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# E v o l D i r

October 1, 2010

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

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## 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](mailto:Golding@McMaster.CA).

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

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



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### Barcelona Biodiversity Oct1-2 2

Dear colleagues,

Just a reminder that the international symposium “Frontiers in Biodiversity: a Phylogenetic Perspective”, will be held in Barcelona, Spain, in three weeks from today (1st and 2nd of October 2010). There are still some seats available for registration and few slots left for poster presentations.

For further information please visit <http://www.phylofrontiers2010.com/> (please, find below the original posted message)

Hope to see you in Barcelona!

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

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

These are exciting times to conduct research on Bio-

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

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

The symposium will be held at the Institute of Catalan

Studies (Institut d'Estudis Catalans, IEC), located at the heart of Barcelona's old town, in the 17th century Santa Creu Hospital building.

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

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

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

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Miquel A. Arnedo

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

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## Gothenburg SYNGEvol Apr25-29

The First Syngnathid Biology International Symposium

Date: April 25th - 29th, 2011

Purpose: To bring together students and scientific researchers working on various aspects of pipefish, seahorse and seadragon biology. Topics include phylogenetics, phylogeography, sexual selection & mating systems, behavior, conservation and management.

Invited speakers: Ingrid Ahnesjö, Uppsala University, Sweden Adam Jones, Texas A&M University, USA Charlotta Kvarnemo, Gothenburg University, Sweden Nuno Monteiro, Centre for Biodiversity and Genetic Resources, Portugal Tony Wilson, Zoologisches Museum Universität Zürich-Irchel, Switzerland

Location: Situated on the Gullmars Fjord on the rugged west coast of Sweden, the Sven LovÅ©n Centre for Marine Research, Kristineberg is Sweden's oldest operating marine research station (<http://www.loven.gu.se>). Kristineberg is situated in the picturesque fishing village of Fiskebäcksil which can be reached either by bus from Gothenburg's Nils Eriksson central station (Göteborg C) or by bus/ferry via Lysekil södra hamnen (see [www.vasttrafik.se](http://www.vasttrafik.se) for time schedules). The nearest international airport is Gothenburg Landvetter airport. Buses from the airport to the central station run regularly during the day (see [www.flygbussarna.se](http://www.flygbussarna.se) for prices. Another option for travelers is Oslo airport (Lufthavn). There you can take a bus (GoByBus < <http://www.gobybus.se/public/-timetable.aspx> > or Swebus < <http://www.swebus.se/> >) to Torp C (Uddevalla) and connect to busses running to Fiskebäcksil.

Conference fee: 4500 SEK (approx. 500 Euros) Included in the conference fee is lodging in a double room at the Station for all four nights, the registration fee, breakfast, lunch, dinner, coffee breaks and a banquet ticket for Thursday the 28th of April.

Deadline for abstract submission and registration: January 15th, 2011 Please note: Conference participation is limited to 60 persons.

Abstract instructions: Please submit a 250 word abstract including title and author affiliations to [kenyon.mobley@emg.umu.se](mailto:kenyon.mobley@emg.umu.se). Please indicate whether you prefer an oral or poster presentation.

Travel grants: Are you student from a Nordic Marine Academy member institution (see <http://nma.uib.no/nma/default.asp?k=13&idw> for more information)? If so, you may be eligible for reimbursement of travel costs of up to 3500 SEK (380 Euros) and a reduced conference fee of 3620 SEK. Other external funding for conference goers may be provided by travel grants from the Fisheries Society of the British Isles (<http://www.fsbi.org.uk/travel-grants/>) and the Animal Behavior Society (<http://www.animalbehavior.org/ABS/Grants/>).

Contact information: Kenyon Mobley, UmeÅ© University ([kenyon.mobley@emg.umu.se](mailto:kenyon.mobley@emg.umu.se)) Gunilla Rosenqvist, Norwegian University of Science and Technology ([gunilla.rosenqvist@bio.ntnu.no](mailto:gunilla.rosenqvist@bio.ntnu.no)) Anders Berglund, Uppsala University ([anders.berglund@ebc.uu.se](mailto:anders.berglund@ebc.uu.se))

More info and updates: <http://syngbio.mezoka.com/>  
\*\*Sponsored by the Nordic Marine Academy\*\*

Kenyon Mobley <[kenyon.mobley@emg.umu.se](mailto:kenyon.mobley@emg.umu.se)>

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## Heraklion Biogeography Jan7-11 Registration Open

Registration is now OPEN for the 5th Biennial Conference of the International Biogeography Society Heraklion, Crete, Greece; 7-11 January, 2011

For more information about the conference, and to register, please visit <http://www.biogeography.org/html/Meetings/2011/index.html> . The meeting is built around four successive SYMPOSIA (8th & 9th January) on broad foundational and cutting-edge topics and approaches in biogeography and macroecology, each with a suite of leading international scientists and \*openings for contributed papers\*:

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

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

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

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

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

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

- Foster communication and collaboration between bio-

geographers in disparate academic fields. - Increase both the awareness and interests of the scientific community and the lay public in the contributions of biogeographers. - Promote the training and education of biogeographers so that they may develop sound strategies for studying and conserving the world's biota.

dawsonmartin@sbcglobal.net

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## KansasCity Arthropod Genomics Jun9-12

ARTHROPOD GENOMICS SYMPOSIUM, June 9-12, 2011, in Kansas City

Please SAVE THE DATES of. June 9 to June 12 on your calendar and plan to attend the 5th ANNUAL ARTHROPOD GENOMICS SYMPOSIUM.

DATES: June 9 to 12, 2011 PLACE: Kansas City Marriott on the beautiful Country Club Plaza SPONSOR: K-State Arthropod Genomics Center, Kansas State University TENTATIVE SCHEDULE: Thursday afternoon, June 9 - Pre-Symposium Workshop Thursday evening, June 9 - Keynote presentation and welcome reception Friday & Saturday, June 10 and 11 - Platform and Poster sessions Sunday morning, June 12 - Roundtable discussion with the ArthropodBase Consortium. All are invited to attend! Noon, Sunday, June 13 - Activities will conclude.

Speakers who are experts in arthropod genomics and bioinformatics with applications in genomics will be announced soon! Additional speakers will be selected from contributed posters.

Demonstrations: Database and bioinformatics tools developers will be available at the meeting to provide hands-on demonstrations.

Visit our website, [www.k-state.edu/agc](http://www.k-state.edu/agc), for updates as details are finalized. We hope you will plan to attend!!!

Please help us "paperlessly publicize" the Symposium and share this announcement with colleagues and students!

Doris Merrill, Program Coordinator K-State Arthropod Genomics Center Division of Biology, Kansas State University 104 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, [dmerrill@k-state.edu](mailto:dmerrill@k-state.edu) [www.k-state.edu/agc](http://www.k-state.edu/agc)

[dmerrill@ksu.edu](mailto:dmerrill@ksu.edu)

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## KansasCity Genomics Nov5-7

8th Ecological Genomics Symposium, November 5, 6, and 7, 2010, in Kansas City

\*\*\*Please help us “paperlessly publicize” the Ecological Genomics Symposium by forwarding this announcement to colleagues and students!\*\*\*

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

Download a flyer to < [http://ecogen.ksu.edu/downloads/Brochure\\_2010.pdf](http://ecogen.ksu.edu/downloads/Brochure_2010.pdf) > post!

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

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

### PLENARY SPEAKER:

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

### FEATURED SPEAKERS:

+Seth R. Bordenstein, Vanderbilt University, “Microbial symbiosis and mobile genetic elements”

+Maitreya Dunham, University of Washington, “Comparative functional genomics in yeasts”

+Audrey P. Gasch, University of Wisconsin-Madison, “Natural variation in stress sensitivity and genomic expression in *Saccharomyces cerevisiae*”

+Corbin Jones, The University of North Carolina at Chapel Hill, “Genetics of host specialization in *Drosophila*: Insights into the interplay of speciation and adaptation”

+John K. McKay, Colorado State University, “Evolutionary genetics of local adaptation in *Arabidopsis* and

beyond”

+Marilyn Roossinck, The Samuel Roberts Noble Foundation, “Plant virus biodiversity and ecology”

+Michael J. Wade, Indiana University, “The plasticity load: The cost of flexibility in a variable environment”

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

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

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

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

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

CORPORATE SPONSORS: JMP Genomics and Roche-NimbleGen.

### DEADLINES:

Tuesday, 9/21/10, Student travel fellowship application materials are due.

Friday, 10/8/10, Registration deadline at early bird rates.

Friday, 10/8/10, Poster Abstracts are due for oral presentation consideration.

Friday, 10/8/10, Hotel Rooms must be reserved to receive reduced group rate.

Wednesday, 10/27/10, Poster Abstracts are due if NOT being considered for oral presentation.

Ecological Genomics Institute Directors:

Dr. Loretta Johnson  
 Dr. Michael Herman  
 Kansas State University, Division of Biology  
 ECOLOGICAL GENOMICS INSTITUTE  
 Doris R. Merrill, dmerrill@k-state.edu  
 Program Coordinator  
 Kansas State University  
 Biology, 104 Ackert Hall  
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 (785) 532-3482, [www.ecogen.k-state.edu](http://www.ecogen.k-state.edu)  
 dmerrill@ksu.edu

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### Laxenburg Austria Speciation Dec13-15

Dear colleague,

Speciation 2010, the first European conference on speciation research, will take place in Laxenburg, near Vienna, Austria, during December 13-15, 2010. We would be most grateful to you if you could kindly share this information with potentially interested colleagues in your research group or department.

The conference will be held in the former summer palace of the Habsburg family, home of the International Institute for Applied Systems Analysis (IIASA), and will be organized as part of the European Science Foundation's Research Networking Programme Frontiers of Speciation Research (FroSpects), funded by 18 national research agencies.

The aim of Speciation 2010 is to bridge between different approaches to speciation research and to promote integrative perspectives that interface empirical insights with theoretical advances and bring together developments in ecology, systematics, and genetics. Indicative topics include, but are not limited to, the diversity of diversification processes, signatures of speciation, species cohesion, speciation models for specific systems, the role of interspecific interactions, speciation and bioinvasions, hybridization and adaptive radiations, genetics and genomics of speciation, biodiversity losses through reverse speciation, speciation in ecosystems, evolutionary biogeography, and macro-ecological explanations of biodiversity.

Participation is open to everyone. Thanks to support

by ESF and IIASA, we only charge a small registration fee to cover lunches, coffee breaks, and bus transfers.

In addition to about 20 invited presentations, the conference will feature contributed talks and a poster session. Confirmed invited speakers include Nick Barton, Austria; Louis Bernatchez, Canada; Dan Bolnick, USA; Jerry Coyne, USA; Tatiana Giraud, France; Andrew Hendry, Canada; Chris Jiggins, UK; Kerstin Johansson, Sweden; Eva Kisdi, Finland; Isabelle Olivieri, France; Anna Qvarnström, Sweden; Jörgen Ripa, Sweden; Michael Rosenzweig, USA; Maria Servidio, USA; Skúli Skúlason, Iceland; Radka Storchová, Czech Republic; and Diethard Tautz, Germany.

Registration is open at [www.speciation.iiasa.ac.at](http://www.speciation.iiasa.ac.at). With many thanks and best wishes,

Åke Brännström & Ulf Dieckmann

Conference poster: <http://www.iiasa.ac.at/Research/EEP/FroSpects/Speciation2010.pdf> About Speciation 2010: <http://www.speciation.iiasa.ac.at> About FroSpects: <http://www.iiasa.ac.at/Research/EEP/FroSpects> About ESF: <http://www.esf.org> About IIASA: <http://www.iiasa.ac.at> Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

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[dieckmann@iiasa.ac.at](mailto:dieckmann@iiasa.ac.at)

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### London Attenborough Fortey Dec16

What's in a name? Attenborough & Fortey on animals Lecture Thursday, December 16, 2010 at 7:00 PM (GMT) London, United Kingdom | Ondaatje Theatre, Royal Geographical Society

Sir David Attenborough and Professor Richard Fortey  
 With his delight and enthusiasm for biodiversity, Sir David shares some of his favourite encounters with animals. Prof. Fortey explains why scientific names are more than just labels, with stories of trilobites and field adventures.

This is a fundraiser for the ICZN - we thank you for your support. Please consider making a further dona-

tion. For information on the work of the ICZN, see our website [www.iczn.org](http://www.iczn.org). Books by the speakers will be available for sale at the event. A cash bar will be open both before and after the lecture in the historic RGS Map Room.

<http://iczn.org/content/international-commission-zoological-nomenclature-fun> draising-lecture or buy your tickets here: <http://iczn2010.eventbrite.com/> Dr Ellinor Michel

Executive Secretary International Commission on Zoological Nomenclature Natural History Museum, London SW7 5BD +44 (0)207-942-5653 (alternative number - 5516) [iczn-em@nhm.ac.uk](mailto:iczn-em@nhm.ac.uk)

[www.iczn.org](http://www.iczn.org) [iczn-em <iczn-em@nhm.ac.uk>](mailto:iczn-em@nhm.ac.uk)

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## London LERN Nov11

I would like to draw you attention to the LERN 2010 annual conference. It is for students in evolutionary biology, and takes place the 11th of November in London. The call for abstracts is now open. I would be very grateful if you could send this information to Evoldir.

<http://londonevolutionarynetwork.wordpress.com/-category/conferences/conference-2010/> Regards

Alexanda Alvergne

Alex Alvergne <[a.alvergne@ucl.ac.uk](mailto:a.alvergne@ucl.ac.uk)>

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## Lund GeneticsMigration Dec6

CAnMove symposium â Genetics of Migration Centre for Animal Movement, Lund University, 6th December 2010

The aim of this symposium is to provide a plenum for scientists to present key studies and state-of-the-art insight into the field of migration covering different taxa and using various approaches. We want to provide a platform to merge and discuss the current state of the field of genetics of migration and identify future directions and methodological approaches to be focused upon.

The symposium will be centred on a backbone of six

talks presenting case studies across a variety of taxa, and introducing different methodological approaches. We will close the symposium with a plenary discussion to synthesise future directions, methodological approaches, and assess possibilities and pitfalls thereof. With this symposium we hope to encourage dialogue and the exchange of ideas, and to foster collaboration and promote debate.

Registration: Attendance of the symposium is free, if you want to attend, please register here. The deadline for applications is October 22nd. (Link to online-registration: <http://canmove-dev.ekol.lu.se/-conf/index.php>)

There will be no talks other than those listed on the programme, but we welcome poster presentations. We especially encourage Ph.D. students to present and discuss their work here.

Please find further information about accommodation and transportation to Lund in "More information" to the right.

Should you have any questions regarding the symposium please do not hesitate to contact me ([miriam.liedvogel@zooekol.lu.se](mailto:miriam.liedvogel@zooekol.lu.se))

Welcome!

Link to online registration: <http://canmove-dev.ekol.lu.se/conf/index.php> Symposium-Homepage for further information:<http://www.canmove.ekol.lu.se/conferences-and-meetings/-canmove-symposium-genetics-of-migration> Local organisers: Miriam Liedvogel, Staffan Bensch and Susanne Åkesson

Miriam Liedvogel <[miriam.liedvogel@zooekol.lu.se](mailto:miriam.liedvogel@zooekol.lu.se)>

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## Marseilles 15thEvolutionaryBiol Sep20-23

Dear all,

We are pleased to announce you that the 15th Evolutionary Biology Meeting at Marseilles will take place from September 20th to September 23rd 2011.

