme Maintenance of color polymorphism and evolution of reproductive isolation. As a model species we use the wood tiger moth (Parasemia plantaginis). This species has a wide geographical distribution and it exhibits color polymorphism locally and geographically. Some main goals of the project are 1) to understand relative importance of between- versus within-population processes for color polymorphism and 2) genomic analyses to elucidate genetics of color and associated phenotypic traits. Another main themes in the project are evolution of predator-prey interactions; evolution of aposematism and mimicry.

Postdoc is available at the University of Jyvaskyla, Finland. www.jyu.fi Other main themes in our research group are predator-prey interactions and evolution of warning signals and evolution of pathogen virulence.

Applicants should have a PhD degree in a relevant biological discipline, and a strong interest in evolutionary biology. We expect strong experience with molecular ecology methods. You will join the Centre of Excellence in Evolutionary Research at University of Jyvaskyla (http://www.jyu.fi/science/-laitokset/bioenv/-evoluutiotutkimus/en/).

The position will be available for 1 year initially, with the possibility of a 1-4 year extension. Applications should be sent by 31st January 2009 (to carita.a.lindstedt@jyu.fi), and be accompanied by a short research statement, a CV and the names of 3 referees. The starting day is flexible but would ideally start no later than April 2009.

Apply by sending (1) a signed letter of application (no more than one A4 page), including the motivation for your application (2) a CV and (3) two reference names with contact details (phone number and e-mail address) by February 15th 2009, to

Informal enquiries welcome

We are welcoming applicants for the PhD student to join our international Evolutionary ecology of the species interactions -group to work on the theme Maintenance of color polymorphism and evolution of reproductive isolation. As a model species we use the wood tiger moth (Parasemia plantaginis). This species has a wide geographical distribution and it exhibits color polymorphism locally and geographically. Some main goals of the project are 1) to understand relative importance of between- versus within-population processes for color polymorphism and 2) genomic analyses to elucidate genetics of color and associated phenotypic traits. Another main themes in the project are evolution of predator-prey interactions; evolution of aposematism and mimicry.

PhD-position is available at the University of Jyvaskyla, Finland. www.jyu.fi Other main themes in our research group are predator-prey interactions and evolution of warning signals and evolution of pathogen virulence.

Applicants should have a McS -degree in a relevant biological discipline, and a strong interest in evolutionary biology. You will join the Centre of Excellence in Evolutionary Research at University of Jyvaskyla (http://www.jyu.fi/science/-laitokset/bioenv/-evoluutiotutkimus/en/).

The position will be available for 4 years. Applications should be sent by February 15th 2009 (to carita.a.lindstedt@jyu.fi), and be accompanied by a signed letter of application (no more than one A4 page), including the motivation for your application, short research statement, a CV and the names of 3 referees. The starting day is flexible but would ideally start no later than April 2009.

Informal enquiries welcome

Johanna Mappes <mappes@bytl.jyu.fi>

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## UMaryland EvolutionaryGenomics

POST-DOC POSITION in EVOLUTIONARY GENOMICS

A POSTDOCTORAL FELLOW position is open in Joana Silva$^1$s group at the Institute for Genome Sciences (http://www.igs.umaryland.edu/), at the University of Maryland School of Medicine, for an enthusiastic, highly motivated individual interested in studying eukaryotic genome evolution. In particular, this project aims to understand the molecular mechanisms that underlie the evolution of genome nucleotide composition, and uses the genus Plasmodium as a system. The project includes both laboratory and molecular evolution analysis components, and is tightly integrated with the genome sequence and annotation information available for several Plasmodium species.

The ideal candidate will have a doctoral degree in Molecular Biology, Genetics, Evolution, or a related field, and will be thoroughly familiar with the fields of molecular evolution and phylogenetics. The candidate must have extensive experience with traditional molecular biology techniques (including DNA isolation, PCR, cloning, primer design) and molecular evolution and phylogeny estimation software (e.g., PAML, HyPhy, DnaSP, PAUP*, MrBayes, BEAST). This position is ideally suited for someone capable of integrating traditional (single-gene) approaches with genomics data and methodologies, and of making use of state-of-the-art bioinformatics and sequencing technology infrastructures. Programming skills in languages such as C/C++ and Perl, and experience with relational databases and SQL, are a plus. A publication record in evolutionary biology is a must. The initial appointment is for two years and is available immediately.

The successful candidate will benefit from a community of very interactive research labs, a large group of bioinformatics programmers and a variety of laboratory, sequencing and computational resources available in a world class genomics institute, that supports basic, genomic and translational research. To apply, please send a CV, a statement of research interests (include reason for applying to this position; 2 pages maximum) and contact information for three references to IGS-jobs@som.umaryland.edu <mailto:IGS-jobs@som.umaryland.edu> . Additional inquiries about the position can be sent to Joana Silva: jcsilva@som.umaryland.edu.

AA/EOE/ADA

jcsilva@som.umaryland.edu jcsilva@som.umaryland.edu

## UOviedo EvolutionaryGenetics

Post-doc Juan de la Cierva in Evolutionary Genetics

Post-doc researchers interested in seed dispersal ecology and genetics may apply to a Juan de la Cierva Programme fellowship for developing a project entitled Effects of landscape configuration on individual dispersal kernels of bird-dispersed trees in the Cantabrian woodlands: ecological vs genetic approach. The Juan de la Cierva Programme funds three-year contracts with a gross salary of 25,250 euros per year.

The successful candidate will lead his/her project and will integrate in a multidisciplinary research team composed of two collaborative labs: the Plant-Animal Interactions Lab at the University of Oviedo (Daniel García, www.uniovi.es/danielgarcia), which will act as host lab for the candidate, and the Unit of Forest Genetics and Ecophysiology at CIFOR-INIA (Santiago C. González-Martínez, www.plantevol.arrakis.es/-scgonzalez.htm). Research work will be funded by current projects from both labs and future complementary applications made by the candidate.

The aim of the project is to model seed dispersal kernels in Crataegus monogyna and Ilex aquifolium from estimates of dispersal distance obtained from the analysis of individual genotypes of seeds and trees, and to relate the shape of kernels to the configuration of the fragmented landscape in the Cantabrian mountains. The work will require field sampling, intensive analysis of populations genetic structure using molecular tools (isolation and characterization of loci microsatellite for C. monogyna and I. aquifolium, genotyping of mother focal plants and seeds), and kernel modelling using both ecological (inverse modelling) and genetic (paternity/parentage and indirect) methods.

The call and the candidate requirements are published in the web page of the Spanish Ministry of Science (see below). In short, the candidate should have a PhD degree obtained after September, the first, 2005, and at least a 12-month post-doc experience if the PhD degree was obtained between September the first, 2005 and 31st of August, 2007. Selection of candidates is based on their own scientific quality (publication in highly-scored international journals, background in Population Genetics and Ecology, and training in molecular techniques) and on the quality of the project and the hosting lab.