Do not hesitate to visit our website for any further information regarding the meeting we have been organizing for 14 years: <http://sites.univ-provence.fr/evol-cgr/> Best regards,

Gaëlle Pontarotti AEEB

Universite EGEE <Egee@univ-provence.fr>

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**MissouriBotanicalGarden EvoDevo  
Oct15-16**

57th Annual Systematics Symposium Missouri Botanical Garden 15-16 October 2010

With support from the National Science Foundation

Evo-Devo

Organizing committee: Elizabeth "Toby" Kellogg <mailto:tkellogg@umsl.edu>

**REGISTRATION**

This form is available in PDF format < <http://www.mobot.org/MOBOT/research/symposium/pdf/registration2010.pdf> > or a Word <<http://www.mobot.org/MOBOT/research/symposium/word/registration2010.doc> > document format

Friday 7:30 - 9:30 p.m. Informal mixer in Ridgway Center. Saturday 8:30 a.m. - 8:30 p.m. Talks in Ridgway Center

David Kingsley

Title to be announced

Elena Kramer

Genome-level views of novel floral organ morphology

Linda Nagy

Title to be announced

Jill Preston

Evo-devo of flower symmetry: recent advances and future directions

Neelima Sinha

Leaf development in the post-genomic era

Greg Wray

Evolvability of a developmental gene regulatory network

John Doebley

Evening Speaker. Domestication as a model for understanding the evolution of plant form

**SPACE LIMITS REGISTRATION TO 400; PLEASE REGISTER EARLY**

Registration must be accompanied by a \$95.00 regis-

tration fee, which also covers the cost of refreshments at the Friday mixer and lunch and dinner on Saturday (but see below). Information on local hotels and motels will be available to registrants. No refunds will be granted after 24 September. There is no guarantee of food being available if you register after 30 September. For electronic payment, please call Mary McNamara <mailto:mary.mcnamara@mobot.org> at 314-5775169 or Sandy Lopez <mailto:sandy.lopez@mobot.org> at 314-577-9520.

I plan to attend the Systematics Symposium. Enclosed is my \$95.00 registration fee. Please make checks payable to "Missouri Botanical Garden"

I enclose my registration fee of \$95.00 \_\_\_\_\_

I request vegetarian meals: \_\_\_\_\_

My name and professional address:

Phone:\_\_\_\_\_ Fax:\_\_\_\_\_ e-mail address:\_\_\_\_\_

Please indicate if you are a) a graduate student \_\_\_\_\_ or b) an undergraduate student \_\_\_\_\_

Mail registration form to: Systematics Symposium Missouri Botanical Garden P.O. Box 299 St. Louis, MO 63166-0299

For further information, contact: Robert Magill Email: bob.magill@mobot.org

phone: 314 577 9520 Fax: 314 577 0828

Robert E. Magill | Senior Vice President, Science & Conservation | Missouri Botanical Garden

P.O. Box 299, St. Louis, MO 63166 | ph (314) 577-5161 | fx (314) 577-0828

Bob Magill <Bob.magill@mobot.org>

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**NHM London Systematists Decl**

12th YOUNG SYSTEMATISTS FORUM

Wednesday 1 December 2010, starting at 9 am

Venue: Flett Lecture Theatre, Natural History Museum, London, UK

The annual Young Systematists Forum represents an exciting setting for postgraduate students and young postdoctoral researchers to present their data, often for the first time, to a scientific audience interested in taxonomy, systematics and phylogenetics. This well-established event provides an important oppor-



tunity for budding systematists to discuss their research in front of their peers within a supportive environment. Supervisors and other established systematists are also encouraged to attend. Note that this Forum is held the day after the Molluscan Forum ([www.Malacsoc.org.uk](http://www.Malacsoc.org.uk)), also at the Natural History Museum. This has been arranged so that both meetings can be attended.

Prizes will be awarded for the most promising oral and poster presentation as judged by a small panel on the day.

Registration is FREE. Send applications by e-mail to David Bass ([d.bass@nhm.ac.uk](mailto:d.bass@nhm.ac.uk)), supplying your name, contact address and stating whether or not you wish to give an oral or poster presentation. Space will be allocated subject to availability and for a balanced programme of animal, plant, algal, microbial, molecular, and other research. Non-participating attendees are also very welcome - please register as above.

Abstracts must be submitted by e-mail in English no later than 15th November 2010. The body text should not exceed 150 words in length. If the presentation is co-authored, the actual speaker (oral) or presenter (poster) must be clearly indicated in BOLD text.

All registered attendants will receive by e-mail further information about the meeting, including abstracts, one week in advance. This information will also be displayed on the Systematics Association website ([www.systass.org](http://www.systass.org)).

Dr David Bass Zoology Department Natural History Museum Cromwell Road London SW7 5BD UK

David Bass <[david.bass@zoo.ox.ac.uk](mailto:david.bass@zoo.ox.ac.uk)>

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## PuertoRico EvolutionClimate Feb11-18

Dear colleagues and friends,

We would like to invite you to attend to our session on our "Evolutionary rules in the brave new ocean - Climate change and life-history strategies" session (see below for description) at the upcoming ASLO Aquatic Sciences Meeting, being held 11-18 February 2011 in San Juan, Puerto Rico. The deadline for submission is the 11 October 2010. For more information and abstract submission, please visit the meeting website: <http://www.aslo.org/meetings/sanjuan2011/> Please do

not hesitate to contact me if you have any question regarding the session. Looking forward meeting you in Puerto Rico for stimulating discussions on life-history and climate change.

Best regards Sam Dupont, Frank Melzner and Mike Thorndyke [Sam.dupont@marecol.gu.se](mailto:Sam.dupont@marecol.gu.se);

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Session Description: Among anthropogenic stressors, global warming and ocean acidification - the decrease in the pH of the oceans caused by their uptake of anthropogenic carbon dioxide from the atmosphere - are of great concern and are believed to be a major threat for near-future ecosystem health. Rates of change are increasingly fast and we can only guess at the kinds of organisms that will suffer ("losers") or benefit ("winners") from this mayhem that is radically altering ecosystem structure. The aim of this session is to summarize recent findings suggesting that a life-history strategy is a major parameter determining species sensitivity. A variety of life history strategies exist that enable marine species to reproduce successfully across a wide range of habitats. These include planktotrophy, lecithotrophy, brooding, asexual reproduction, hybridization, etc. The proportion of each strategy is believed to be a consequence of a range of selective pressures and recent findings suggest that these rules may be change in near-future oceans. To understand near-future ocean, we need to understand these new evolutionary rules that will shape ecosystems.

Sam Dupont <[sam.dupont@marecol.gu.se](mailto:sam.dupont@marecol.gu.se)>

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## QueensU Belfast Systematics Jul4-8 CallProposals

Dear all,

I'm writing to announce that the next Systematics Association biennial meeting will be held at Queen's University Belfast from the 4-8 July 2011.

We are currently working on arranging the details of the event, and we hope to have some more information on the Systematics Association website ([www.systass.org](http://www.systass.org)) very soon. In particular, we have started arranging the scientific program for the biennial, and are keen to involve as wide a cross-section of the systematics community as possible. If you would like to arrange a symposium, or have suggestions for symposium topics you would like to see at next year's meeting, please get in

touch with me, the Programme Secretary, soon.

We look forward to seeing some of you in Belfast next year, Yours,

James Cotton

James Cotton Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge. CB10 1SA UK

01223 494864

james.cotton@sanger.ac.uk

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### SaltLakeCity Speciation Jan3-7

Dear All,

We are organizing the symposium “Speciation in the Sea” that will be held during the 2011 SICB (Society for Integrative and Comparative Biology) Meeting in Salt Lake City, Utah (Jan 3-7 2011). Please check out the website and the list of speakers at: <http://www.sicb.org/meetings/2011/symposia/speciation.php> If you are interested in presenting in a session complementing this symposium, please register soon at this website (<http://sicb.org/meetings/2011/abstracts/index.php3>). The registration dead line is Friday, September 10, 2010.

Hope to see you in Salt Lake City!

Maria Pia Miglietta, Anuschka Faucci and Francesco Santini

Maria Pia Miglietta Research Assistant Professor Department of Biological Sciences University of Notre Dame 100 Galvin Life Sciences Center, Notre Dame, IN, 46556

<http://www.personal.psu.edu/mum31>  
mmigliet@nd.edu

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### StanfordU ComplexTraits Oct14-15

SYMPOSIUM: Genes & Environment: Finding the Missing Heritability of Complex Traits

Stanford University, October 14 & 15, 2010

Generously supported by Society in Science, the

Branco Weiss Fellowship - <http://www.society-in-science.ethz.ch/> Public registration to attend this one and a half day symposium is now open at <http://www.gxe2010.org> - admission is FREE and will be handled on a “first come first serve” basis. Space is limited and pre-registration is required.

Why is it that humans vary in their susceptibility to major diseases, such as cancer, depression, schizophrenia, and HIV/AIDS? What determines complex human traits? Is it genes, the environment, a combination of both, or something else? These questions lie at the heart of a debate that has been raging for decades, namely the nature vs. nurture debate. Modern technology has allowed us to dig deep into the genetic variation in human populations and associate that variation with traits of interest. However, the results of these so-called genome wide association studies (GWAS) have been sobering: While some traits are clearly associated with particular genetic variants, most variation in traits cannot be explained by variation in genes. This poses a paradox: Many traits cluster in families, but genetic variation seems to explain little variation. Where does the missing heritability come from?

At Stanford University, 9 world-renowned experts on these questions and leaders in their fields will speak at the GxE 2010 symposium. At this one and a half day event, talks will be alternating with moderated discussion in a medium-sized setting that allows and fosters personal interactions.

The speakers are, in alphabetical order:

- Jeanne Brooks-Gunn, Virginia and Leonard Marx Professor of Child Development, Teachers College & College of Physicians and Surgeons, Columbia University - Steve Cole, Vice President, Research and Development, Hope Lab & Associate Professor of Medicine, University of California, Los Angeles - Marcus Feldman, Burnet C. and Mildred Finley Wohlford Professor of Biological Sciences & Director, Morrison Institute for Population and Resource Studies, Stanford University - James H. Fowler, Professor of Medical Genetics and Political Science, University of California, San Diego - David Goldstein, Professor of Molecular Genetics and Microbiology & Director, Center for Human Genome Variation, Duke University - Ahmad Hariri, Professor of Psychology and Neuroscience & Director, Laboratory of Neurogenetics, Duke University - Stephen Manuck, Distinguished University Professor of Health Psychology and Behavioral Medicine & Director, Initiative for Neurobehavioral Genetics, University of Pittsburgh - Eric Turkheimer, Professor, Department of Psychology & Director of Clinical Training, University of Virginia - Anne Wojcicki, co-founder, 23andMe

More information about the symposium can be found online at <http://www.gxe2010.org> The organizers,

Marcel Salathé & George Slavich

Genes & Environment 2010: Finding the Missing Heritability of Complex Traits October 14 & 15, 2010 Stanford University <http://www.gxe2010.org> Marcel Salathé, PhD Assistant Professor of Biology and Society in Science: Branco Weiss Fellow CIDD - Center for Infectious Disease Dynamics The Pennsylvania State University 516 Mueller Laboratory University Park, PA, 16802

mobile: (408) 386-8916 work: (814) 867-4431 email: [salathe@psu.edu](mailto:salathe@psu.edu) web: [salathegroup.com](http://salathegroup.com)

“salathe@psu.edu” <[salathe@psu.edu](mailto:salathe@psu.edu)>

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## UFlorida SEPEEG Registration

Dear All,

You can now register for SEPEEG, the Southeastern Population Ecology and Evolutionary Genetics meeting! Go to the website to register, or for more information: [http://web.me.com/mlwayne/SEPEEG\\_2010/-registration.html](http://web.me.com/mlwayne/SEPEEG_2010/-registration.html) See you there, Marta and Charlie

Marta L. Wayne, PhD Colonel Allan R. and Margaret G. Crow CLAS Term Professor P.O. Box 118525 Department of Biology University of Florida Gainesville, FL 32611-8525 (courier: B30 Bartram Hall) vox: 352-392-9925 fax: 352-392-3704 <http://www.biology.ufl.edu/People/faculty/mlwayne.aspx> [mlwayne@ufl.edu](mailto:mlwayne@ufl.edu)

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## UWisconsin AppliedEvolution Oct1-2

Special Symposium on Applied Evolution

Friday & Saturday, October 1-2, 2010

Ebling Auditorium, University of Wisconsin-Madison

The Center of Rapid Evolution (CORE) and The James F. Crow Institute for the Study of Evolution at the University of Wisconsin-Madison are holding a special event to foster discussion and outreach on Applied Evo-

lution. The goal is to position the University of Wisconsin as a leader in the study of rapid and applied evolution and to inform the public on how evolutionary insights are critical for addressing serious problems in conservation, medicine, and agriculture. The events include a keynote address on rapid evolution, public outreach lectures by distinguished University of Wisconsin faculty on diverse topics in applied evolution, and panel discussions. Everyone is welcome to attend.

Friday, October 1

KEYNOTE ADDRESS 3:30 pm-4:30 pm

Introduction by James F. Crow

Distinguished Professor Richard Lenski, from Michigan State University, will speak on the topic of rapid evolution in his talk, The Dynamics of Phenotypic and Genomic Evolution during a 50,000 Generation Experiment with *E. coli*.

CAMPUS DISCUSSION 4:45-5:45 pm

Don Waller (Professor of Botany) will lead a discussion on “University of Wisconsin as a leader in research on the study of Rapid Evolution.” A reception will follow.

Saturday, October 2

AFTERNOON LECTURES 1:00-4:00 pm

Distinguished UW-Madison faculty will discuss diverse ways in which evolutionary research could contribute greatly toward the understanding and solving of real-world problems in a series of 20- minute presentations.

Carol Lee (1 pm, Rapid evolution of freshwater invaders and the pathogens they carry)

Irwin Goldman (1:30 pm, Evolution you can taste: crop domestication and breeding for a hungry planet)

Johanne Brunet (2 pm, Escape and establishment of genetically modified organisms)

Tony Goldberg (2:30 pm, West Nile virus in Chicago: the evolution of a virus in real time with real-world consequences)

Nicole Perna (3 pm, Friends and enemies - evolution of bacterial pathogen and nonpathogen genomes)

Mark Berres (3:30 pm, Where did the chicken come from, and where is it going?).

PANEL DISCUSSION 4:00-5:00 pm

A panel discussion on “How is evolution useful in daily life?” will take place as the final event. Panelists will include Irwin Goldman (Professor of Horticulture), David Baum (Professor of Botany and Director of the JF Crow Institute for the Study of Evolution), Johanne Brunet (Research Ecologist with the US Department

of Agriculture Agricultural Research Service and Associate Professor of Entomology), and Mark Berres (Assistant Professor of Animal Science). A reception will follow.

The events are free of charge and open to the public, and will be held in the Microbial Sciences Building, located on Linden Dr. and Babcock St., across from Steenbock Library (see <http://www.map.wisc.edu/> for nearby parking lots). For additional information, please contact Professor Carol Lee at [carollee@wisc.edu](mailto:carollee@wisc.edu) or Mara McDonald at [mamcdona@wisc.edu](mailto:mamcdona@wisc.edu) or 263-8941.

Co-sponsored by The University of Wisconsin College of Agricultural & Life Sciences, The Laboratory of Genetics, The Department of Botany, and The Department of Zoology.

Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 [carollee@wisc.edu](mailto:carollee@wisc.edu)

<https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html> [carollee@wisc.edu](mailto:carollee@wisc.edu)

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## UWisconsinMadison AppliedEvolution Oct1-2

The Center of Rapid Evolution (CORE) at the University of Wisconsin- Madison is holding the following event. Everyone interested in rapid and/or applied evolution is welcome to attend.