The application should be performed by the hosting Institution, through the official web of the Spanish Ministry, after a previous selection of the candidates made by the research supervisors (Daniel García and Santiago C. González-Martínez).

For a pre-selection of candidates, they should send an e-mail letter of interest, their CVs, and the e-mail of two colleagues for recommendation references to Daniel García (danielgarcia@uniovi.es) and Santiago C. González-Martínez (santiago@inia.es), before the 31st of January, 2009.

Instructions: Instructions, documents and FAQs are in http://web.micinn.es/contenido.asp?menu1=-1&menu2=3&dir=03_Plan_IDI/00-LIAs/-00@LIARRHH/02-Contratacion/01-JCierva

Daniel García Depto. de Biología de Organismos y Sistemas Universidad de Oviedo C/ Rodrigo Uría s/n, Oviedo 33071, Spain danielgarcia@uniovi.es www.uniovi.es/danielgarcia fax: 34 985 104866

AND

Santiago C. González-Martínez Center of Forest Research, INIA Carretera de La Coruña km 7.5, 28040 Madrid, Spain Ph +34 913471499 Fax +34 913572293

e-mail: santiago.c.gonzalez.martinez(nosp@m)gmail.com web: www.plantevol.arrakis.es/-scgonzalez.htm Find me in Skype: santiago.c.gonzalez.martinez Have a look to Evoltree NoE at www.evoltree.eu santiago.c.gonzalez.martinez@gmail.com

## Uppsala EvolutionComplexTraits

Postdoc: Genetics and Evolution of Complex Traits

We are looking for Post-Docs to join our young and growing group working in Computational Genetics. We provide a supportive environment, giving you the opportunity to develop your career to the next level. We are looking for enthusiastic and motivated individuals and strongly believe in an interdisciplinary approach, so we encourage applicants with a non-standard background to apply. We are based in Uppsala, Sweden at the Swedish University of Agricultural Sciences and also have links with Uppsala University. Initially the appointments will be for one year, with the possibility of extension for up to four years.

An increased understanding of the genetics and evolution of complex traits is not only of fundamental scientific interest but is of paramount importance for future developments in most areas of biology, including human medicine and agriculture. We aim to provide new insights into complex-trait genetics by using and developing new computational methods in the areas of mathematical modelling, statistical analysis and simulation. We also conduct empirical work where we establish our own experimental animal populations and characterize these phenotypically and genetically using e.g. genome-resequencing and high-density genotyping - all with an aim to validate and replicate important findings.

A successful applicant should have relevant scientific education (Ph.D. degree or similar) and an interest in quantitative, population and/or evolutionary genetics. A strong mathematical / statistical background and programming experience is an advantage.

Aside from work, you will have the chance to get to know Uppsala, which is a pretty university town, notable for its castle and cathedral. It is 40 minutes by train from Stockholm. We get some snow in winter and beautiful long summer days.

If you are interested in joining our team or have more questions about us or our work, please contact Örjan Carlborg (Orjan.Carlborg@hgen.slu.se)

We look forward to hearing from you!

Weblinks: http://www.computationalgenetics.se http://www.slu.se http://www.lcb.uu.se http://-/en.wikipedia.org/wiki/Uppsala Selected recent publications: * Carlborg, Ö. and Haley, C. Epistasis: too often neglected in complex traits studies? Nature Reviews Genetics 2004 5: 618-625. * Carlborg, Ö., Jacobsson, L., Åhgren, P., Siegel, P., Andersson, L. Epistatsis and the release of genetic variation during long-term selection. Nature Genetics 2006 38:418-20. * Gjuvsland, A., Hayes, B., Plahte, E., Omholt, S., Carlborg, Ö. Statistical epistasis is a generic feature of gene regulatory networks. Genetics 2007 175:.411-420. * Le Rouzic, A., Siegel, P. and Carlborg, Ö. Phenotypic Evolution from Genetic Polymorphisms in Radial Network Architectures. BMC Biology 2007, 5:50. * Alvarez-Castro, J., le Rouzic, A. and Carlborg, Ö. How to perform meaningful estimates of genetic effects. PLOS Genetics 2008 May 2; 4(5):e1000062 * Le Rouzic, A., Alvarez-Castro, J. and Carlborg, Ö. Dissection of the genetic architecture of body weight in chicken reveals the impact of epistasis on domestication traits. Genetics 2008 179:1591-1599.

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Orjan.Carlborg@hgen.slu.se Orjan.Carlborg@hgen.slu.se

## UTennessee EvolutionaryTheory

Postdoctoral Fellowship Opportunities with NIMBioS

The National Institute for Mathematical and Biological Synthesis (NIMBioS) provides an opportunity for postdoctoral scholarship at the interface between mathematics and biological science at the University of Tennessee. Highest priority will be given to those with explicit plans to develop their ability to effectively carry on research across these fields. We are particularly interested in requests to support research that integrates diverse fields, requires synthesis at multiple scales, and/or makes use of or requires development of new mathematical/computational approaches. NIMBioS Postdoctoral Fellows are chosen based upon indications that the applicant's research plans are consistent with the mission of NIMBioS, the applicant has the demonstrated ability to carry out the proposed research, and the opportunities provided through NIM-

BioS will enhance the capacity for the research to be completed in an efficient and timely manner. For additional information on NIMBioS, visit www.nimbios.org < http://www.nimbios.org/ > . Support: annual stipend of $51,000, full University of Tennessee employee fringe benefits, and an annual travel allowance of $2,000. To Apply: Submit a brief project description, references, and CV following the guidelines available at http://www.nimbios.org/postdocs/postdoc.html to Dr. Chris Welsh at cwelsh@utk.edu. Deadline: NIMBioS postdoctoral requests for support are reviewed twice a year and the selected researchers are offered positions at NIMBioS where they conduct research that is mostly self-directed. The deadline for activities beginning 1 September 2009 is 1 March 2009.

Dr. Christopher Welsh Deputy Director, NIMBioS 569 Dabney Hall Knoxville, TN 37996 (865)974-9334

cwelsh@utk.edu

“Welsh, Christopher J E” <cwelsh@utk.edu>

## UToronto BehaviouralEvolution

The Rowe and Sokolowski labs are seeking a Postdoctoral Fellow to join an investigation of the pleiotropic effects of the rover/sitter foraging gene on the life history and mating behaviour of Drosophila melanogaster. A successful candidate will have a Ph.D. in evolutionary biology, evolutionary genetics, behaviour genetics or a related field. Expertise in manipulation of Drosophila is beneficial but not essential. Duration of appointment is two years, with the second year contingent upon performance during first year.

This is a joint project that would involve research in the labs of Profs. Locke Rowe and Marla Sokolowski, within the Department of Ecology and Evolutionary Biology at the University of Toronto.

Toronto is a vibrant, multicultural city on the shore of Lake Ontario, with rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life. The EEB department is home to an interactive, collegial group of ecologists, geneticists, and evolutionary biologists, and currently supports a strong group of Post-Doctoral Fellows with diverse research interests.

To apply, please submit by email a CV, a statement of past and current research interests (no more than one page), and the names and contact information for two references to Penelope Gorton (p.gorton@utoronto.ca). Deadline for applying is March 30, 2009.

For further information about our research programs, please visit our websites and the departmental website:

http://labs.eeb.utoronto.ca/rowe/ http://www.erin.utoronto.ca/~w3forage/ http://www.eeb.utoronto.ca/ Contact: Locke Rowe, 416-978-1486, locke.rowe@utoronto.ca Marla Sokolowski, 905-828-5326, marla.sokolowski@utoronto.ca

John Stinchcombe <john.stinchcombe@utoronto.ca>

## UToronto EvolutionaryBiol

The Department of Ecology and Evolutionary Biology < www.eeb.utoronto.ca > at the University of Toronto invites applications for Departmental Postdoctoral Fellowships in the areas of Ecology and Evolutionary Biology, broadly defined. One position is available this year, and we expect that another will become available next year through an ongoing EEB Post-Doctoral Fellowship Program. Positions may continue for two years, subject to review after one year, and can begin as early as July 1, 2009. The salary is $40,000 Canadian per year, with research expenses covered by the Post-Doctoral Advisor.

The Fellow will be a fully participating member in the Department. Candidates must identify and communicate with a potential advisor (or advisors) in advance of the application process. All full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors (see < www.eeb.utoronto.ca/postdoc/ > for a list of potential supervisors). Opportunities for teaching in an upper level course may be available.

To apply, applicants should first contact and obtain the agreement of a faculty advisor (or co-advisors). Afterwards, applicants should submit a cover letter clearly indicating the proposed faculty advisor(s), a curriculum vitae, copies of 2 publications, and a short (1-3 pages) description of past research accomplishments and future research plans. Applicants should include names and e-mail addresses for two potential referees. Applicants should also indicate the date they will be available to begin the position. All application materials must be submitted as PDF’s in a single email to: Elizabeth Rentzelos <chairsec.eeb@utoronto.ca>.

For more information about the Department, contact your potential supervisor. Queries regarding the fellowship program should be directed to Demetrios Voudouris <demetrios.voudouris@utoronto.ca> Review of applications will begin on March 20, 2009.

Toronto is a vibrant, multicultural city on the shore of Lake Ontario, with rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life. The EEB department is home to an interactive, collegial group of ecologists, geneticists, and evolutionary biologists, and currently supports a strong group of Post-Doctoral Fellows with diverse research interests.

–

John Stinchcombe Department of Ecology and Evolutionary Biology University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

http://labs.eeb.utoronto.ca/stinchcombe/
john.stinchcombe@utoronto.ca

## Vienna EvolutionGeneExpression

A 2-year postdoctoral position is available to work on the evolution of gene expression in Drosophila

Background: The recent technological breakthrough of massively parallel sequencing has the potential to replace currently existing methods for expression profiling. In addition to intraspecific transcriptome analyses, this method also allows the comparison of gene expression between species.

The successful candidate will serve a central role in bridging the gap between experimentalists generating expression data and functional biologists performing tests on interesting obtained from the expression analyses. We are searching for an individual with strong bioinformatic sills, a solid background in biology, and excellent communication aptitude.

The post is based at the Institute of Population Genetics at the VUW, Vienna. The Vienna Research Area has a strong network of research groups interested in population genetics, statistical genetics and bioinformatics providing an excellent scientific environment (e.g. N. Barton, R. Bürger, U. Diekmann A. Futschik, A. v. Haeseler, J. Hermisson, I. Hofacker, C. Kosiol, P. Schuster, K. Sigmund, C. Vogl).

The position is immediately available and the search continues until the position is filled.

Applications should be sent to C. Schlötterer (christian.schloetterer@vu-wien.ac.at), including the names and emails of two academic references and a brief description of the research interests.

Christian Schlötterer Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390
http://i122server.vu-wien.ac.at/pop/index.html

# WorkshopsCourses

## Banff MathematicalEvolutionaryBiol May10-17

BIRS International Summer School on The Mathematics of Invasions in Ecology and Evolutionary Biology.

Date: May 10-17, 2009

Location: Banff International Research Station

Website: www.mast.queensu.ca/ ˜ summerschool/index.htm The summer school is aimed at graduate students in applied mathematics, biology and epidemiology, who wish to learn important mathematical techniques for modeling biological invasions. The emphasis will be on practical, hands-on experience for building and analyzing models, coupled with lectures on key techniques. Examples will be drawn from a variety of areas including ecological invasions of so-called 'pest' species, and the emergence of novel pathogens like SARS and avian influenza. A major focus will be on techniques for incorporating evolutionary change in the mathematical models.

Each student will be expected to develop and analyze a model of their choosing during the period of the summer school, in collaboration with a small group of other students.

Organizers: Troy Day (Queen's), Fred Brauer (UBC), James Watmough (New Brunswick), Jianhong Wu (York), Rachel Bennett (Queen's)

Please visit the course website for more information and to apply.

Troy Day Departments of Mathematics & Biology Jeffery Hall Queen's University Kingston, ON, K7L 3N6, Canada Phone: 613-533-2431 Mobile: 613-217-2431 Fax: 613-533-2964 tday@mast.queensu.ca http://www.mast.queensu.ca/˜tday/ troy.day@mac.com

## BodegaBay AppliedPhylogenetics Mar7-13

Note: Due to the holiday season we have extended the deadline for applications. The new deadline is Friday 9 January. Students will be notified via e-mail by 12 January of acceptance.

UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California

March 7-13, 2009

Sponsored by the

University of California, Davis and Bodega Marine Laboratory (additional financial support provided by the University of Rochester, and NESCent)

Introduction. Phylogenetic methods have revolutionized modern systematics and become indispensable tools in evolution, ecology and comparative biology, playing an increasingly important role in analyses of biological data at levels of organization ranging from molecules to ecological communities. The construction of phylogenetic trees is becoming a methodology that is well-defined, with broad agreement on the central issues and questions. A nearly standard set of topics is now taught as part of the curriculum at many colleges and universities. On the other hand, application of phylogenetic methods to interesting problems outside of systematics is an area of special excitement, innovation, and controversy, and perspectives vary widely.