Special Symposium on Applied Evolution

Center of Rapid Evolution (CORE), University of Wisconsin

October 1-2, Ebling Auditorium, University of Wisconsin-Madison

Friday, October 1: Special Keynote talk on Rapid Evolution

3:30 pm Richard Lenski

Title: The Dynamics of Phenotypic and Genomic Evolution during a 50,000 Generation Experiment with *E. coli*

4:30 Discussion

Reception

Saturday, October 2: Public Symposium on Applied Evolution

1:00 pm Carol Lee: Rapid evolution of freshwater invaders and the pathogens they carry

1:30 Irwin Goldman: Evolution you can taste: crop domestication and breeding for a hungry planet

2:00 Johanne Brunet: Escape and establishment of genetically modified organisms

2:30 Tony Goldberg: West Nile virus in Chicago: the evolution of a virus in real time with real-world consequences

3:00 Nicole Perna: Friends and enemies - evolution of bacterial pathogen and nonpathogen genomes

3:30 Mark Berres: Where did the chicken come from, and where is it going?

4:00 Panel Discussion: How is evolution useful in daily life?

Reception

Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 [carollee@wisc.edu](mailto:carollee@wisc.edu)

<https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html> [carollee@wisc.edu](mailto:carollee@wisc.edu)

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## UWisconsinMadison AppliedEvolution Oct1-2 2

Special Symposium on Applied Evolution

Friday & Saturday, October 1-2, 2010

The Center of Rapid Evolution (CORE) at the University of Wisconsin-Madison (<https://mywebspace.wisc.edu/carollee/web/Lee/CORE.html>)

will be holding a special event to foster discussion and outreach on Applied Evolution. The goal is to position the University of Wisconsin as a leader in the study of rapid and applied evolution and to inform the public on how evolutionary insights are critical for addressing serious problems in conservation, medicine, and agriculture. The events include a special keynote address on rapid evolution, public lectures by distinguished University of Wisconsin faculty on diverse topics in applied evolution, and panel discussions. All events will be held in Ebling Auditorium, University of Wisconsin- Madison. Everyone interested in Rapid and/or Applied Evolution is welcome to attend.

Friday, October 1

KEYNOTE ADDRESS 3:30 pm-4:30 pm

Professor Richard Lenski, eminent researcher from Michigan State University and a member of the US National Academy, will discuss the topic of rapid evolution in his talk, The Dynamics of Phenotypic and Genomic Evolution during a 50,000 Generation Experiment with *E. coli*.

CAMPUS DISCUSSION 4:45-5:45 pm

A campus-wide discussion will focus on “University of Wisconsin as a leader in research on the study of Rapid Evolution,” followed by a reception.

Saturday, October 2

AFTERNOON LECTURES 1:00-4:00 pm

Distinguished UW-Madison faculty will discuss diverse ways in which evolutionary research could contribute greatly toward the understanding and solving of real-world problems in a series of 20-minute presentations. The speakers will be Carol Lee (1 pm, Rapid evolution of freshwater invaders and the pathogens they carry), Irwin Goldman (1:30 pm, Evolution you can taste: crop domestication and breeding for a hungry planet), Johanne Brunet (2 pm, Escape and establishment of genetically modified organisms), Tony Goldberg (2:30 pm, West Nile virus in Chicago: the evolution of a virus in real time with real-world consequences), Nicole Perna (3 pm, Friends and enemies - evolution of bacterial pathogen and nonpathogen genomes), and Mark Berres (3:30 pm, Where did the chicken come from, and where

is it going?). Each talk will be followed by a 10-minute answer and question session.

PANEL DISCUSSION 4:00-5:00 pm

A panel discussion on “How is evolution useful in daily life?” will take place as the final event. Panelists will include Irwin Goldman (Professor of Horticulture), David Baum (Professor of Botany and Director of the JF Crow Institute for the Study of Evolution), and Johanne Brunet (Research Ecologist with the US Department of Agriculture Agricultural Research Service and Associate Professor of Entomology).

The events are free of charge and open to the public, and will be held in the Microbial Sciences Building, located on Linden Dr. and Babcock St., across from Steenbock Library (see <http://www.map.wisc.edu/> for nearby parking lots). For additional information, please contact Professor Carol Lee at [carollee@wisc.edu](mailto:carollee@wisc.edu) or Mara McDonald at [mamcdona@wisc.edu](mailto:mamcdona@wisc.edu) or 263-8941.

Sponsored by Center of Rapid Evolution (CORE), The James F. Crow Institute for the Study of Evolution, The University of Wisconsin College of Agricultural & Life Sciences, The Department of Zoology and The Department of Botany.

Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 [carollee@wisc.edu](mailto:carollee@wisc.edu)

<https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html> Carol Eunmi Lee <[carollee@wisc.edu](mailto:carollee@wisc.edu)>

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## Barcelona PrimateGenomics

INSTITUTE FOR EVOLUTIONARY BIOLOGY  
(UPF/CSIC) in Barcelona, Spain

PhD contract available

The Evolutionary Genomics Group in the Comparative and Computational Genomics program of the IBE (<http://www.ibe.upf-csic.es/>) is willing to recruit a PhD student.

The research group that the successful candidate will join studies genomic variation at both the intraspecific and interspecific levels in hominids. Besides several other research projects, the group runs the Population Genomics Node of the Spanish National Bioinformatics Institute (<http://www.inab.org>), working in close collaboration with the National Genotyping Centre (<http://www.cegen.org>). The group is located at the Evolutionary Biology Unit of the Pompeu Fabra University (<http://www.upf.edu>) and is part of the Barcelona Biomedical Research Park (<http://www.prbb.org>), a renowned centre for Biomedical research that hosts, besides the University, other institutions such as the CRG (Centre for Genomic Regulation) or the CMRB (Barcelona's Centre for Regenerative Medicine). All these organizations share a thrilling and dynamic scientific atmosphere, driven by leading groups in fields such as bioinformatics, molecular biology and evolution. The PRBB is located close to Barcelona's City Centre (right in front of the beach).

The PhD project will be directed by Dr. Tomas Marques-Bonet.

<http://www.upf.edu/ibe/research/research-groups/-marques.html> The project will consist in the detailed analysis and fine characterization of copy number variants in primate genomes.

Candidates should hold a Bachelor's degree (or equivalent) in Biology, Computer sciences or similar. Candidates with strong programming, knowledge on next-generation sequence methods (454 and Illumina) and

experimental background are especially encouraged to apply.

Motivated and potentially competitive applicants should send, before December the 20th and preferably via e-mail, a CV and a short letter of interest including the names of two persons able to provide references to:

Tomas Marques-Bonet ([tomas.marques@upf.edu](mailto:tomas.marques@upf.edu))

Institut de Biologia Evolutiva (UPF-CSIC) Departament de Ciències Experimentals i de la Salut Parc de Recerca Biomèdica de Barcelona Plaça Charles Darwin, 1 08003 Barcelona

[tomas.marques@upf.edu](mailto:tomas.marques@upf.edu)

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## ColoradoStateU EvolutionaryBiology

PhD position in evolutionary ecology at Colorado State University

The Hufbauer lab is filling PhD position in evolutionary biology to work on a collaborative project between CSU and CU Boulder at the interface of demography, modeling and ecological genetics.

The project focuses on the contributions of demography and genetics in the founding and spread of new populations, combining a model biological system (*Tribolium* flour beetles) and quantitative models. The student at CSU will conduct the experiments in the lab of Ruth Hufbauer at Colorado State University (<http://lamar.colostate.edu/~hufbauer/>). We will collaborate closely with mathematical biologists at CU Boulder in Brett Melbourne's lab (<http://www.colorado.edu/eeb/facultysites/melbourne/>).

Previous experience conducting lab experiments using insects or other model organisms would be helpful, and a strong background in evolutionary ecology is vital. The ability to start as early as January 2011 would be a bonus, but at the latest summer 2011.

Please get in touch with Ruth for additional details. When you write, please send a CV that includes information on coursework and grades. Applications can either go through BSPM (<http://www.colostate.edu/Dept/bspm/>) or GDPE (<http://www.ecology.colostate.edu/>).

Ruth A. Hufbauer Associate Professor BSPM, GDPE Colorado State University 1177 Campus Mail Fort Collins, CO 80523-1177 USA

office: C147 Plant Sciences (970) 491-6945 lab: E113/115 Plant Sciences (970) 491-5984 fax: (970) 491-3862 email: [hufbauer@lamar.colostate.edu](mailto:hufbauer@lamar.colostate.edu) <http://lamar.colostate.edu/~hufbauer/> <http://www.invasionsrcn.org/> [hufbauer@lamar.colostate.edu](mailto:hufbauer@lamar.colostate.edu)

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## CRI-FEM Evolutionary Genetics Conifers

PhD opportunity on “Evolution of regulatory elements of adaptive genes in Conifers” Project code: PJ10 AM 03

Contact person: VAROTTO CLAUDIO, PhD [claudio.varotto@iasma.it](mailto:claudio.varotto@iasma.it)

Institutions: Edmund Mach Foundation - Environment Department (IT), University of California at Davis - Department of Plant Sciences (USA)

The project is a collaboration between the group of Dr. Claudio Varotto at the Research and Innovation Centre (CRI) of the Edmund Mach Foundation (<http://www.iasma.it/>), and the group of Prof. David Neale (<http://dendrome.ucdavis.edu/NealeLab/>). The successful candidate will carry out the project mainly at CRI-FEM with a stage of at least 6 months at the University of Davis, California (USA).

We offer a competitive scholarship, subsidized meal benefits, a foreign office providing support for accommodation search and bureaucratic aspects. We aim to help our candidates to develop their creative abilities of students to carry out original scientific research. The training environment of CRI offers an integrated approach on problems related to the domain of natural resources, biodiversity, genomics as well as food production, health, and biotechnologies.

The Institute is located in the wonderful setting of the Eastern Italian Alps, a few Km north of Trento, a renowned location for both summer and winter holi-

days (hiking, climbing, biking, skiing).

**PROJECT SUMMARY DESCRIPTION** The aims of this project are: 1) the identification of regulatory elements (REs) in the promoters of genes involved in adaptive responses in conifers; 2) the analysis of patterns of REs nucleotide variation in conifers; 3) the assessment of the adaptive potential of polymorphisms affecting the REs identified in natural populations of selected conifer species.

Conifers are extremely important tree species, both from an ecological and an economical point of view. Several candidate genes for stress adaptation have recently been identified in conifers or characterized in model species. While most of the studies currently focus on the identification of signals of selective pressure acting on the coding sequences, little is known about regulatory regions.

We are looking for a highly motivated and dynamic candidate to carry out a PhD project aimed at the identification of regulatory elements (REs) in the promoters of genes involved in adaptive responses in conifers. Natural genetic variation affecting the REs identified will be assessed in natural populations of selected conifer species and associated to adaptive differences among them. Population genetics studies will then provide the framework for the statistical identification of naturally occurring regulatory variation in adaptive genes in selected conifer species.

**FELLOWSHIP DESCRIPTION FEM** - Research and Innovation Centre welcomes applications for a 3-year PhD research fellowship starting on Spring 2011 to support brilliant and highly motivated students developing their career in the fields of evolutionary biology / population genetics. The project is part of a larger PhD programme encompassing 11 fellowships. The official language of the programme is English. We welcome applications from students of all countries. Applications can be sent starting from 13 September 2010.

**GENERAL INFORMATION** Applicants will be assessed on the basis of their curriculum and of the letter(s) of references. Referee forms sent by the applicants will not be considered. The grant is for three years and the expected start is February 2011 (Spring 2011 at the latest). The gross salary is 20.000 Euros per year. Students will also benefit of funding for travelling as the projects include a minimum period of 6-months stage at the University of California at Davis. Please clearly indicate the preference for Project code PJ10 AM 03 in your application form. Selected candidates are awarded a 3-years fellowship. The scholarship can be additionally extended for up to 1 year, pending the approval of the FEM PhD Fellowships Committee.

Please note that the CRI issues a specific certificate of attendance, but candidates are asked to register either at the doctoral school of the University partner of the project or of another University, in order to get the conferral of the PhD degree. The selected candidate has 1 year time from the start of the contract to register at the University doctoral school. If the candidate fails to register within the first year, the scholarship will be interrupted.

**ADMISSION REQUIREMENTS** Candidates should hold a Master's degree or equivalent in fields relevant to the research project (e.g. genetics, biology, ecology, environmental or natural science, ). Experience in the fields of evolutionary biology / population genetics are highly preferred but not compulsory. Documented molecular biology laboratory experience and basic computer skills are required.

— / —

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>

## Dalhousie MicrobeDiversity

The Doolittle, Bielawski and Beiko labs at Dalhousie University, in collaboration with Olga Zhaxybayeva (West Virginia) and Marc Ereshefsky (Calgary) are looking for several PhD students and postdocs to join the project "Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes", recently funded by the Canadian Institutes of Health Research as part of the Canadian Microbiome Initiative. The main aim of this project is to understand human-associated microbial communities not only in terms of who is there, but also in terms of what key genetic and metabolic processes are characteristic of different clinical scenarios. This purely bioinformatic project involves the analysis of large genomic and metagenomic datasets from public repositories and from several collaborating research groups.

Key elements of the project include

(i) Analysis of publicly available microbial genomic and metagenomic datasets to delineate appropriate units of diversity. To what extent is it useful to consider microbial species and speciation as key determinants of a microbiome? (ii) Uncovering the determinants

of phenotype for microbes and microbial communities. What important genes, metabolic and evolutionary processes (particularly neutral evolution, adaptation, recombination, and lateral gene transfer) are characteristic of complex individual and community phenotypes (pathogen vs. commensal, healthy vs. diseased)? (iii) Development and deployment of software. We will build a modular suite of software tools that incorporates insights gained from (i) and (ii), and from other sources. The main software framework and graphical interface will be implemented in Python, but management and analysis of large data sets will require certain modules to be written in C/C++.

Individuals with backgrounds in population genetics, microbial genomics, molecular evolution, phylogenetics, bioinformatics, computer science, mathematics or statistics are encouraged to apply. Applications will be considered on an ongoing basis, with positions beginning immediately. Successful applicants will join a thriving multidisciplinary team that is already developing and applying bioinformatics software (see <http://kiwi.cs.dal.ca/Software> for examples), and will have access to several high-performance computing clusters as well as conference travel opportunities, and be active participants in Dalhousie's Centre for Comparative Genomics and Evolutionary Bioinformatics (<http://cgeb.dal.ca/>).

Interested and qualified applicants should send a curriculum vitae and a one-page statement of interest to [microbiome@lists.dal.ca](mailto:microbiome@lists.dal.ca).

[beiko@cs.dal.ca](mailto:beiko@cs.dal.ca)

## DukeU MarinePopulationGenetics

Duke University Deep-Sea Population Genetics We seek at least two exceptional graduate students interested in population genetics and connectivity to join us at Duke in an NSF- recommended study of deep-sea invertebrates from chemosynthetic environments. Our study sites include seeps in the Caribbean, Gulf of Mexico, and Atlantic seaboard and 7 research cruises, at least one of which will use the deep-diving research submersible Alvin. Our team includes oceanographers and modelers at NC State (Roy He and Dave Eggleston) and larval biologists at the University of Oregon (Craig Young and Svetlana Maskalova). Together, this team will integrate biophysical and genetic data in a seascape approach to understanding connectivity. We



are looking for students who already have some research exposure to genetics, have great hands in the lab, will embrace the at-sea experience, have experience in scientific writing, and (ideally) have started programming in “R”. Students accepted to Duke’s PhD programs are guaranteed full support for 5 academic years through a combination of fellowships, teaching assistantships and research assistantships. In addition, we offer 4 years of summer support for each student and a dive to the seafloor in Alvin.

US students are encouraged to apply for a prestigious NSF Graduate Research Fellowship for work at Duke. The website is: [http:// www.nsfgrfp.org/](http://www.nsfgrfp.org/). Deadline for life sciences is 22 November.

Exceptional international students are encouraged to apply for Fulbright and national fellowships for study in the US.

Because Cliff and I are in different parts of Duke, an effective strategy for admission is for potential applicants to consider submitting to the Duke Graduate School through the Biology Department, through the Division of Marine Science and Conservation, and through the University Program in Genetics and Genomics. My understanding is that this strategy will improve chances of acceptance and of a fellowship for qualified applicants.