In March, 2009, for the tenth year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic tools are being applied. We cover a range of topics in biogeography, ecology, conservation biology, phylogenomics, functional morphology, macroevolution, speciation, and character evolution. The course starts with recent advances in phylogenetic methodology, and then focuses on methods and tools that can be brought to bear on these "applied" issues in the context of a given phylogeny.

The course will be held entirely at the Bodega Marine Lab on the Northern California coast, which has extensive computing resources and on-site housing. The course format will involve equal parts of lecture, discussion, and training in software and internet tools. One afternoon during the week will be left free for field trips to local natural areas.

Specific Topics to be Covered

* Finding, evaluating and interpreting phylogenetic trees; phylogenetic databases * Recent advances in tree reconstruction: Bayesian inference; stochastic optimization strategies; divide-and-conquer methods; Garli; gene-tree species tree resolution * Analysis of character evolution–theory: parsimony, likelihood and

Bayesian approaches; null models and statistical testing * Analysis of character evolution–form and function of complex character systems * Phylogeography; coalescent methods for inferring migration rates and patterns * Phylogenetic comparative methods * Phylogenetic perspectives on biodiversity and conservation biology * Data mining of sequence databases for phylogenetic analysis * Estimation of divergence times from sequence data, analysis of diversification rates * Ecological Phylogenetics, biogeography

Instructors for the main workshop.

* Peter Wainwright * Brad Shaffer * Brian Moore * Michael Donoghue * Bruce Rannala * Jonathan Eisen * Rich Glor * Justen Whittall * Greg Pauly * Samantha Price * Stephen Smith * Phil Spinks * Robert Thomson

plus guest lecturers!!

Prerequisites. Students should have some familiarity with phylogenetic methods through previous coursework. Some experience with PAUP, PHYLIP, or other programs for phylogeny reconstruction will be assumed.

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is $450. This includes room and board at BML for duration of the course (arriving March 7, leaving March 14) and transportation from Davis to BML.

Application Deadline. Applications are due by January 9, 2009. Please send a completed application form (available at http://bodegaphylo.wikispot.org/2009_Course_Announcement) and one letter of recommendation from your major advisor. Applications should be sent via email as PDFs to pqspinks@ucdavis.edu. Sorry, but due to the limited size of the class, postdocs and faculty are discouraged from applying. Students will be notified via e-mail by 12 January of acceptance.

Send all application materials to

Dr. Phillip Q. Spinks Department of Evolution and Ecology 2320 Storer Hall University of California Davis Davis, CA 95616 email:pqspinks@ucdavis.edu

pqspinks@ucdavis.edu pqspinks@ucdavis.edu

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## DTU-Aqua Denmark ThermalAdaptation Jun15-19

Workshop announcement:“Thermal adaptation in aquatic ectotherms”, Denmark, June 15-19 2009.

Dear all

We would like to announce the workshop “Thermal adaptation in aquatic ectotherms” to be held in Denmark from the 15th to the 19th of June 2009. The workshop is funded by the ThermAdapt network under the European Science Foundation and organized by the Section for Population Genetics, National Institute of Aquatic Resources, Technical University of Denmark. The workshop will be held at the Mols Laboratory, a field station located in a national park near Aarhus.

Background

Aquatic organisms are expected to be affected by future climate changes, but knowledge about their response to these challenges is generally lacking. Understanding thermal adaptation requires insights from cellular through organism to population levels of biological organization. In this workshop, we intend to bring together researchers from population genetics and molecular and evolutionary physiology in a cross-disciplinary environment to foster exchange of ideas and improve our understanding of responses to thermal changes in aquatic organisms and populations. The workshop will be organized as sessions with presentations by all workshop participants, leaving good time for discussions both during and between sessions.

Invited speakers include

Craig Primmer, University of Turku, Finland

Hans Otto Pörtner, AWI, Bremerhaven, Germany

Luc De Meester, Katholieke Universiteit Leuven, Belgium

Patricia Schulte, University of British Columbia, Canada

Thorsten Reusch, Leibniz-Institut fuer Meereswissenschaften, Kiel, Germany

Attendance

Attendance is limited to 35 participants. Accommodation and meals are funded by the ThermAdapt network. Please send an email to Jakob Hemmer-Hansen (jhh@aqua.dtu.dk) with a short description of your area of research if you are interested in participating in the workshop.

Relevant information

Getting there:

The Mols field station is located just 15 minutes from Aarhus Airport (Tirstrup) and 45 minutes from the city of Aarhus. Transport to/from trains and planes will be arranged.

ThermAdapt network:

http:// www.esf.org/ activities/ research-networking-programmes/ life-earth-and-environmental-sciences-lesc/ current-esf-research-networking-programmes-in-life-earth-and-environmental-sciences/ thermal-adaptation-in-ectotherms-linking-life-history-physiology-behaviour-and-genetics-thermadapt.html

Section for Population Genetics, Technical University of Denmark:

http://www.aqua.dtu.dk/English/-Recreational_fisheries/Population_genetic_group.aspx

Mols field station:

http://www.naturhistoriskmuseum.dk/molslab/

Organizers

Jakob Hemmer-Hansen Dorte Bekkevold Thomas Damm Als Einar Eg Nielsen

Michael Møller Hansen Section for Population Genetics National Institute of Aquatic Resources (DTU Aqua) Technical University of Denmark Vejlsoevej 39 DK-8600 Silkeborg Denmark

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## GulbenkianPT GTPBcourses Mar3-6

Dear Evoldir members

The Gulbenkian Training Programme in Bioinformatics (GTPB) has now issued its list of courses for 2009.

At least two of them (MEPA and MMPG) are of yinterest to the evoldir community

MEPA09 - Molecular Evolution, Phylogenetics and Adaptation - March 3-6 IB09- Introductory Bioinformatics ENSGEN09 - Browsing on genomes with ENSEMBL, Mining with BIOMART ENSAPI09 - Compara API, Programming workshop MDAGB09 - Microarray Data Analysis IPN09 - Interactions, Pathways and Networks BFB09 - Biostatistical Foundation in Bioinformatics WPAT09 - Workflows and Programatically Accessible Tools MLB09 - Machine Learning in Bioinformatics MMPG09 -Molecular Markers and Population Genetics TM09 -Translational Medicine MBL09 - Mining Biomedical Literature BPB09 - Bioinformatics using Python for Biologists MDARB09 - Microarray Data Analysis using R and Bioconductor GB09 - Genome Bioinformatics RNAB09 - RNA Bioinformatics BCR09 - Bioinformatics in Cancer Research SB09 - Structural Genomics PDA09 -Proteomics Data Analysis

MEPA09 is scheduled for March 3-6th, applications are about to open

GTPB courses are displayed in our website http://-gtpb.igc.gulbenkian.pt where information is regularly updated.