DUKE University Graduate School Application Instructions (General): <http://gradschool.duke.edu/admissions/index.php> MARINE SCIENCE AND CONSERVATION [http://gradschool.duke.edu/depts\\_progs/degree\\_progs/ms.php](http://gradschool.duke.edu/depts_progs/degree_progs/ms.php) BIOLOGY [http://gradschool.duke.edu/depts\\_progs/degree\\_progs/biology.php](http://gradschool.duke.edu/depts_progs/degree_progs/biology.php) UNIVERSITY PROGRAM IN GENETICS AND GENOMICS [http:// gradschool.duke.edu/depts\\_progs/degree\\_progs/gg.php](http://gradschool.duke.edu/depts_progs/degree_progs/gg.php)

Interested and qualified students should contact Cliff and me for further information.

Cindy Van Dover Director, Duke University Marine Laboratory Chair, Division of Marine Science and Conservation Nicholas School of the Environment 135 Marine Lab Road Beaufort NC 28516 tel: 252-504-7655 fax: 252-504-7648 [c.vandover@duke.edu](mailto:c.vandover@duke.edu)

and

Cliff Cunningham Professor Biology Department Duke University 130 Science Drive Durham NC 27708 tel: 919-660-7356 [cliff@duke.edu](mailto:cliff@duke.edu) <http://www.biology.duke.edu/cunningham> Cindy Van Dover <clv3@duke.edu>

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## ETH Zurich 2 MicrobialEvolution

### Two PhD Positions in Experimental Microbial Ecology

The Molecular Microbial Ecology Group at the Swiss Federal Institute of Technology-Zürich (ETH-Z) and the Swiss Federal Institute of Aquatic Science and Technology (Eawag) has two PhD positions available in experimental microbial ecology. Both positions seek to understand the evolution and implications of cross-feeding, whereby one microorganism consumes metabolic intermediates produced by another microorganism. The objectives of the project are to better understand why cross-feeding sometimes occurs within microbial communities and how cross-feeding can promote diversity within these communities. Denitrification of nitrate to nitrogen gas is used as a model cross-feeding pathway, which has important implications for water quality, air quality, and global warming. The positions are expected to largely focus on experimental work, but may incorporate theoretical components as well. Both positions will begin January 1st, 2011, but this is to some degree negotiable. The positions are funded by the Swiss National Science Foundation for three years, include an annual salary of approximately 57,000 CHF, and cover all tuition costs.

The Molecular Microbial Ecology Group provides a unique opportunity to conduct research in microbial ecology. The group is located at Eawag, which has a broad range of expertise in environmental sciences, including ecology, microbiology, chemistry, and toxicology. The group is also part of the Department of Environmental Sciences at ETH-Z and maintains strong interactions with various groups in experimental and theoretical biology. Both Eawag and ETH-Z are located within the Zürich metropolitan area. The city of Zürich is continuously ranked among the top cities in the world for quality of life and is within close proximity to the Swiss Alps.

Interested applicants should have a Masters degree or equivalent in biological or environmental sciences and have a strong background in experimental microbiology, microbial ecology, and / or microbial evolution. The ability to conduct research independently and to communicate in English is essential. Those interested should send (as PDFs) a cover letter outlining their motivation to work on the project, a CV, a brief summary of research experiences and interests, and contact in-

formation for at least two academic references to Dr. David Johnson (david.johnson@eawag.ch). Review of applicants will begin on November 1st. Informal inquiries before application are encouraged.

Dr. David R. Johnson Swiss Fed Inst Aquatic Sci Technol (Eawag) Dept. Environmental Microbiology Ueberlandstrasse 133 BU-F13 8600 Zürich, Switzerland

Phone: +41 (0)44 823 55 20 Fax: +41 (0)44 823 50 28  
E-mail: david.johnson@eawag.ch

Johnson David Russell <david.johnson@env.ethz.ch>

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## ETH Zurich PopBiol GeneticsInfectiousDiseases

### PHD AND POSTDOC POSITIONS IN POPULATION BIOLOGY AND GENETICS OF INFECTIOUS DISEASES AT THE ETH ZURICH

Positions for two PhD student, a junior and a senior postdoc are available in the groups of Sebastian Bonhoeffer and Roland Regoes at the ETH Zurich. In our groups we study the population biology and genetics of infectious diseases. For more information on our groups see [www.tb.ethz.ch](http://www.tb.ethz.ch). One of the PhD students and the senior postdoc would work in the group of Sebastian Bonhoeffer. The broad research area of these two positions will be the theoretical population genetics of infectious disease (see [www.tb.ethz.ch/research/-Bonhoeffer](http://www.tb.ethz.ch/research/-Bonhoeffer)). Applicants for the PhD position should have strong quantitative skills. We therefore encourage people with a background in mathematics, biostatistics, bioinformatics or physics to apply. For applicants for the senior postdoc position a track-record in studying the emergence and the control of drug-resistance is an advantage. The postdoc position comes with a high degree of independence, and it would be great if you developed your own projects, possibly also involving the more junior members of the group. A strong background in mathematical modelling and computation is required for this position.

The other PhD student and the junior postdoc would work with Roland Regoes, studying the population biology of immune responses against viruses. In the last years Roland Regoes and his group members studied the dynamics of cytotoxic T lymphocyte killing in vivo, and the neutralization of HIV by antibodies (see [www.tb.ethz.ch/research/Regoes](http://www.tb.ethz.ch/research/Regoes)), and the PhD student and the postdoc could work on some of these top-

ics initially. While our research is conducted in close collaboration with experimental immunology and virology laboratories (eg Annette Oxenius and Alexandra Trkola), we are seeking candidates with strong quantitative skills (for example, trained mathematicians, biostatisticians, or physicists).

The starting dates of these positions are fairly flexible. We envisage some time at the end of this year.

Our groups are strongly linked with the experimental ecology group of Paul Schmid-Hempel, and the microbial evolution group of Martin Ackermann at the Institute of Integrative Biology of the ETH Zurich (see <http://www.ibz.ethz.ch/> for more details).

Zurich is a great place to live and to do research. It is the home of two big universities (the University of Zurich and the ETH), and is an attractive city in beautiful surroundings with a multinational population and many educational and recreational opportunities.

To apply send a letter describing your interest in this position, a CV and the names and contact addresses of two referees by email to our secretary Rita Jenny: rita.jenny@env.ethz.ch. Please write "Application for postdoc/PhD position with Sebastian Bonhoeffer/Roland Regoes" into the subject line of your email. The deadline of the application is October 31, 2010. Informal enquires to roland.regoes@env.ethz.ch or sebastian.bonhoeffer@env.ethz.ch are also welcome.

Sebastian Bonhoeffer and Roland Regoes Institute of Integrative Biology, ETH Zurich [www.tb.ethz.ch](http://www.tb.ethz.ch)  
roland.regoes@env.ethz.ch

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## ETHZurich TheoreticalEvolutionaryBiology

### PhD Position in Theoretical Evolutionary Biology

A PhD position is available at ETH Zurich under the supervision of Dr. Jan Engelstädter. The aim of the project is to develop mathematical models for the evolution of genetic exchange in bacteria, with the overarching goal of gaining a better understanding of why sex and recombination are so abundant in nature. An important applied aspect in this project concerns the evolution of resistance to antibacterial compounds in pathogens, which is a major problem in public health. Starting date of the position is January 1st 2011, but this is to some degree negotiable. The position is funded by the Swiss National Science Foundation for three

years.

The successful applicant will be based at the main campus of the ETH Zurich close to the town center. She or he will belong to both the Molecular Microbial Ecology group, led by Prof. Martin Ackermann, and to the Theoretical Biology Group, led by Prof. Sebastian Bonhoeffer. This environment provides ample opportunities for collaborations with other theoreticians as well as experimental biologists. The groups are very international and the working language is English. (Some knowledge of German may be helpful for living in Zurich but is not necessary.) Zurich is a beautiful city that offers many cultural and outdoor activities and a high general quality of life.

Applicants should have a keen interest in evolutionary questions and be highly motivated to address such questions with mathematical models. A strong background in either evolutionary biology (including population biology and genetics) or mathematics is essential, as is the ability to conduct research independently and to communicate proficiently in English. Knowledge of a programming language (e.g., C/C++ or R) is desirable, but not necessary. A Master degree in biology, mathematics, physics or a related field is required for the position.

Applicants should send (as PDFs) a cover letter outlining their motivation to work on this project, a CV, a brief summary of research experiences and interests, and contact information of at least two academic referees to [jan.engelstaedter@env.ethz.ch](mailto:jan.engelstaedter@env.ethz.ch). Reviewing of applications will start on October 18th. Informal inquiries before application are encouraged.

— Dr. Jan Engelstädter Theoretical Biology Institute of Integrative Biology (IBZ) ETH Zurich, Universitätsstr.16 ETH Zentrum, CHN K12.1 CH-8092 Zurich Switzerland

phone: +41 44 6320659 fax: +41 44 6321271 <http://www.tb.ethz.ch/people/ejan>  
[jan.engelstaedter@env.ethz.ch](mailto:jan.engelstaedter@env.ethz.ch)

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## Frankfurt EvolutionPollination

This is a MIME message. If you are reading this text, you may want to consider changing to a mail reader or gateway that understands how to properly handle MIME multipart messages.

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charset=UTF-8 Content-Transfer-Encoding: 8bit

A PhD position in “Movement/Pollination ecology” is available at the Biodiversity and Climate Research Centre (BiK-F), Lab K. Böhning-Gaese, in Frankfurt am Main, Germany.

The successful applicant will investigate the determinants of bird pollination and plant reproduction in South African heathlands. He/she will examine how resource distributions shape bird movements and plant reproduction, combining observational and experimental approaches. The project is carried out in close collaboration with another PhD-student (supervised by Frank Schurr, University of Potsdam) and aims at a deeper understanding of spatial interactions between plants and animals. The applicant should hold a master/diploma in Biology or a related field, and needs to have expertise in conducting ecological field work and a strong interest in statistical modelling, preferably with R. He/she is expected to carry out several field work periods in South Africa and to analyze the data with advanced statistical methods. Experience in tropical/subtropical ecosystems, in experimental pollination studies and basic ornithological knowledge are an advantage. Good written and oral English language skills are required. Please send your application by e-mail attachment in a single pdf file, mentioning the reference of this position (#B40), and including a letter outlining your suitability and motivation, a detailed CV, contact details of 2 referees, a list of your most important publications and a summary of your thesis before September 30th to [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de). For scientific enquiries please write to [matthias.schleuning@senckenberg.de](mailto:matthias.schleuning@senckenberg.de). More details about the announcement and application procedures are found at: [http://www.bik-f.de/files/-stellenausschreibungen/b40\\_phd.schleuning\\_web.pdf](http://www.bik-f.de/files/-stellenausschreibungen/b40_phd.schleuning_web.pdf)

— Dr. Matthias Schleuning Senckenberg Research Institute Biodiversity and Climate Research Centre BiK-F Senckenberganlage 25 D-60325 Frankfurt am Main Germany

Phone: (+49) 69 / 75 42 - 1892 Fax: (+49) 69 / 75 42 - 1800 E-Mail: [mschleuning@senckenberg.de](mailto:mschleuning@senckenberg.de)

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## Italy 11 EvolutionaryBiology

FEM PhD Fellowships CALL for applications 2010-2011

11 FEM Fellowships starting on Spring 2011 FEM - Research and Innovation Centre welcomes applications for 3-years research fellowships to support brilliant and highly motivated students to get the PhD title in the fields covered by the Centre . We welcome applications from students of all countries. The official language of the programme is English. Applications can be sent from 13 September 2010.

General information Eleven (11) scholarships are available for PhD research in the fields covered by the strategic research areas of our Centre: Environment and Natural Resources Area , Food Quality and Nutrition Area, Genomics and Crop Biology Area. Applicants will be assessed on the basis of their curriculum and of the letters of references. Referee forms sent by the applicants will not be considered. The grant is for three years and the expected start is February 2011 (Spring 2011 at the latest). The gross salary is 20.000 Euros per year. Students will also benefit of funding for travelling to our projects. IASMA partner institutions as the projects include a minimum period of 6-months-stay at the institution co-responsible for the single PhD project. There is a general empowerment of the student choice when applying to our PhD research projects. Candidates can postulate for one to three specific projects. Selected candidates are awarded a 3-years fellowship. The scholarship can be additionally extended for up to 1 year, pending the approval of the FEM PhD Fellowships Committee. Please note that the CRI issues a specific certificate of attendance, but candidates are asked to register at the doctoral school of the University partner of the project or of another University, in order to get the conferral of the PhD degree. The selected candidate has 1 year time from the start of the contract to register at the University doctoral school. If the candidate fails to register within the first year, the scholarship will be interrupted.

Admissions requirements Candidates should hold a Master's degree or equivalent in fields relevant to the research projects (e.g. biology, chemistry, ecology). The candidature should also be accompanied by 2 letters of references.

#### DEADLINES

CRI PhD Office receives applications from September 13 to October 18, 2010.

HOW TO APPLY To apply, send by e-mail the application form, your cv (1 page max) and two referee forms, not later than 18 October 2010, at the following address: [phdfem@iasma.it](mailto:phdfem@iasma.it). The referee forms must be sent by your referees: referee forms sent by the applicants will not be considered.

13 September 2010

FEM PhD Office Research and Innovation Centre Fondazione Edmund Mach - IASMA via E. Mach, 1 38010 San Michele all'Adige (TN) Tel + 39 0461 615601- 559 Fax +39 0461 615183

[phd.fem <phd.fem@iasma.it>](mailto:phd.fem@iasma.it)

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### MississippiStateU IguanaPopulationGenetics

The Welch Lab at Mississippi State University is looking for graduate students to work on the population genetics of Caribbean rock iguanas. We are interested in recruiting both MS and PhD students that would like to pursue a degree in Biological Sciences. Students will also be able to choose between applied conservation genetics research projects as well as more basic research projects focused on the evolutionary dynamics of natural populations. Island populations of iguanas are particularly useful for these types of studies because gene flow between islands is typically low, and population sizes vary providing natural replicates for study. This research is facilitated by extensive collaboration with leading conservation biologists in the field. Participants in the Welch lab will primarily be asked to conduct molecular genetic analyses. However, fieldwork is highly encouraged. Three students working on one project have already conducted extensive work in the Turks and Caicos Islands. Funding for students will initially be provided by means of teaching assistantships with the potential for research assistantships dependent on the availability of external funding. We are looking for students to start at any point in 2011. Please contact Mark Welch at [welch@biology.msstate.edu](mailto:welch@biology.msstate.edu) if you are interested. Also, a CV that includes information regarding prior education including coursework and grades would be appreciated.

Mark E. Welch, PhD Mississippi State University

The Department of Biological Sciences PO BOX GY  
Mississippi State, MS 39762

[welch@biology.msstate.edu](mailto:welch@biology.msstate.edu)

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## NorthCarolinaStateU PlantSystematicsEvolution

Ph.D. Student: Evolutionary developmental genetics of inflorescence architecture in Dogwoods - North Carolina State University

We are looking for a Ph.D. student to participate in a NSF-funded project investigating the genetic bases of inflorescence evolution in the dogwood family. The student will be working with a multidisciplinary team of three faculty members in the Department of Plant Biology and Department of Genetics at NCSU. Background and training in plant genetics, evolutionary development or molecular systematics is required. A MS degree and experiences in working with flowering plants in the interface of the three areas are preferred. Experimental skills in plant genetic transformation, RNA in-situ hybridization, RT-PCR or qRT-PCR, and phylogenetics are desired. English skills in writing, speaking, and reading are expected.

The student will be supported by a combination of research funding and teaching assistantship. Women and other minority categories are encouraged to apply. Please send application by e-mail attachment to [jenny\\_xiang@ncsu.edu](mailto:jenny_xiang@ncsu.edu) including a letter outlining your suitability for the position, a detailed CV, and contact details of 3 referees. The position is available in the Spring 2011.

Jenny Xiang

Qiu-Yun (Jenny) Xiang, Ph.D. Associate Professor Department of Plant Biology North Carolina State University Gardner Hall 2115 Raleigh, NC 27695-7612 USA Phone: 919-515-2728 Fax: 919-515-3436 Homepage: <http://www4.ncsu.edu/~qyxiang> Jenny Xiang <[jenny\\_xiang@ncsu.edu](mailto:jenny_xiang@ncsu.edu)>

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## StockholmU InsectCoevolution

\*PhD position in Ecology/Evolution\* \*\*Coevolution in tritrophic systems\*\* \*\*

At the Department of Botany, Stockholm University, ref. no. 2/2010

Coevolution underlies the diversity of life, and is therefore an essential process in evolutionary research. In food webs, evolution may be affected by several species and the understanding of underlying processes necessitates a multifaceted approach. This project aims to explore coevolution in tritrophic food webs associated with the plant purple loosestrife (*Lythrum salicaria*). The project will explore the complexity of coevolutionary processes through a collaboration between plant ecology, insect ecology, insect immunology and chemical ecology. This collaboration is needed to provide a more complete picture on the ecological and evolutionary effects of species interactions. As a PhD-student in this project, you will therefore get a broad experience on modern coevolutionary research.

Further information: Professor Peter Hambäck, Dept. of Botany, Stockholm University, 106 91 Stockholm. Ph +46 (0)8 161288 e-mail: [peter.hamback@botan.su.se](mailto:peter.hamback@botan.su.se)

\*The application\* should include a letter of intent, a certified curriculum vitae that includes information on previous education, two copies of the masters thesis (or 'examensarbete'), other documents supporting your competence and suitability for the position, and address and phone number to two reference persons. The application can be written in English or Swedish.

The minimum requirements are completed exam on advanced level, or studies corresponding to at least 4 years education, or 240 credit points, including 60 credit points at advanced courses. Previous studies should include at least 15 credit points in ecology, or corresponding courses, and a completed master thesis (or 'examensarbete') of at least 30 credit points, in ecology or in a related field.

Applications will be evaluated based on the applicant's knowledge of ecological theory and applications, field-work experience, written and spoken English, creativity, power of initiative, independence and ability to collaborate. Evaluations will be based on results on University courses, quality of master's thesis, references, interviews and the letter of intent. The successful candidate must possess a driving license in order to carry out the field work.

A PhD education is 4 years (48 months). During the first two years the student receives a scholarship (Sw: "utbildningsbidrag") and during the last two years the student has a PhD position (Sw: "doktorandanställning").

The application should be labeled with the reference number 2/2010, and should be received at the following address no later than 6 October, 2010:

Registrator Anna Kjellin, Department of Botany,

Stockholm University, SE-10691 Stockholm, Sweden. You may also send your application to [anna.kjellin@botan.su.se](mailto:anna.kjellin@botan.su.se).

Union representatives: Bo Ekengren, SACO ([saco@saco.su.se](mailto:saco@saco.su.se)), Lisbeth Häggberg, ST ([lisbeth@st.su.se](mailto:lisbeth@st.su.se)) +46 8 162000, Gunnar Stenberg, SEKO, +46 70-316 43 41, and PhD student representative ([do@sus.su.se](mailto:do@sus.su.se)).

Peter Hambäck <[peter.hamback@botan.su.se](mailto:peter.hamback@botan.su.se)>

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## UAlaska Fairbanks PlantSystematics

M.S. student position in molecular plant systematics at the University of Alaska Fairbanks

The Ickert-Bond lab (<http://users.iab.uaf.edu/~stefanie.bond/>) at the University of Alaska Fairbanks is seeking to fill a position for a M.S. student to pursue research in molecular plant systematics to begin January 2011. While receiving graduate training in molecular plant systematics, the student will act as a herbarium assistant in the UA Museum of the North Herbarium (<http://www.uaf.edu/museum/collections/herb/>) helping to coordinate a large digitization project focused on imaging and databasing vascular plant collections.

**APPLICATION** Applicants should have a strong interest in plant systematics and be working towards a career or further degree involving collections based research, phylogenetics, taxonomy, and/or evolutionary biology.

Applications should include: 1) cover letter indicating specific interest in this position, 2) general statement of research interests and experience 3) CV, including names and contact information for at least three references. Please send materials to Dr. Steffi Ickert-Bond ([smickertbond@alaska.edu](mailto:smickertbond@alaska.edu)).

The student selected for this position will be required to successfully enroll as a graduate student in the Department of Biology and Wildlife at the University of Alaska Fairbanks. For information about policies and entrance requirements pertaining to university admission see: <http://www.uaf.edu/admissions/grad/us/> and the Biology & Wildlife website: <http://www.bw.uaf.edu/> Location: Fairbanks is a modern community of 90,000 people in the interior of Alaska. A two-hour drive from Denali National Park, the area also has world-class cross-country skiing and numerous outdoor op-

portunities. Experience the last frontier by seeing the northern lights for over half the year, attending dog sled races and backpacking in the arctic wilderness.

Steffi Ickert-Bond <[smickertbond@alaska.edu](mailto:smickertbond@alaska.edu)>

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## UBasel Biogeography

PhD Position in Biogeography 2010, Basel, Switzerland

Project title: Life history and Biogeography: a comparative evolutionary study of the Terrestrialisation of African amphibians September 7, 2010

PhD-POSITION IN Biogeography. We are looking for a highly motivated graduate student interested in biogeography. The research of our group is focussed on diversification patterns - and the processes that govern them. The research in our group has focused primarily on the phylogenetic diversification of amphibians (our model group), and mainly on the continent of Africa (our model area). The research is characterized by the integration of a broad range of techniques - fieldwork, taxonomy, molecular and morphological systematics, traditional descriptive and modern biogeographic approaches - used to interpret patterns of diversity in Africa, particularly in rainforest habitats. The SNF funded project seeks to address fundamental questions on how life history strategies in African amphibians have developed over time and space. We address this question by looking at the biogeographical correlates that might explain the evolution of the diversity of developmental terrestrialization in African amphibians. This will be investigated through state of the art methods and novel approaches that combine ecological and evolutionary approaches. We will look for significant correlations between life history strategy traits and environmental parameters (e.g. climate and habitat). Complementing this we will conduct phylogenetic analyses to reconstruct evolutionary trees (time-trees). Understanding the overall patterns by which life histories have changed through evolutionary time will elucidate potential mechanisms of how, and under what circumstances key innovations, such as terrestrialization, have developed spatially and temporally. **BACKGROUND.** Applicants should have a MSc degree (or equivalent) in a relevant field, and a strong background and keen interest in systematics. Previous experience in molecular systematics is necessary, and an interest in learning GIS and climatic niche modelling techniques would be important. **RESEARCH**

GROUP AND INSTITUTE. Our research group is part of the Biogeography Institute at the University of Basel, which hosts groups sharing a common interest in biogeography (see [www.biogeography.unibas.ch](http://www.biogeography.unibas.ch) for more information). For the project we are also collaborating with other international institutes in Jena, Berlin, Trento and London. POSITION AND APPLICATION. The PhD-position is funded through a Swiss National Science Foundation (SNF) research grant for the duration of three years. Starting date is negotiable, but should ideally be between 1st November 2010 and 1st January 2011. Please send your application documents (CV, list of publication, short summary of your current research, a statement on your reasons to pursue a PhD, contact details for two referees) by e-mail and as single pdf to: Dr. Simon Loader, Dept. of Environmental Sciences, Institute of Biogeography, University of Basel, Klingelbergstr. 27, CH-4056 Basel, Switzerland. E-mail: [Simon.Loader@unibas.ch](mailto:Simon.Loader@unibas.ch); internet: [www.biogeography.unibas.ch/loader](http://www.biogeography.unibas.ch/loader) Applications received on or before **\*\*Friday, 1st October 2010\*\*** will be given full consideration

Dr Simon Loader Dept. of Environmental Sciences  
Institute of Biogeography University of Basel Klingelbergstr. 27 CH-4056 Basel Switzerland

Tel: ++41 61 267 07 23 e-mail: [Simon.Loader@unibas.ch](mailto:Simon.Loader@unibas.ch)  
Homepage: <http://www.biogeography.unibas.ch/loader>  
Personal Homepage: <http://web.mac.com/simon.loader>  
Tanzanian Herps Homepage: <http://www.tanzaniaherps.org/>  
Associate Editor, The Herpetological Journal <http://www.ingentaconnect.com/content/bhs/thj>  
Simon Loader <[Simon.Loader@unibas.ch](mailto:Simon.Loader@unibas.ch)>

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### **UBritishColumbia ConservGenomics**

A PhD graduate assistantship is available in the laboratory of Dr. Michael Russello at The University of British Columbia (Okanagan Campus) in the area of population and conservation genomics starting May 2011. I am looking for a highly motivated graduate student to join our group studying fine-scale adaptive population divergence in a number of systems centering on vertebrate species of conservation concern. There are opportunities for both laboratory and field-based research, although all projects involve the use of high-throughput DNA-based methodologies. Individuals with experience and/or interest in SNP dis-

covery using next-generation sequencing are especially encouraged to apply. Please visit my website for further details: <http://people.ok.ubc.ca/mirussel/> Candidates should have a strong undergraduate background in biology, and prior research experience with molecular laboratory techniques and bioinformatics is desirable. For more information contact Michael Russello at [michael.russello@ubc.ca](mailto:michael.russello@ubc.ca). Additional information about our Biology graduate program at UBC can be found at the following website: <http://web.ubc.ca/okanagan/biol/graduate.html> [michael.russello@ubc.ca](mailto:michael.russello@ubc.ca)

Michael Russello Assistant Professor Department of Biology University of British Columbia Okanagan Campus Kelowna, British Columbia Canada

[michael.russello@ubc.ca](mailto:michael.russello@ubc.ca)

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### **UEdinburgh PopulationQuantitative**

Ph.D. Studentship at The Roslin Institute (University of Edinburgh)

We are currently recruiting a Ph.D. student (ONLY UK RESIDENTS) to evaluate and apply novel statistical techniques for diversity-based gene mapping. This four-year studentship is funded by a Genesis Faraday CASE BBSRC award with an enhanced stipend and other benefits provided by Genesis Faraday and the CASE partner, Aviagen Ltd.

The rationale for this gene-mapping approach is that variation will be reduced in regions of the genome subject to positive selection. Patterns of genome-wide diversity may reveal regions that have been under strong selection and contain genes with large phenotypic effects. This project will focus on the development, evaluation and application of methods of testing for selection using both simulated and genomic poultry data. This studentship will thus provide training in population and quantitative genetics, statistical methods, scientific computing and bioinformatics.

The student will be based at The Roslin Institute and the Institute of Evolutionary Biology (IEB) at the University of Edinburgh. The Edinburgh genetics research community is thriving, with strong expertise in population and quantitative genetics, making it an exciting place to study. The student will also spend time at Aviagen Ltd (Edinburgh), one of the major poultry breeders in the world with a strong commitment to research.

We are seeking an enthusiastic individual with an interest in population and evolutionary biology or animal genetics and aptitude with computer-based numerical analyses. The UK-based candidate should possess a good quality first degree in a relevant subject. Enthusiasm, dedication and aptitude are the most important characteristics; additional training in genetics and genome analysis are available at IEB.

The project involves a collaboration between Pam Wiener (Roslin), Chris Haley (MRC Human Genetics Unit), Brian Charlesworth (IEB) and Kellie Watson (Aviagen). Applications including a full CV with names and addresses (including email addresses) of two academic referees, should be sent to:

Pam Wiener, The Roslin Institute, The University of Edinburgh, Roslin, Midlothian, EH25 9PS. Email: pam.wiener@roslin.ed.ac.uk. Informal queries requesting further information are welcome. Closing date: 11 October 2010.

Pam Wiener The Roslin Institute University of Edinburgh Roslin Midlothian EH25 9PS phone: 44 (0) 131 527 4464 fax: 44 (0) 131 440 0434

pam.wiener@roslin.ed.ac.uk

Please send your application or enquiries to Saskya van Nouhuys (saskya.vannouhuys@helsinki.fi). Your application should include a short CV, a one page explanation of your motivation and suitability for the project and the e-mail addresses of three references. We will begin interviews in November 2010, and the position will start spring 2011. –

Saskya van Nouhuys <http://www.eeb.cornell.edu/sdv2/saskya%20www/index.html> Academy research fellow Metapopulation Research Group <http://www.helsinki.fi/science/metapop/> Department of Biological and Environmental Sciences Mobile phone: + 358 40 508 2549

and

At Cornell University:

Visiting Associate Professor Department of Ecology and Evolutionary Biology <http://www.eeb.cornell.edu/> Adjunct Associate Professor Department of Entomology <http://www.entomology.cornell.edu/> Fax: (607) 255-8088 phone (607) 327-0014

saskyavn@gmail.com

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## UHelsinki ParasitoidPopulationBiology

We are looking for a PhD student with a background in population or community ecology, and an interest in parasitoids, to join the Metacommunity Ecology Group, which is part of the Metapopulation Research Group at the University of Helsinki (<http://www.helsinki.fi/science/metapop/>). Potential research topics are (1) parasitoid metacommunity structure, (2) sex ratio and spatial population structure of contrasting parasitoid species, and (3) patterns and mechanisms of parasitoid virulence and host susceptibility. The project will have a field and laboratory component and, depending on the student can also have a mathematical component. The applicant must have a Masters Degree or equivalent. For information about the research system see: <http://www.helsinki.fi/science/metapop/metacom/>. We have a strong international research environment with opportunities for mixing among ecologists, molecular ecologists and mathematicians. The position is for completion of a PhD within four years, and includes a salary of about 2,300 /month.

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## UKansas EvolutionaryBiol

Graduate positions: opportunities for Graduate Study in Evolutionary Biology at The University of Kansas

The Department of Ecology and Evolutionary Biology (EEB) at the University of Kansas ( <http://www2.ku.edu/~eeb/> ) has an active and energetic group of faculty with research interests in evolutionary genetics who are currently recruiting graduate students. Graduate opportunities are available with the faculty listed below as well as with other faculty in EEB at The University of Kansas. If you are interested in applying, please contact faculty members directly.

PhD candidates in EEB are provided competitive support packages (for more information, go to <http://www2.ku.edu/~eeb/graduate/> ). In addition, exceptional PhD students who are US citizens may be eligible for scholarships from the Self Foundation ( <http://www.ku.edu/~selfpro/> ). The Self Graduate Fellowship is a four-year award including annual stipend, full tuition and fees, and a professional development program.

Faculty



Dr. Justin Blumenstiel: <http://www.people.ku.edu/~jblumens/> Research - evolutionary genetics, epigenetics, genetic conflict, RNA silencing

Dr. Paulyn Cartwright: <http://www.people.ku.edu/~pcart/labwebsite/> Home.html Research - Hydrozoan phylogenetics and evolution, evolution of development, character evolution, transcriptomics

Dr. Jennifer Gleason: <http://www.people.ku.edu/~jgleason/home.html> Research - sexual selection, behavioral genetics, quantitative genetics, evolution of behavior, *Drosophila*

Dr. Lena Hileman: <http://www.people.ku.edu/~lhileman/HilemanLab/> Home.html Research - evolution of floral morphology, evolution of development, molecular evolution, epigenetics

Dr. Mark Holder: <http://phylo.bio.ku.edu/> Research - phylogenetic methods, bioinformatics, modeling sequence evolution

Dr. John Kelly: <http://www2.ku.edu/~eeb/faculty/kellyj.shtml> Research - plant genetics and evolutionary theory

Dr. Maria Orive: <http://www2.ku.edu/~eeb/faculty/orive.shtml> Research - theoretical evolutionary genetics, gene flow, population structure

Dr. Joy Ward: <http://web.ku.edu/~jwardlab/index.shtml> Research - ecological genomics, plant physiology, climate change

lhileman@ku.edu

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## UKonstanz EvoDevo

PhD position in evo-devo phenotypic plasticity research at the University of Konstanz, Germany

We are looking to recruit a PhD student with an interest in vertebrate evo devo, to examine the molecular basis of phenotypic plasticity in an adaptive trait of cichlid fishes, and its importance to evolution. It is known that diet can directly influence jaw morphology in some African cichlids, however the epigenetic mechanism by which this occurs remains uncharacterized. The project combines animal physiology with a range of modern molecular biology techniques to test the theory that strain-mediated remodeling plays a fundamental role in the observed phenotypic plasticity. This PhD student position is a part of a newly funded DFG-project in our laboratory, and will provide a Ph.D. salary for

three years. The candidate should have experience in one or more of the following techniques: cloning, microarray, QRT-PCR or in situ hybridization.