I will send a message to EVOLDIR when applications open for MEPA09 and MMPG09, but the announcement of our 2009 program may also be of interest to the community.

Thanks Pedro

Pedro Fernandes GTPB Coordinator Instituto Gulbenkian de Ciência Apartado 14 2781 OEIRAS PORTUGAL http://gtpb.igc.gulbenkian.pt Pedro Fernandes <pfern@igc.gulbenkian.pt>

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## HinxtonUK AdvancedDrosophilaGeneticsGenomics Aug9-23

Wellcome Trust Advanced Course in Drosophila Genetics and Genomics

9-23 August 2009

Wellcome Trust Genome Campus, Hinxton UK

This will be an advanced, discussion-based course on the genetics and genomics of Drosophila. The intended audience is postdoctoral and graduate students now working in a fly lab, or students who have recently completed a PhD in another field and are moving into Drosophila research for their postdoctoral studies. However, students with other backgrounds will be considered on their merits.

Topics covered will include: - advanced genetics - developmental genetics - genetic analysis of sex determination - the Drosophila genome(s) - databases and resources - evolutionary genetics - neurogenetics - genetic analysis of complex characters - genetic screens - mosaics and P-element systems - meiosis

Course organisers: Michael Ashburner (University of Cambridge, UK) Scott Hawley (Stowers Institute for Medical Research, USA) Casey Bergman (University of Manchester, UK)

Guest lecturers: Steve Russell (University of Cambridge, UK) Ruth Lehmann (New York University School of Medicine, USA) Daniel St Johnston (The Gurdon Institute, Cambridge, UK), Kent Golic (University of Utah, USA) Brian Charlesworth (University of Edinburgh, UK), Trudy Mackay (North Carolina State University, USA), Leslie Vosshall (The Rockefeller University, USA) Bruce Baker (Stanford University, USA).

Prerequisites: Applicants should be postdoctoral scientists or senior PhD students actively engaged in Drosophila research. The course is subsidised by the Wellcome Trust for scientists based at academic institutions anywhere in the world.

Cost: This is a residential course, without exception, and although the course is subsidised by the Wellcome Trust for academics there is a charge of £1400 towards board and lodging (sharing a twin room with en suite bathroom, subject to availability), or £1800 (private room and en suite) for academic applicants.The fee for commercial (non- academic) applicants is £3600.

Bursaries: Limited bursaries are available for academics (50 per cent of fee) and are subject to open competition.

Applications: Applicants will be required to complete an application form containing their CV together with a 300-word outline of the relevance of the course to their research. Please note that documentation supporting their application will be required from the applicant's supervisor/ head of department.

Application deadline: 10 April 2009

For full details please visit: http://www.wellcome.ac.uk/Professional-resources/Courses-and-conferences/Advanced-Courses/Courses/WTX027650.htm casey.bergman@manchester.ac.uk casey.bergman@manchester.ac.uk

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## KelloggBiol TheoPopBiol June

Mathematics and Field Ecology Summer Program

**Scholarship Support Available**

15 June - 31 July for Undergraduate and Graduate Students at Kellogg Biological Station, Michigan State University http://www.kbs.msu.edu/ELME Kellogg Biological Station (KBS) will once again host the summer program known as ELME, Enhancing Linkages between Mathematics and Ecology. ELME is a course-work based research experience designed for students with an interest in applying mathematics to questions in ecology and evolution. The program is designed for students both with and without formal training in mathematics. Participants in the full program take 3 one-week math courses on topics that are relevant to ecology/evolution and then apply these tools in a four-week field ecology/evolution course. Students can enroll in a subset of the ELME courses if that better fits their needs and schedules.

Mathematics 1-week courses:

Introduction to Theoretical Population Biology - MTH 490.431 Robin E. Snyder, Case Western Reserve University June 15 - June 19

Game Theory and Adaptive Dynamcis- MTH 490.432 Christopher Klausmeier, Kellogg Biological Station, MSU June 22 - June 26

Maximum Likelihood Analysis in Ecology - MTH 490.433 Don Schoolmaster, Kellogg Biological Station, MSU June 29 - July 3

Ecology 4-week course:

Field Ecology and Evolution - ZOL/PLB 440 Gary Mittelbach, and Jen Lau, Kellogg Biological Station, MSU July 6 - July 31

Undergraduate Fellowships ($1500, plus housing, travel, and tuition) are available for students enrolling in the full ELME program. Graduate scholarships are available for tuition and housing. More information about KBS and the ELME program is available at http://www.kbs.msu.edu/ELME. The application deadline for enrollment and scholarships is 2 March 2009.

– Donald R. Schoolmaster Jr. Ph.D. ELME Coordinator Postdoctoral Research Associate Kellogg Biological Station 3700 Gull Lk. Dr. Hickory Corners, MI

schoolm4@msu.edu schoolm4@msu.edu

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## LaFouly Switzerland EvolutionaryBiol Jun20-26

Evolutionary Biology Workshop in the Alps

La Fouly, Switzerland, 20-26 June 2009

This is a graduate course based on a concept developed by Steve Stearns and John Maynard Smith. Target participants are advanced master students and students in the first half of their PhD. Taking place in a beautiful small Alpine village (La Fouly), it will allow you to focus while being able to enjoy the landscape and the Alpine flora. The goals are to develop the following skills:

* developing your scientific ideas through discussions in groups; * thinking critically and expressing oneself clearly; * turning a general idea into a research project; * discovering the many layers of a scientific project: digging deep; * writing a grant proposal and defending it; * interacting with the faculty in an informal setting

It is you, the students, who will be in charge in this course. You will work with *your* ideas, you will decide yourself what the important questions in broadly defined evolutionary biology are, you will choose one, and propose a research project that will address it. The faculty will visit the groups during the discussions to answer your questions and provide coaching and they will give you feedback on your proposal, but they will generally take the back seat. Additionally, the faculty will give informal talks about their research and be available for informal discussion. The language of the course is English.

Faculty: Mark Kirkpatrick (University of Texas, Austin), John Taylor (University of California, Berkeley), Ian Sanders and Tad Kawecki (both University of Lausanne, Switzerland).

Costs: there is no tuition fee; the participants will cover the costs of room and board (approximately CHF 420.-).

For more information see http://www.unil.ch/ee/page63533.html To apply, send a single file (pdf or rtf) containing a short motivation letter, a cv and the name of your scientific advisor to to tadeusz.kawecki@unil.ch, with “Evolution Workshop Application” in the subject field. Deadline March 15.

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lausanne, Switzerland tadeusz.kawecki@unil.ch

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## LakeTahoe InvasiveSpecies Mar19-22

Special Workshop: Synthesizing Ecology and Evolution for the Study of Invasive Species

Organizers: Carol Lee, Kristina Schierenbeck, Robert Holt

We have organized a workshop to promote the integration of ecological and evolutionary perspectives and approaches into the study of invasive species. Our aim is to create a venue in which discussion among the participants would lead to novel synthetic research and papers that reflect the novel syntheses. For example, the integration of population genetics and population dynamics could yield insights into the lag period of invasions, evolutionary responses to novel environments, and range expansions, oscillations, and extinctions. Also, integrating empirical data on ecological factors, such as predation or competition, with genetic factors, such as quantitative genetic variance or the genomic architecture of critical traits, could enhance our understanding of factors that limit invasions, improve the efficacy of predictive models, including those that might aid in biological control. Invasive species provide an ideal testing ground for many basic evolutionary theories, and we hope that this workshop will help expand this potential.

This event will be held March 19-22, 2009 at North Lake Tahoe, California, USA. The workshop will consist of talks by invited speakers (listed below), group discussions, and posters sessions. Conference attendance will be limited to 100, so we recommend registering early!

The workshop will take place during prime ski season at the scenic Granlibakken Conference Center & Lodge, which is nestled between trees, mountains, and Squaw and Alpine Ski Resorts. The Reno-Tahoe International Airport provides ready access to Lake Tahoe, and from a number of major airports.

The all-inclusive meeting package of $799.00 (single-occupancy) or $608.00 (double occupancy) includes conference registration fees; three nights lodging (Thursday, Friday, and Saturday), dinner on Thursday, three meals on Friday and Saturday, and breakfast and lunch on Sunday. Day passes to the conference (conference attendance + lunch) are available at $120 per day or $252 for the entire conference.

We recommend that you plan on arriving a few days early or a stay a few days later if you plan to take advantage of the local skiing, showshoeing, ice-skating, and hiking opportunities. On site amenities include ski lessons and on-site cross country ski trails.

The registration deadline is February 15. You may register at http://www.granlibakken.com < https://silk.csuchico.edu/exchweb/bin/redir.asp?URL=3Dhttp://www.granlibakken.com > . The user name and password are: usda09

If you would like to present a poster, please submit a title to Kristina Schierenbeck (ka.schierenbeck@ars.usda.gov) by March 10.

List of Invited Speakers and Tentative Titles:

Richard Gomulkiewicz, Robert Holt & Scott Nuismer Genetic complexity, adaptation, and invasion in harsh environments

Alex Perkins Effects of evolutionarily labile interspecific interactions on spatial spread dynamics

Judith Miller The fate of neutral mutations arising during invasions

Andrew Kanarek & Colleen Webb Allee effects and invasion success through coupled evolutionary and ecological dynamics

Carol Eunmi Lee, Yuseob Kim & Davorka Gulisija Testing for genetic signatures of selection during independent invasions into novel environments

Marc Kramer Application of climate models to understand and model environmental processes

Andy Suarez, Neil Tsutsui & David Holway Insights into invasion success from comparing the biology of ant invaders in their native and introduced ranges

Kevin Rice The role of trans-generational plasticity (i.e. maternal effects) in biological invasions

George Gilchrist & Raymond Huey Developmental plasticity evolves during biological invasions

Heinz Müller-Schärer Adaptive evolutionary change in an invasive plant: Tracking its evidence

Elizabeth Leger & Erin Espeland Evolution of native plants in response to invaders

George Roderick & Maria Navajas Evidence for evolutionary change in classical biological control and what this says about invasions

Kristina A. Schierenbeck USDA/ARS, Research Leader Exotic & Invasive Weeds Unit 920 Valley Road Reno, Nevada 89512

Work: 775-784-6057 ext. 222 Cell: 530-591-9907

Ka.Schierenbeck@ARS.USDA.GOV

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## Montreal Population Genomics Genetic Epidemiology May19-22

Montreal - May 19-22 2009

www.MontrealSpringSchool.ca

Description:

The main objective of the School is to provide training in rapidly developing disciplines that are becoming increasingly important in health sciences. It includes genetic epidemiology and human evolutionary genetics, population genomics and bioinformatics. The training will be based on real-data examples from the research of the instructors' laboratories. In one module we will also present genealogical resources specific to Quebec and introduce informatics methods for their use in population analysis and epidemiology. The School consists of four days of lectures and computer labs, starting with basic concepts and methods of analysis in biostatistics and population genetics before turning to genetic epidemiological applications.

Application Procedures:

If you wish to participate in the workshop, please visit our website for instructions and to download the application form. All applications should be submitted no later than Friday, February 27, 2009.

Because of a limited number of places, participants will be selected based on their academic/scientific background, research record, and their specific research interests and needs.

Registration fees: 250$

Faculty:

Alexandre Alcais, Paris, France Philip Awadalla, Montreal, Canada

Luis B. Barreiro, Chicago, IL Louis Houde, Trois-Rivières, Canada

Lluis Quintana-Murci, Paris, France Marie-Hélène Roy-Gagnon, Montreal, Canada

Hélène Vézina, Chicoutimi, Canada Rob Sladek, Montreal, Canada (Invited speaker)

Scientific Committee:

Jamie Engert, Montreal, Canada France Gagnon, Toronto, Canada

Maja Krajinovic, Montreal, Canada Julian Little, Ottawa, Canada

Erwin Schurr, Montreal, Canada Terry-Lynn Young, St. Johns, Canada

Organized by:

Damian Labuda, Philip Awadalla and Marie-Hélène Roy-Gagnon for the Réseau de Médecine Génétique Appliquée (RMGA) of the Fonds de la recherche en santé du Québec (FRSQ), CHU Sainte-Justine Research Centre, and Departments of Pediatrics, Biochemistry, Social and Preventive Medicine, and Robert Cedergren Centre for Bioinformatics and Genomics of the Université de Montréal.

To apply or for more information please contact:

Ms. Dominika Kozubska E-mail: info@montrealspringschool.ca Phone: 514-345-4691

Or visit our website: www.montrealspringschool.ca

Damian Labuda, Ph.D., D.Sc. Professor, Pediatrics Department, Montreal University Sainte-Justine Hospital Research Center, room B-607 b 3175 Cote Sainte-Catherine Montreal, PQ Canada H3T 1C5

tel: (514) 345-4931 ext.3586 [sec. 3282] fax: (514) 345-4731 damian.labuda@umontreal.ca Damian Labuda <damian.labuda@umontreal.ca>

## NESCent DatabaseInteroperability Hackathon

NESCent Hackathon on Evolutionary Database Interoperability

OPEN CALL FOR PARTICIPATION

The National Evolutionary Synthesis Center (NESCent; http:// nescent.org) is sponsoring an "Evolutionary Database Interoperability" hackathon aimed at enhancing the value (and raising the profile) of important community resources for evolutionary and biodiversity data by increasing their accessibility to users and software. We are broadly soliciting applications for participation from the community. More information about the event is available online at http://evoinfo.nescent.org/Database_Interop_Hackathon .