This project is being conducted within the laboratory of Prof. Axel Meyer, which combines both world-class fish breeding and molecular laboratory facilities. The Ph.D. student will have the opportunity to join the newly formed International Max Planck Research School in Organismal Biology, housed here at the University of Konstanz. This is an excellent opportunity to join an exciting research environment.

Please send a statement of your research interests, your CV and two letters of reference by the 15th of October.

Helen Gunter

[helen.gunter@uni-konstanz.de](mailto:helen.gunter@uni-konstanz.de)

<http://www.evolutionsbiologie.uni-konstanz.de/index.php?section=109>

<http://www.zukunftskolleg.uni-konstanz.de/>

[-personen/fellows/helen-gunter/](http://www.zukunftskolleg.uni-konstanz.de/-personen/fellows/helen-gunter/)

Helen Gunter

<[helen.gunter@uni-konstanz.de](mailto:helen.gunter@uni-konstanz.de)>

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## UMassAmherst EukMicrobialEvolution

GRADUATE STUDENT POSITIONS Molecular/Genome Evolution in Microbial Eukaryotes Smith College - UMass Amherst

I am looking for highly motivated students to work on molecular systematics and genome evolution of microbial eukaryotes. Applicants should have skills/interest in molecular systematics, bioinformatics, microbiology and/or molecular evolution. Potential projects include: 1) bioinformatic and/or experimental analyses of eukaryotic phylogeny and 2) characterization of genome properties from microbial eukaryotes, with a focus on ciliates and amoeboid lineages.

Research in the my lab aims to elucidate principles of evolution in eukaryotes through analyses of microbial groups, and to assess how these principles apply (or fail to apply) to other organisms. Currently we focus on four interrelated areas: (1) Characterizing evolutionary relationships among eukaryotes; (2) Reconstructing the ciliate tree of life through multigene analyses; (3) Exploring the evolution of ciliate and foraminifera genomes; (4) Describing the phylogeography of coastal marine ciliates.

Graduate students in the lab join either through the MS program at Smith College or the Ph.D. program in Organismic and Evolutionary Biology (OEB) at the University of Massachusetts Amherst. Interested individuals should visit the web sites below and contact Dr. Laura Katz directly (lkatz@smith.edu)

Laura Katz, Smith College <http://www.science.smith.edu/departments/Biology/lkatz/-Research.htm> OEB at UMass Amherst <http://www.bio.umass.edu/oeb/> Smith College MS in biology <http://www.smith.edu/biology/graduate.php> lkatz@smith.edu

## UOtago NZ Genetics Cryptic Female Choice

Ph.D. Project Opportunity Available to Investigate the Genetic basis of Cryptic Female Choice in Chinook Salmon

We are currently seeking a student with interests in genetics, evolution, and/or behavioural ecology to conduct research into the genetic basis of possible cryptic female choice in Chinook salmon.

**Project Description** In many species females can control fertilisation after mating via behavioural, morphological, and physiological mechanisms - a process called cryptic female choice (CFC). While widespread, it is generally unknown, if and how CFC might be exerted in external fertilisers, where eggs and sperm are shed simultaneously into the surrounding water. We demonstrated in salmon that ovarian fluid, a viscous substance released with eggs during spawning, differentially alters male sperm function in a female-dependent fashion, and thus that females may exert cryptic control of male reproductive success (Rosengrave et al.2008. A mechanism for cryptic female choice in chinook salmon. *Behavioral Ecology* 19: 1179-85). The rationale for this CFC is unknown, but our hypothesis is that ovarian-fluid-mediates sperm selection promoting favoured genetic combinations that enhance offspring fitness. We will test this hypothesis using a novel combination of computer assisted sperm analysis, compositional analyses, replicated paired-male competitive in vitro fertilisation experiments that mimic the gametic microenvironment, and genetic screens of MHC class I, class II and microsatellite loci to establish parentage. Using these approaches we will determine (i) the effects of a given female's ovarian fluid on a male's sperm func-

tion, (ii) how this male x female interaction influences male reproductive success, (iii) whether particular male and female genotype combinations (MHC I, II and microsatellites) are associated with greater or lesser sperm performance and male reproductive success, and (iv) whether any compositional differences among gametic fluids explain the patterns we observe. Our expectation is that the successful PhD student will focus on tasks ii), and iii), while contributing to the others.

**The Ideal Candidate** The ideal candidate will possess experience in molecular genetics, evolutionary genetics and behavioural ecology. They will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research programme. They will be a competent laboratory worker, with experience of all routine molecular genetic techniques, particularly microsatellite genotyping and sequencing, and should be computer literate with familiarity with database management and statistical analyses. Minimum qualifications: B.Sc. (Hons) and/or M.Sc. in Genetics, Molecular Biology, Molecular Ecology or equivalent with an A- average or better.

**Scholarship Funding** Financial support should be available for a high achieving student with an A- average or better via a University of Otago or Departmental scholarship see <http://www.otago.ac.nz/-study/scholarships/>.

**Illegibility** The University of Otago and Departmental scholarships are open to all nationalities. However, overseas candidates for whom English is not a first language must satisfy the English Language Requirements of the University to be eligible for study (see [http://www.otago.ac.nz/international/-postgraduate/english\\_requirements.html](http://www.otago.ac.nz/international/-postgraduate/english_requirements.html)). Other eligibility criteria are detailed here [http://www.otago.ac.nz/international/postgraduate/-entrance\\_requirements.html](http://www.otago.ac.nz/international/postgraduate/-entrance_requirements.html). How to Apply Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmill. Please send your Curriculum Vitae, a copy of your academic transcript, a sample of your written scientific work and the names of three referees with a covering letter to:

Professor Neil J. Gemmill Centre for Reproduction and Genomics (www.crg.org.nz < <http://www.crg.org.nz> > ) e-mail: neil.gemmill@otago.ac.nz <mailto:neil.gemmill@otago.ac.nz>

The closing date for the main round of University of Otago Scholarships is 1 November 2010 so interested applicants should contact me as soon as possible to avoid missing this deadline.

Neil J. Gemmill Professor and Director Centre for Re-

production and Genomics Department of Anatomy & Structural Biology University of Otago, PO Box 913 Dunedin 9054 New Zealand

Phone: +64 3 479 6824 Fax: +64 3 479 7254

neil.gemmell@otago.ac.nz

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## UPerpignan EvolutionaryEpigenetics

PhD position in Environmental and Evolutionary Epigenetics

A PhD position is available at the Center for Tropical and Mediterranean Biology and Ecology (UMR5244, CNRS/University of Perpignan, France) to work on the relation of environmentally induced genetic and epigenetic changes and adaptive evolution. The position is funded by the French National Research Agency (ANR) and will be performed in collaboration with the Institute of Human Genetics (UPR1142 CNRS Montpellier, France), Oregon State University (US) and the CPqRR/FIOCRUZ (Brazil). The PhD student will work with Christoph Grunau (Perpignan) and Jérôme Buard (Montpellier). Specifically, the PhD project consist of studying stress-induced changes in epigenetic, genetic and transcription status by whole (epi)genome approaches (massive sequencing based) to deliver an integrated view of events that lead to adaptive evolution in the human blood fluke *Schistosoma mansoni*.

The candidate should have a strong interest in the relation of epigenetics to evolution. A good background in either molecular biology, evolutionary biology, comparative genomics of parasitology is required. Candidates of all nationalities can apply, but they should be proficient in spoken and written English. French language skills, although helpful, are not essential.

The position is for three years. The student will be enrolled into the interdisciplinary graduate school "Energy and Environment (E2)". Net salary is 1300-1600 Euros/month including social security and full health/dental insurance.

Deadline for application is December 27, 2010 but candidates must contact Ch. Grunau (christoph.grunau@univ-perp.fr) before the end of November 2010. Applicants should send a letter of motivation, a CV (1-2 pages) and the names and email-addresses of one or two referees by email.

Perpignan is located in Southern France at the Mediterranean Sea close to the border with Spain. The region has a rich cultural and natural heritage. The town has an airport with daily connections to Paris and the UK, and is linked through the high-speed train (TGV) system to mayor European cities.

Further information: <http://methdb.univ-perp.fr/-epievo/> <http://cbetm.univ-perp.fr> Christoph Grunau <grunau@methdb.net>

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## UPuertoRico EvolutionaryButterflyGenomics

Fellowship for a Hispanic, USA resident Ph.D. student is offered at the University of Puerto Rico in the Lab of Riccardo Papa.

Riccardo Papa: I am a new Faculty member starting a lab at the University of Puerto Rico, Rio Piedras. Since I was an undergraduate student, I was attracted by the incredible diversity of shape and color of each living organism. With my research, I try to understand the origin and evolution of natural diversity. My research interests focus on the interaction between the environment and its living organisms, with particular emphasis on understanding how new phenotypes arise and evolve in association with the surrounding ecosystem. My work explores phenotypic plasticity as a source of variation for natural selection and adaptation to work upon. To investigate what governs pattern diversity, what limits it, and what promotes its potentials, I combine methods of pure genetics, phylogenetics, developmental cell biology, and functional genomics. I am especially interested in butterfly wings patterns, because I am attracted to the possibility of combining population biology (natural selection and adaptation), with genetics and developmental biology.

I am seeking a Ph.D. student interested in working on an interdisciplinary project in the area of evolutionary biology. Specific project can be discussed with the applicant. The candidate should have a strong background in molecular and evolutionary biology and be highly motivated. Ability to work in a team is essential. The project is expected to be very demanding but rewarding and asks for an independent and creative mind. The candidate should have a strong interest in experimental molecular work on insects and a good working knowledge of bioinformatics. Proficiency of the English language is required. The study will involve field and

laboratory work and will present the possibility to carry out part of the study at UC Irvine (California) or at the Smithsonian Tropical Research Institute in Panama. A stipend for at least the first two years is guaranteed, but the applicant has to meet the following requirements: a) Hispanic origin, b) USA resident.

Additional information: My work is in collaboration with an extended group of colleagues that creates a vibrant and enjoyable scientific community. My lab is located at the University of Puerto Rico- Rio Piedras (<http://www.uprrp.edu/>). The University is in San Juan, the capital of Puerto Rico, a very energetic city that offers a wide variety of restaurants and activities blended with a Caribbean life style (<http://www.topuertorico.org/city/sanjuan.shtml>). The island is a mix of historical and naturalistic sites with plenty of exotic beaches. The international Luis Muñoz Marín airport is in the main city and connects San Juan to the major cities in the USA, Europe and South America (<http://www.san-juan-airport.com/>). Puerto Rico is bilingual: Spanish and English. As part of my lab, I have insectaries in the botanical garden where I can rear butterflies ([http://en.wikipedia.org/wiki/San\\_Juan\\_Botanical\\_Garden](http://en.wikipedia.org/wiki/San_Juan_Botanical_Garden)). You can also go to my Lab website (under construction) to get more information about me and my research: <http://www.wix.com/ricpapa/Papa-Riccardo-Lab> Recommended articles to read: - Counterman B. A, Araujo-Perez F., Hines H. M., Baxter S. W., Morrison C. M., Lindstrom D. P., Papa R., Ferguson L., Joron M., French-Constant R. H., Smith C. P., Nielsen D. M., Chen R., Jiggins C. D., Reed R. D., Halder G., Mallet J., McMillan W. O (2010). Genomic hotspots for adaptation: The population genetics of Müllerian mimicry in *Heliconius erato*. *Plos Genet.* 5; 6 (2): e1000796. - Papa R., Martin A., Reed R. D. (2008). Genomic hotspots of adaptation in butterfly wing pattern evolution. *Current Opinion in Genetics and Development* 18: 559-564. - Joron M., Papa R., Beltrán M., Chamberlain N., Mavárez J., Baxter S., Bermingham E., Humphray S., Rogers J., Beasley H., Barlow K., French-Constant R., Mallet J., McMillan, W. O., Jiggins C. D. (2006). A Conserved Supergene Locus Controls Colour Pattern Diversity in *Heliconius* Butterflies. *Plos Biol.* 4 (10): e303. - Martin A, Kapan DD, Gilbert LE, 2010 Wing Patterns in the Mist. *PLoS Genet* 6(2): e1000822. doi:10.1371/journal.pgen.1000822 - Quek, S. P., B. A. Counterman, P. Albuquerque de Moura, M. Z. Cardoso, C. R. Marshall, W. O. McMillan and M. R. Kronforst. 2010. Dissecting mimetic radiations in *Heliconius* reveals divergent histories of convergent butterflies. *Proc. Natl. Acad. Sci. USA* 107: 7365-7370. - Chamberlain, N. L.\*, R. I. Hill\*, D. D. Kapan, L. E. Gilbert and M.

R. Kronforst. 2009. Polymorphic butterfly reveals the missing link in

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## USheffield BehaviouralEvolution

Ph-D position in Behavioural Ecology of House Sparrows - Univ. Sheffield, UK

The PhD student will work in a team on our house sparrow population on Lundy Island - on “personality and fitness consequences”.

Requirements: We are seeking motivated and independent team player to join our house sparrow research group. The fieldwork on Lundy Island will be conducted for 4 months per year, requiring a committed and collaborative individual. Ideally, you have previous research experience, fieldwork experience, and are interested in birds and behavioural ecology. Experience in handling birds and/or a ringing licence are an advantage. The graduate position is for 3 years, with a flexible starting date before January 2011. The supervisors are Prof. Terry Burke, Dr. Julia Schroeder (Sheffield University) and Dr. Shinichi Nakagawa (Otago University, NZ). For any questions and to apply, contact [julia.schroeder@sheffield.ac.uk](mailto:julia.schroeder@sheffield.ac.uk).

This is a re-advertisement and if you applied before you do not need to apply again.

Project description: In behavioural and evolutionary biology, there has been a recent explosive interest in the phenomenon known as behavioural syndromes (i.e., animal personality or consistent behavioural differences between individuals across diverse contexts). A realisation of the ubiquity of behavioural syndromes in the wild has shaken the traditional view of animal behaviour in which behavioural phenotypes are expected to be infinitely flexible so as to be adaptive in any given context. Despite much interest in animal personality research, very little is yet known about how different personalities can affect the fitness of animals. We will use a long-term monitored population of house sparrows on Lundy Island to investigate the link between fitness and personality in the wild. There are five personality traits recognised: activity, boldness, exploration, ag-

gressiveness and sociability. We will particularly focus on the first three personality traits. Our previous studies have demonstrated that two behavioural traits, parental care and fidelity (quantified by extra-pair mating), are repeatable within individuals, meaning, for example, that some individuals express consistently high parental care or that others are successful at gaining extra-pair paternity through their lifetime. Obviously these two traits have significant fitness consequences. A critical feature of this study is that all individuals are monitored through time and DNA profiling will be used to confirm the pedigree. Consequently, it will be possible to attach precise fitness measures to alternative behaviours. The project will therefore be among the first to investigate intricate interactions among these fitness-related behavioural traits (parental care and mate fidelity) and personality traits (e.g., activity, boldness and exploration).

julia.schroeder@gmail.com

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## UToronto Mississauga Evolutionary Biol

Two Ph.D. positions in Evolution and Ecology

When: starting Fall 2011

Where: Ecology and Evolutionary Biology Graduate Program ([www.eeb.utoronto.ca](http://www.eeb.utoronto.ca)), University of Toronto Mississauga (<http://www.utm.utoronto.ca/~w3bio/homepage/>)

Who: Lab of Marc Johnson ([www.evoeco.org](http://www.evoeco.org))

Details:

Our lab will be moving to the University of Toronto Mississauga (Canada) in July 2011 and we are looking to take on two Ph.D. students to start in fall 2011. Ph.D. students in our lab have the ability to work on a wide range of problems at the intersection of evolution and ecology. Ongoing projects in the lab include: the evolutionary consequences of sex, micro- and macroevolution of plant defense, the causes and consequences of coevolution, the ecological consequences of genetic diversity, and the effects of climate change on plant-herbivore interactions. Students will have the ability to learn a wide range of techniques and skills in their projects, including lab and field work, molecular biology, phylogenetics, insect/plant rearing, chemistry, stats, theory, etc. Students are also free to work within existing projects or develop new systems and questions.

If you are interested in applying to work in the lab and would like more information please visit the lab web page ([www.evoeco.org](http://www.evoeco.org)) and write to me at [marc\\_johnson@ncsu.edu](mailto:marc_johnson@ncsu.edu).

Marc

Marc Johnson, Ph.D. Assistant Professor Department of Plant Biology North Carolina State University Box 7612, Raleigh NC 27695 U.S.A. Office: 919-515-0478, Lab: 919-515-0479 Fax: 515-3436 [www.evoeco.org](http://www.evoeco.org) [marc\\_johnson@ncsu.edu](mailto:marc_johnson@ncsu.edu)

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## UZurich Phylogenetics

Integrative phylogenetic/niche modeling Ph.D. position at the University of Zurich

Project description: The selected Ph.D. student will participate in a broad collaborative project entitled "Effects of climate change on past, recent, and future biodiversity of alpine/arctic plants: Integrative evidence from phylogenies, population genetics, ecological niche modeling and new insights for conservation", funded by a ProDoc grant from the Swiss National Science Foundation (SNF) within the Zürich-Basel Plant Science Center (PSC).

Recent improvements in our ability to reconstruct the history of biodiversity through timed phylogenies, estimate changes in genetic diversity, and predict the potential distribution of selected species with ecological niche models (ENMs) now allow us to infer the evolution of ecological preferences and distributional ranges at different temporal scales, from the present, to the past and the future. The Ph.D. student based at the University of Zürich will use a combination of phylogeny and ENM to test (i) the model of allopolyploid speciation by secondary contact in arctic/alpine plants; (ii) whether island colonization by plants with specialized breeding systems is associated with a change of reproductive strategy, ecological preferences, and genetic variation. The biological model system used to address these questions is *Primula* section *Aleuritia*, because it includes a range of ploidy levels and phylogeny-based hypotheses of polyploid species origins are available (see Guggisberg A., Mansion G., & Conti E. 2009. Disentangling reticulate evolution in an arctic-alpine polyploid complex. *Systematic Biology* 58:55-73). The project stems from a direct collaboration between Elena Conti (phylogeny-biogeography; University of Zurich)

and Christoph Randin (ecological niche modeling; University of Basel), with additional expertise provided by Stephen Smith (National Evolutionary Synthesis Center, USA) and Jérôme Goudet (University of Lausanne). Position characteristics: We offer a highly cooperative and stimulating working environment in motivated teams, interdisciplinary collaboration with leading research institutions, and opportunities for publication in high-ranking scientific journals. Salary according to the Swiss National Science Foundation (SNF) guidelines. Funding is available for 3 years. Requirements: Applicants must hold a master degree in biology or related disciplines. Practical experience in molecular techniques and phylogenetic analysis (or phylogeography/population genetics) highly desirable. Excellent knowledge of the English language, written and oral, required. High motivation, ability to work in an interdisciplinary team and social competence are expected. How to apply: Send the following documents by email AS A SINGLE PDF FILE to Prof. Elena Conti, [ContiElena@access.uzh.ch](mailto:ContiElena@access.uzh.ch): I) a one- to two- page application letter clearly addressing the following questions: a) Why are you interested in a Ph.D. position in this research topic? b) What are your career goals?; II) your detailed curriculum vitae, including a list of field collecting, molecular, analytical, and linguistic skills, presentations at scientific meetings, and publications (if applicable); III) a copy of your undergraduate and graduate academic record; IV) names and full addresses of two or three referees selected from your academic advisors. In your email subject line, use the title: "Ph.D. application ProDoc PSC". Applications that do not follow the above-specified guidelines will be no further evaluated.

Deadline for application: Applications will be screened as they arrive, thus we encourage each applicant to send in his/her pdf file as soon as possible. The closing date for applications is October 15, 2010.

Starting date: As soon as a suitable candidate is selected, but no later than February 1, 2011.

Prof. Elena Conti, Ph.D. University of Zurich, Institute for Systematic Botany Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 44 634 8424 Fax: 0041 44 634 84 03 email: [ContiElena@access.unizh.ch](mailto:ContiElena@access.unizh.ch) <http://www.systbot.uzh.ch/Personen/ProfessorenundDozenten/ElenaConti.html>  
Elena Conti <[ContiElena@access.uzh.ch](mailto:ContiElena@access.uzh.ch)>

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## VictoriaU KiwiGenomics

PhD scholarship in kiwi ecology and genomics

A PhD scholarship is available to study ecology and genomics of kiwi within the Allan Wilson Centre at Victoria University of Wellington in New Zealand. The candidate will join a group of researchers (Drs Kristina Ramstad, Nicola Nelson, Hugh Robertson, and Fred Allendorf) using a genomics approach to assess potential inbreeding effects on the persistence of kiwi populations.

The PhD candidate will investigate fitness measures (e.g., nesting and hatching success) of little spotted kiwi populations on remote offshore islands and in the urban sanctuary of Zealandia. In addition, they will develop broader research in kiwi conservation genomics, reproductive ecology, and/or population modeling (depending on their area of interest) and conduct their work directly with Maori community groups (the indigenous people of New Zealand).

Applicants should hold an MSc degree (or equivalent preparation for a PhD) in animal behaviour, conservation biology, population genetics, or evolutionary ecology. They should be independent, self-motivated and capable of completing project goals with minimal direct supervision. They should be in good health and have a high level of physical fitness as they will be following study animals through difficult terrain, off trail, both during daylight hours and at night, in remote field settings. Excellent writing and communication skills (English) are a must. A background in field research and demonstrated ability to organize and conduct field research projects with diverse human interest groups are a plus, as are enthusiasm, a positive attitude, a willingness to work hard, and the capacity to work collaboratively within a team.

The scholarship includes a tax-free stipend of at least NZ\$25,000 per annum plus tuition fees of approximately NZ\$6,300 plus seed funding (\$5,000NZ per year) for field work for a period of up to three years.

Review of applications will begin immediately. Those interested in applying should send their CV to Kristina Ramstad [kristina.ramstad@vuw.ac.nz](mailto:kristina.ramstad@vuw.ac.nz) <<mailto:kristina.ramstad@vuw.ac.nz>> to obtain further information about the projects and how to apply.

For information on the Allan Wilson Centre: <http://www.allanwilsoncentre.ac.nz/> For information on Victoria University: <http://www.victoria.ac.nz/sbs/>  
 Kristina Ramstad Postdoctoral Fellow \* Allan Wilson Centre for Molecular Ecology & Evolution

School of Biological Sciences \* Victoria University of Wellington P.O. Box 600 \* Wellington \* New Zealand

Ph +64 4 463-7443 \* Fax +64 4 463-5331  
 Website <http://awcmee.massey.ac.nz/people/-KRamstad/index.htm> Kristina Ramstad  
 <Kristina.Ramstad@vuw.ac.nz>

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## Vienna PopulationGenetics

PhD positions in Population Genetics

Over the past years, Vienna has developed into one of the leading centres of population genetics. The Vienna Graduate School of Population Genetics has been founded to provide a training opportunity for PhD students that builds on this outstanding on site expertise.

We invite applications from highly motivated and outstanding students with a background in one of the following disciplines: bioinformatics, statistics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply.

Available topics include:

- New algorithm and models to analyze population genetic massive parallel sequence data - The footprint of adaptive gene introgression after secondary contact
- Probabilistic models for the population genetics of molecular evolution - The genetics of two closely related species of *Aquilegia* - Evolution of gene expression in *Drosophila* - Association mapping in outbred *Drosophila* populations - Measuring interspecific gene flow by massively parallel sequencing - Genetic basis of local adaptation - Admixture mapping with Bayesian probabilistic models for genome wide population genetic data - Mathematical models of spatially varying

selection in subdivided populations - Functionally significant genetic variation in lifespan in natural populations - Statistical methods for detecting selective sweeps using genome-wide data - Population genetic estimators from NGS data

Applications need to be received by 13.02.2011 and include CV, motivation letter, university certificates and an indication of the two preferred topics in a single pdf. Two letters of recommendation need to be sent directly by the referees.

All information about the about the Vienna Graduate School of Population Genetics, the training program and the application procedure can be found at [www.popgen-vienna.at](http://www.popgen-vienna.at) - Dr. Julia Hosp Coordinator Vienna Graduate School of Population Genetics University of Veterinary Medicine Veterinärplatz 1 A-1210 Vienna [www.popgen-vienna.at](http://www.popgen-vienna.at) Tel: +43 1 25077 4338 Fax: +43 1 25077 4390

[julia.hosp@gmail.com](mailto:julia.hosp@gmail.com)

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## WWU-Muenster EcologyAndEvolution

A PhD position is available in the newly established group of Evolutionary Functional Genomics in the Institute for Evolution and Biodiversity at WWU Muenster (Germany).

We are looking for an enthusiastic, dedicated, and well-motivated individual who would like to join the lab to investigate the role of environmental nutrient limitations in the evolution of genomes and proteomes, using a computational approach.

Applicants should have a Master degree (or equivalent) in biology, bioinformatics or related disciplines and a strong interest in computational and/or quantitative approaches. Applicants should send a single PDF file containing a statement of research interests, full curriculum vitae, and contact information of two referees to Claudia Acquisti ([claudia.acquisti@uni-muenster.de](mailto:claudia.acquisti@uni-muenster.de))

[claudia.acquisti@uni-muenster.de](mailto:claudia.acquisti@uni-muenster.de)

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PortlandStateU PlantEvolution .....	48	WashingtonU EvolutionaryAnthropology .....	65
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### Albuquerque Bioinformatics programming

Job: Engineering Support Job ID: 635089 Location:  
Albuquerque, NM

About Sandia

Sandia National Laboratories is the nation's premier science and engineering lab for national security and technology innovation. We are a world-class team of scientists, engineers, technologists, post docs, and visiting researchers all focused on cutting-edge technology, ranging from homeland defense, global security, biotechnology, and environmental preservation to energy and combustion research, computer security, and

nuclear defense.

To learn more, visit California Website: <http://ca.sandia.gov/casite/> or New Mexico Website: <http://www.sandia.gov/>. Department Description

The Bioenergy and Defense Technologies department, which is part of Sandia's Biological and Materials Sciences Center, supports mission areas in biodefense, emerging infectious disease, and biofuels. The department conducts fundamental research in cell biology, immunology, and microbiology and develops advanced measurement technologies, such as fluorescence microscopy, vibrational spectroscopies, and x-ray and neutron scattering. Current research projects include understanding receptor activation and cell signaling processes, pathogenesis, and plant physiology, as well as algal biochemistry and cultivation characterization for biofuels applications. We conduct research for the National Institutes of Health, the Department of Home-



land Security, the Department of Defense, U.S. industry, and Sandia's Laboratory Directed Research & Development program. To learn more, visit <http://bio.sandia.gov> . How to Apply

Visit <http://tinyurl.com/233kmec>, follow the instructions to upload a resume, and complete the submission process to indicate your interest in this position.

#### Job Details

**SUMMARY:** Run routine data pipeline programs and database tools to analyze sequence data

**DUTIES:** - Use existing applications, such as, alignment programs, sequence assemblers and BLAST to perform routine analytical tasks - Collaborate with scientific staff to use software specifications for data pipelines - Maintain daily operation of ?omics-oriented pipelines

#### Required

- Bachelors degree in Bioinformatics, Computer Science, Computer Engineering, or four years of relevant software engineering experience or education - Ability to operate in a UNIX/Linux operating environment - Fluency in object-oriented Perl, and one or more relational database management systems. Knowledge of one or more programming languages such as C++, C#, R, Java. Familiarity with web technologies such as HTML, CSS, PHP, Ajax - Programming expertise in statistical analyses software packages, such as SAS, MATLAB, Mathematica and/or the R Project for Statistical Computing, languages and tools

#### Desired

- Parallel and grid-based computing programming experience - Ability to support production data management and software pipeline operation - Ability to provide support to senior-level scientific staff

#### Security Clearance

Sandia is required by DOE directive to conduct a pre-employment background review that includes personal reference checks, law enforcement record and credit checks, and employment and education verifications.

Applicants for employment must be able to obtain and maintain the appropriate DOE security clearance if required for a position. Applicants offered employment with Sandia are subject to a federal background investigation to meet the requirements for employment including access to classified information or matter.

Substance abuse or illegal drug use, falsification of information, criminal activity, serious misconduct or other indicators of untrustworthiness can cause a clearance to be denied by the DOE, rendering the inability

to perform the duties assigned and resulting in termination of employment.

#### Citizenship

Sandia is a Department of Energy (DOE) national laboratory; as such, many of our jobs require a DOE security clearance, which requires U.S. citizenship. If this position requires a Department of Energy (DOE)-granted security clearance, U.S. citizenship and employee eligibility for clearance processing will be required at the time of hire.

If you hold dual citizenship and you accept a job offer for a position that requires a DOE-granted security clearance, you may be asked by DOE to renounce your foreign citizenship and retain only your U.S. citizenship.

#### Benefits

At Sandia you will receive many benefits as a valued employee of a premier national multi-program engineering and science research laboratory. In our Total Rewards package you will enjoy competitive pay, great benefits, a stimulating, positive environment and learning opportunities that will help build your career. More information may be found on our Careers website.

#### EEO

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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>

## Albuquerque Bioinformatics programming 2

Job: Engineering Support Job ID: 635089 Location: Albuquerque, NM

Summary, duties and requirements for a master's level bioinformatician/programmer:

\* **SUMMARY:** programming to support the development of integrated flexible pipelines and databases/analytical tools to facilitate analyses next generation sequence data

\* **DUTIES:**

- Using object-oriented, bioinformatics-relevant programming and database languages (e.g., C++, C#, Java, Perl, Python, MySQL; BioPerl, BioSQL, BioPy-

thon, BioRuby) and existing applications, such as alignment programs, sequence assemblers and BLAST to establish data pipeline and to perform specific analytical tasks

- Collaborate with scientific staff to develop software specifications for data pipeline

- Maintain daily operation of -omics-oriented pipeline, including preparing scripts, queries, extracting data requested by researchers, and arraying data in prescribed formats

- Scan similar research and analytical activities and track use of innovative tools and methods that are in the published research and in the public domain for possible use in local methods and software development

**\* REQUIREMENTS:**

- Bachelors &/or Master's degree in bioinformatics, Computer Science, Computer Engineering, or four years of relevant software engineering experience or education

- Ability to operate in a UNIX/Linux operating environment

- Fluency in object-oriented Perl, and one or more relational database management systems. Knowledge of one or more programming languages such as C++, C#, R, Java. Familiarity with web technologies such as HTML, CSS, PHP, Ajax

- Programming expertise in statistical analyses software packages, such as SAS, MATLAB, Mathematica and/or the R Project for Statistical Computing, languages and tools

- Parallel and grid-based computing programming experience

- Ability to support production data management and software pipeline operation

- Ability to provide support to senior-level scientific staff

- Excellent oral and written communication, presentation and interpersonal skills

- Ability to keep current with emerging software and programming technologies/techniques

- Ability to use advanced software tools in an innovative fashion to address systems, data analysis and data presentation problems

- Knowledge of methods for organizing, storing, analyzing, and presenting large data sets

- Proficiency with existing bioinformatics tools, methods and databases such as sequence similarity, assem-

bly, alignment and annotation tools; NCBI, EMBL, DDBJ, BRENDA, KEGG, SwissProt, Gene Ontology, etc. databases

“Quinn, Erin Elizabeth” <eequinn@sandia.gov>

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## AmericanMusNatHist CuratorialAssociate

Curatorial Associate, American Museum of Natural History

The American Museum of Natural History is one of the world's preeminent scientific and cultural institutions. Since its founding in 1869, the Museum has advanced its global mission to discover, interpret and disseminate information about human cultures, the natural world and the universe through a wide-ranging program of scientific research, education and exhibition. The Museum is renowned for its exhibitions and scientific collections, which serve as a field guide to the entire planet and present a panorama of the world's cultures.