A hackathon is an event at which a group of programmers who otherwise do not have the opportunity to interact on a routine basis meet with users and domain experts to collaboratively develop working code that is of utility to the community as a whole. The Database Interoperability Hackathon will bring together developers from a number of emerging standards for evolutionary data exchange (NeXML; http://nexml.org ), data and metadata semantics (CDAO; http://www.evolutionaryontology.org ), and programmatic access of evolutionary data providers (PhyloWS; http://evoinfo.nescent.org/PhyloWS) with database programmers and metadata experts from a variety of evolutionary and biodiversity community resources. In addition, the mix of people will include programmers of embeddable widgets, mash-up and aggregation applications that can showcase the value of the effort for research applications.

We also welcome comments and suggestions for issues in database interoperability that could be addressed at the event but are not yet on our radar. Please email the organizers at hackathon3@nescent.org with any suggestions you have.

GOALS AND ACTIVITIES

The focus of the programming aspect of the meeting will be to promote interoperability among online evolutionary databases through the following core set of activities. 1) Mapping the data and operation semantics of the participating online resources to an ontology, CDAO. 2) Implement a NeXML transformation for participating online resources as a formally defined query input and data output. 3) Implementation of programmable web-service interfaces following the emerging PhyloWS standard. 4) Showcase some of the possibilities that can arise from achieving data provider interoperability through small integration and/or mash-up oriented prototype applications.

Supporting activities will include discussing input from end-users, discussing compliance with emerging reporting standards (MIAPA) and documentation of solutions and open problems on the hackathon wiki.

ORGANIZATION

The event will be 5 days in duration and will take place at NESCent in Durham, North Carolina, on March 9-13, 2009. Participant travel, accommodation, expenses for meals, etc, will be paid by NESCent. Logistical and travel details will be communicated to accepted and confirmed participants.

The specific development targets will be selected by the participants through a hackathon wiki, a mailing list, and one or more conference calls. The exact agenda for the event will be developed similarly, but will be largely devoted to coding time. At the event itself, participants will self-organize into small subgroups (of 2-5) focused on particular targets.

The NeXML, CDAO, and PhyloWS standards are products of the Evolutionary Informatics working group (http://evoinfo.nescent.org), under the auspices of whom this event is being organized.

CALL FOR PARTICIPATION

We invite all individuals interested in attending to apply by responding to the questions below. We specifically encourage applications from members of underrepresented groups, specifically women and minorities, and from graduate students and postdocs.

1. Please indicate if you would be available for all or only for part of the March 9-13 time period.

2. All code and documentation produced at the event is to be made available immediately under an OSI-approved open-source license or a Creative Commons license. Please indicate if this would pose any difficulty for your participation.

3. Please briefly describe your qualifications (programming languages, metadata standards, experience with data schemas, web-service programming, mash-up programming, etc).

4. Please state what you would most like to accomplish at the hackathon, given your current understanding. If you would not be writing software at the event, please state how you would like to contribute and how you would expect to benefit.

5. Please indicate if you are a member of an underrepresented group

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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

## Portugal MolEvol

GTPB - the Gulbenkian Training Programme in Bioinformatics

Course Announcement - Applications are OPEN

Dear EvolDir mailing list member,

Registration is now open for

MEPA09 - Molecular Evolution, Phylogenetics and Adaptation

Please visit the GTPB website for details: http://gtpb.igc.gulbenkian.pt or go directly to the MEPA09 webpage: http://gtpb.igc.gulbenkian.pt/MEPA09 WARNING: we have received an overwhelming number of positive expressions of interest on this course. Experience from previous editions tells us that it is likely to bevery competitive for seats. Our maximum capacity is 20 seats. Early application is recommended!

Pedro Fernandes

– Pedro Fernandes GTPB Coordinator Instituto Gulbenkian de Ciência Apartado 14 2781 OEIRAS PORTUGAL

Pedro Fernandes <pfern@igc.gulbenkian.pt>

## UMichigan SpeciesTrees Jan10-11

Workshop at the University of Michigan, Jan 10-11, 2009

Estimating Species Trees: a Phylogenetic Paradigm for the 21st Century

NOTE: Given the level of interest in the workshop, we have increased the number of participants that may attend the computer training to 60. There is not a constraint on the number of people that may attend the seminars on Jan 10 - see website for details and registration.

Recent computational and modeling advances have produced methods for estimating species trees directly. Accurate estimates of phylogenetic relationships can be extracted from genetic data with these new approaches, sometimes with less data, by directly modeling the causes of discordance in topology and branch lengths among gene trees. Such inferences are commonly impossible under the traditional phylogenetic paradigm because of the potential for the idiosyncrasies of gene trees to obscure the actual history of species divergence.

We are offering this workshop to not only increase the visibility and use of these methods, but also address a number of significant challenges to estimating species trees, to assure that the advantages these methods offer reach a broad community of users. The goals of the workshop are to: (i) provide an understanding of the theoretical underpinnings of current methodology, (ii) present empirical examples demonstrating the utility of current methodology as well as its limitations, and (iii) offer instruction on the technical aspects involved in using current software. This will be accomplished through the combination of a series of lectures (day one) and hands-on computer training (day two). Participation in the workshop requires registration (go to http://www.ummz.lsa.umich.edu/sptree.html) and is free for those attending the lectures (on Jan 10) and is $25 for those attending the computer training (on Jan 11; see website for programs that will be covered).

Co-organizers: L. Lacey Knowles, University of Michigan, and Laura S. Kubatko, Ohio State University

Schedule: January 10, Location: East Hall Auditorium 1324 8:15 Introduction: L. Lacey Knowles, Species tree and gene tree heterogeneity: concepts, estimation and empirical application 8:30 Scott Edwards, Estimating species trees: empirical comparisons of bayesian, summary statistic and concatenation methods 9:00 Robb Brumfield, Inferring the speciational history of hybridizing manakins (Aves) from multi-locus, multi-allelic data 9:30 Liang Liu, BEST: a bayesian coalescent approach for estimating species phylogenies 10:00 Coffee break 10:30 Karen Cranston, Species trees and gene trees from high-throughput sequence data in rice 11:00 Bret Larget, BUCKy: bayesian untangling of concordance knots (applied to yeast and other organisms) 11:30 Célcile Ané, Detecting phylogenetic discordance on a genome-wide scale 12:00 Lunch break 1:30 Laura Kubatko, Detecting hybridization in the presence of incomplete lineage sorting using multilocus data 2:00 Luay Nakhleh, Efficient search for the species tree in the compatibility graph of gene trees 2:30 Catherine Linnen, Grafting gene trees onto species trees: insights into speciation and adaptation 3:00 Coffee break 3:30 Natalia Belfiore, Multilocus reconstruction of the phylogenetic history of recently diverged species: concatenation vs BEST, a case study with pocket gophers 4:00 Lisle Gibbs, Species trees and speciation history in Sistrurus rattlesnakes inferred from multilocus data 4:30 James Degnan, Probabilities of gene trees in species trees with intraspecific sampling 5:00 Laura Kubatko, Closing remarks (5 minutes) 6:00 Reception and dinner, Hall of Dinosaurs, Museum of Zoology January 11, Location: Shapiro Undergraduate Library, classroom 2054 9:00 James Degnan: program COAL 9:45 Laura Kubatko: program STEM 10:30 Cécile Ané: program BUCKy 11:15 Dennis Pearl: BEST: A Markov Chain Monte Carlo approach to species tree estimation 12:00-1:00 Lunch break 1:00-5:00: Work on datasets

Location of the workshop: University of Michigan, January 10-11, 2009.

Invited speakers for workshop: Liang Liu, Harvard University Laura Kubatko, Ohio State University Dennis Pearl, Ohio State University Célcile Ané, University of Wisconsin James Degnan, University of Canterbury L. Lacey Knowles, University of Michigan Luay Nakhleh, Rice University Karen Cranston, University of Arizona Bret Larget, University of Wisconsin Robb Brumfield, Louisiana State Univ. Lisle Gibbs, Ohio State University Scott Edwards, Harvard University Catherine Linnen, Harvard University Natalia Belfiore, University of California, Berkeley

For more information please contact: Dr. L. Lacey Knowles, knowlesl@umich.edu <mailto:knowlesl@umich.edu>

This workshop has been made possible by funds generously provided by the Museum of Zoology, LSA Dean's Office, and the Office of Vice President for Research, University of Michigan, and NSF.

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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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## UTennessee TheoreticalEvolution Jun1-Jul24

Dear Colleagues,

I would greatly appreciate it if you could please pass this information on to the math and biology undergraduates at your institution.

Sincerely,

Mike

Research Experiences for Undergraduates 2009 Summer Program

National Institute for Mathematical and Biological Synthesis (NIMBioS) at the University of Tennessee, Knoxville

June 1 - July 24, 2009

Undergraduate majors in math, biology, and related fields will live on campus and work in teams with UT professors on state-of-the-art research projects.

The stipend is $3200. Housing and travel allowance are provided.

Project research areas: - plant chemical defenses - codon usage and gene expression - disease modeling

Application information will be available soon on this site. We encourage applicants from diverse backgrounds. Contact Suzanne Lenhart at lenhart@math.utk.edu for further information.

REU Leadership Team: Suzanne Lenhart, Director, Mathematics Department Mike Gilchrist, Ecology and Evolutionary Biology Department Kim Gwinn, Entomology and Plant Pathology Department Steve Wise, Mathematics Department

For more information see: http://nimbios.org/undergraduates/reu.html http://www.nimbios.org/docs/REUflyer.pdf mikeg@utk.edu mikeg@utk.edu

## UVirginia FieldBiology

SUMMER 2009 Field Biology Courses and REU Internships; Mountain Lake Biological Station; MLBS.org Mountain Lake Biological Station (University of Virginia) announces its summer field biology program: 1) Courses - Field-based undergraduate and graduate-level biology credit courses and workshops offered by nationally recruited faculty. 2) NSF REU-Sites Program - Undergraduate independent research internship program now in its 17th year. Work at MLBS focuses on field-based evolution, physiology, and behavior. Courses web page:

http://mlbs.org/courses.html REU web page: http://mlbs.org/REU.html Fliers to Distribute or Post:

http://mlbs.org/download/MLBS_Poster.pdf http://mlbs.org/download/MLBS_Courses.pdf http://mlbs.org/download/MLBS_REU_Poster.pdf **** Learn all about Mountain Lake opportunities at MLBS.org **** Thank you very much, Butch Brodie, Director Eric Nagy, Associate Director

Eric S. Nagy, Ph.D. Associate Director Mountain Lake Biological Station, Department of Biology University of Virginia / P.O. Box 400327 Charlottesville, VA 22904-4327 USA street address: 485 McCormick Road / 219 Gilmer Hall tel: +1-434-243-4989 (+1-540-626-5227 summer) fax: +1-434-982-5626 (+1-540-626-5229 summer) cel: +1-434-906-3122 eml: enagy@virginia.edu skype: flightofthesandor web:

virginia.edu/biology/faculty/nagy.htm MLBS web page: mlbs.org

enagy@virginia.edu

## WoodsHole MolEvol Jul26-Aug7

Workshop on Molecular Evolution, Woods Hole

http://workshop.molecularevolution.org/mbl/ 26 July - 7 August 2009, extended topics session 7 August - 14 August 2009

Application Deadline 2 March 2009

Michael P. Cummings, Director

The Workshop on Molecular Evolution has been the finest course in the subject since it was started in 1988. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. A distinguishing feature of the Workshop is a well-equipped computer laboratory with Apple Macintosh computers and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as AWTY, BEAST, Clustal W and Clustal X, FASTA, FigTree, GARLI, LAMARC, MAFFT, MrBayes, PAML, PAUP*, and PHYLIP provide demonstrations and consultations. This two-week program is designed for established investigators, postdoctoral fellows, and advanced graduate students with prior experience in molecular evolution and comparative genomics. Lectures and computer laboratories total ~90 hours of scheduled instruction. An optional all-computer laboratory of 54+ hours of independent work with guidance and consultation of some faculty and teaching assistants is offered during the third week. Admission is limited and highly competitive, with admissions decisions determined by an international committee. Many participants find the extended topics session to be especially useful.

Topics to be covered include:

- Databases and sequence matching: database searching: protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches - Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis; hypothesis testing - Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters - Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conservation - Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution - Comparative genomics: genome content; genome structure; genome evolution - Molecular evolution integrated at lower levels: biochemistry; cell biology; physiology; relationship of genotype to phenotype

2009 Fees: $2500 (room and board at no additional charge), plus an additional $900 for the extended topics session.

More information is available at http://workshop.molecularevolution.org/mbl/ Direct link to application information is - http://gosnold.mbl.edu/StudentApp/StudentApp.asp?CourseID=3DMOLE mike@umiacs.umd.edu mike@umiacs.umd.edu

# 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.