Job Title: Curatorial Associate, AMNH Division of Invertebrate Zoology

Job Description: To coordinate and oversee the management of the collections of the Division of Invertebrate Zoology. To facilitate the use of these collections by AMNH Curators, Scientific Staff, students, visiting scientists, and to support the activities of the division.

The Curatorial Associate specific professional responsibilities will include:

Management and coordination of collection curation in conformance with AMNH policies and procedures. Maintenance of divisional collection databases. Supervision and coordination of collections compliance activities including internal reports. Interaction with the public and AMNH staff in the presentation and explanation of IZ collections activities. Application for extramural funds to maintain and enhance IZ collections. Other collections related duties as required.

Education and Skill Requirements:

Required Ph.D. in one of the following: Systematics, Organismic Biology, and Invertebrate Zoology. Collections management experience. Relevant computer skills.

Salary: Commensurate with experience.

Please send résumé and cover letter specifying va-

cancy, together with the names of 3 referees, to egaughan@amnh.org

The American Museum of Natural History is an Equal Opportunity Employer. The Museum does not discriminate due to age, sex, religion, race, color, national origin, disability, marital status, veteran status, sexual orientation, or any other factor prohibited by law. Qualified candidates of diverse ethnic and racial backgrounds are encouraged to apply for vacant positions at all levels. Please be advised that due to the high volume of applicants, we are only able to contact those candidates whose skills and background best fit the needs of the open position.

crowley@amnh.org

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## ArizonaStateU BioinformaticsProgrammer

Programmer or Analyst in Bioinformatics

We are seeking a programmer or analyst responsible for the maintenance, development, and debugging of software applications for use in the fields of Computational Biology and Bioinformatics (<http://kumarlab.biodesign.asu.edu>). We have already developed many tools, including MEGA (<http://www.megasoftware.net>), TimeTree (<http://www.timetree.org>), and FlyExpress (<http://www.flyexpress.net>). Come join an active and dynamic team. The scientific programs in CEMI address four primary research themes. 1) personal genomics: predicting adaptive and disease propensities of mutations in individuals; 2) disease origins: tracing pathogen evolution to unravel dynamics of infections and drug resistance; 3) functional proteomics: discovering functionally important elements of genome; and 4) discovery bioinformatics: modeling, analysis, and simulations to discover patterns and test predictions. More information about the Center can be found at <http://cemi.asu.edu>. You can view and apply for this job at: [https://ep.oasis.asu.edu/-psp/asuepprd/EMPLOYEE/PSFT\\_ASUSAPRD/-c/HRS\\_HRAM.HRS\\_CE.GBL?Page=-HRS\\_CE\\_JOB\\_DTL&Action=A&JobOpeningId=-24958&SiteId=1&PostingSeq=1](https://ep.oasis.asu.edu/-psp/asuepprd/EMPLOYEE/PSFT_ASUSAPRD/-c/HRS_HRAM.HRS_CE.GBL?Page=-HRS_CE_JOB_DTL&Action=A&JobOpeningId=-24958&SiteId=1&PostingSeq=1) (JOB ID: 24958; ASU, Tempe Campus)

Extended deadline: September 15, 2010 (with weekly review thereafter)

Sudhir Kumar (s.kumar@asu.edu), Director Center for Evolutionary Medicine & Informatics Biodesign Institute (office A-240) Professor, School of Life Sciences Arizona State University Tempe, Arizona, AZ 85287-5301, USA

s.kumar@asu.edu

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## AuburnU ComparativePhysiology

Position Announcement

Comparative Vertebrate Physiology College of Sciences and Mathematics, Auburn University

The Department of Biological Sciences at Auburn University invites applications for a tenure-track faculty position at the assistant professor level in comparative physiology, beginning Fall, 2011 (pending final budgetary approval). The successful candidate is expected to establish an extramurally funded, internationally recognized research program using vertebrate models, and engage in the training of graduate and undergraduate students. Candidates whose research programs are complementary to or enhance existing areas of strength in the department (evolutionary, environmental, behavioral physiology, and functional morphology) will be given preference. The candidate will have teaching responsibilities in the Anatomy and Physiology teaching program and will have the opportunity to develop upper-division and/or graduate coursework in the area of specialization.

Applicants must have a Ph.D. in Biological Sciences or a closely related discipline, plus relevant postdoctoral experience. Excellent communication skills are required. Desired qualifications include a strong record of publication, teaching experience, and good interpersonal skills. The candidate selected for the position must be able to meet eligibility requirements to work in the United States at the time appointment is to begin and continue working legally for the proposed term of appointment. Women and minorities are encouraged to apply.

Review of applications will begin October 15, 2010, and will continue until a suitable applicant is found. Applicants should submit a curriculum vitae, a description of research interests, a statement of teaching philosophy and experience, and the names and contact information of at least three references to: Dr. Raymond Henry, Physiologist Search Committee Chair,

Department of Biological Sciences, 101 Rouse Life Sciences Bldg, Auburn University, Auburn, AL 36849-5407. Email: [henryrp@auburn.edu](mailto:henryrp@auburn.edu) More information about the department and its programs can be found at the following web site: <http://www.auburn.edu/-cosam/departments/biology/index.htm>

Auburn University is an Affirmative Action/Equal Opportunity Employer.

[henryrp@auburn.edu](mailto:henryrp@auburn.edu)

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## BEACON MichiganStateU EvolutionEducationDirector REPOST

Education Director – BEACON Center for the Study of Evolution in Action

REPOST: note new deadline (October 1, 2010)

The BEACON Center for the Study of Evolution in Action is a newly established NSF Science and Technology Center (STC), funded at \$5 million/year for five years, renewable to ten years. We are recruiting a full-time Education Director who is an accomplished scholar, with a deep understanding of evolution, some knowledge of computation, and a commitment to innovative science education at all levels. Desirable qualifications include a record of administrative leadership and exceptional interpersonal, communication and multi-tasking skills. This is a fixed term position at Michigan State University. The initial appointment is for 12 months, with annual reappointment possible for the duration of the project. Salary and benefits will be competitive, commensurate with experience.

BEACON will advance research and education on the evolutionary dynamics of natural and digital systems and apply new evolutionary principles to engineering and biological problems. BEACON includes over 60 faculty members in biology, engineering and computer science, half at Michigan State University (BEACON headquarters), with others distributed among North Carolina A&T State University, University of Idaho, University of Texas at Austin, and University of Washington. Additional information is available at the BEACON website: <http://www.beacon.msu.edu/>. The Education Director is a member of the BEACON management team, reporting to the BEACON Director. She or he is a member of the Education and Human Resource Development (EHRD) Steering Committee and works

with that committee to initiate and facilitate projects within the educational mission of BEACON, including mentoring postdocs, multidisciplinary graduate training, undergraduate research and education, K-12 and public outreach. The Education Director coordinates educational initiatives among the five BEACON universities as appropriate and works with the leadership and evaluation teams to prepare materials related to EHRD activities to be submitted in BEACON reports. She or he works with BEACON faculty in the preparation of proposals for external support of BEACON EHRD activities and on scholarly publications that follow from these activities. The Education Director will have the opportunity to devote up to 25% of her or his effort to collaborative studies that advance the BEACON research and/or education missions.

Questions and applications should be emailed to Tom Getty, Chair of the BEACON Education Director Search Committee, at [getty@msu.edu](mailto:getty@msu.edu) with “BEACON Education Director” in the subject line. Applications should include a cover letter, a full resume/vita, a two-page statement of purpose emphasizing the applicant’s suitability for the job, and contact information for three references. Application materials should be emailed as a single pdf-file, if possible. We will begin reviewing applications on October 1, 2010 and continue the search until the position is filled.

MSU is an affirmative-action, equal-opportunity employer. MSU is committed to achieving excellence through cultural diversity. The university actively encourages applications and/or nominations of women, persons of color, veterans and persons with disabilities.

– Danielle J. Whittaker, Ph.D. Managing Director  
BEACON Center for the Study of Evolution in Action  
1441 Biomedical and Physical Sciences Building  
Michigan State University East Lansing, MI 48824 (517) 884-2561

[djwhitta@msu.edu](mailto:djwhitta@msu.edu)

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## Brigham YoungU ComputationalBiology

Computational Biology Position Announcement The Department of Biology at Brigham Young University (BYU) invites applications for a continuing faculty status (BYU’s equivalent to tenure) track position in the area of computational biology. We seek exceptional in-

dividuals with a PhD and postdoctoral experience relevant to computational biology, including degrees in areas of biology, computer science, mathematics, and/or statistics. The successful candidate is expected to develop an externally funded research program and teach courses in computational biology and the biology core. The department offers competitive start-up packages and reduced teaching loads for new faculty. The anticipated start date for this position is January or August 2011.

Complete applications will include a cover letter, curriculum vitae, teaching statement, research statement, and a completed BYU employment application form (found at <https://yjobs.byu.edu>). Applicants should provide names and contact information for three references; letters of recommendation will be requested for those candidates that make our short list. The initial review process will begin September 30, 2010 and continue until the position is filled. Inquiries should be directed to Dr. John S.K. Kauwe, Computational Biology Faculty Search, 401 WIDB, Department of Biology, BYU, Provo, UT 84602, USA (or email [bio@byu.edu](mailto:bio@byu.edu)<<mailto:bio@byu.edu>>).

Brigham Young University, an equal opportunity employer, does not discriminate on the basis of race, color, gender, age, national origin, veteran status, or against qualified individuals with disabilities. All faculty are required to abide by the university's honor code and dress and grooming standards. Preference is given to qualified candidates who are members in good standing of the affiliated church, The Church of Jesus Christ of Latter-day Saints. Successful candidates are expected to support and contribute to the academic and religious missions of the university within the context of the principles and doctrine of the affiliated church.

Byron Adams Evolutionary Ecology Laboratories, Department of Biology Brigham Young University Provo, UT 84602

[byron\\_adams@byu.edu](mailto:byron_adams@byu.edu)

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### ChicagoBotanicGarden PlantConservation

Research Scientist/Lecture Position at Chicago Botanic Garden and Northwestern University

As part of a collaborative program in Plant Biology and Conservation ([http://-](http://www.plantbiology.northwestern.edu)

[www.plantbiology.northwestern.edu](http://www.plantbiology.northwestern.edu)) at Northwestern University (NU) and the Chicago Botanic Garden (CBG), a full-time joint position is available as Research Scientist and Lecturer in Plant Biology. The individual will maintain an active research program and work in the new state of the art labs in the Daniel F. and Ada L. Rice Plant Conservation Science Center at CBG (<http://www.chicagobotanic.org/-research/building/?expanddiv=3Dbuilding>), and will also have access to research-support facilities at NU. The individual will also teach undergraduate courses in the Program in Biological Sciences (<http://www.biosci.northwestern.edu/> <<http://www.biosci.northwestern.edu/> > ) at NU. Courses will be focused on the individual's area of expertise. Applicants should have a PhD in botany, biology, or a related field. While the area of expertise is open, we encourage applications from people with expertise in plant physiology, genomics, landscape ecology, and ethnobotany/phytochemistry. Experience teaching in a university setting is highly desirable. A demonstrated enthusiasm for instructing students with diverse educational backgrounds is necessary. The individual will be directly employed by CBG but will hold an appointment at NU. Review of applications will begin on November 15, 2010 and the position will start in September 2011. To apply, please send application materials to Susan Black, 2205 Tech Dr., 2-144 Hogan, Evanston, IL 60208 or via e-mail to [seb451@northwestern.edu](mailto:seb451@northwestern.edu). If sending via e-mail include <sup>3</sup>CBG/NU position<sup>2</sup> in subject line. Applications should include a Cover Letter, CV, Research Statement, Teaching Statement, and 3 letters of recommendation. Women and minorities are encouraged to apply.

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

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### CollegeWilliamMary BiologicalMathematics

Assistant Professor in Biological Mathematics The College of William and Mary

The Department of Biology at The College of William and Mary invites applications for a tenure-track position at the level of Assistant Professor in Biological Mathematics beginning Fall, 2011. The successful candidate will develop a productive, externally funded research program in biological mathematics, broadly con-

strued, that includes collaborations with both faculty and students in the Department of Biology and, potentially, the Program in Neuroscience. Collaboration with faculty in the Departments of Applied Science and Mathematics is also encouraged. Typical teaching duties will be one course per semester; the successful candidate will develop and teach a sophomore level course in mathematical biology suitable for Biology majors and an advanced course that incorporates student research projects. In addition, the successful candidate will help to develop quantitative elements for introductory and advanced Biology courses in collaboration with the instructors of such courses. The assignment to teach a particular course might be substituted partially or entirely by collaborative work with other faculty members to develop and integrate biological mathematics into courses from the introductory to advanced level. An interest in and ability to teach biostatistics is preferred, but this need not be the research focus of the successful candidate. A Ph.D. is required and post-doctoral experience is desirable. Applications should include a curriculum vitae, a statement of current and future research interests, and a statement of teaching interests and experience and should be submitted electronically as a single PDF to <http://jobs.wm.edu>. The system will also prompt you for the names and emails of a minimum of three referees familiar with your research and/or teaching who will be asked to provide a reference letter. Questions should be addressed to Margaret Saha ([mssaha@wm.edu](mailto:mssaha@wm.edu)). Review of applications will begin on November 1, 2010 and will continue until an appointment is made. The College of William and Mary is an EEO/AA Employer and is committed to improving diversity.

Dr. John Swaddle Professor, Biology Director, Environmental Science and Policy Program Millington Hall, Room 220 College of William & Mary Williamsburg, VA 23187-8795 Office: 757.221.2231 Fax: 757.221.6483 <http://jpswad.people.wm.edu/> John Swaddle <[jpswad@wm.edu](mailto:jpswad@wm.edu)>

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### DukeU ResTech ConservationGenetics

Duke Marine Lab: Research Technician: Conservation Genetics The Duke University Marine Laboratory in Beaufort, North Carolina is seeking a full time research technician to work on the conservation genetics of anadromous river herring. The goal of this project,

which is being funded by the National Fish and Wildlife Foundation, is to use genetic and otolith markers to assess the population structure of river herring along the USA Atlantic Coast in order to identify runs that are being impacted by marine bycatch.

The duties of this position include: 1) travel and field work for sample collection, 2) laboratory work at the Marine Conservation Molecular Facility involving DNA extractions, PCR, sequencing, and microsatellite genotyping, 3) tasks related to data collection, database management, and analysis, 4) otolith removal and preparation, 5) general field and laboratory tasks, 6) interacting with researchers and managers involved in other aspects of this project, and 7) training students in proper field and laboratory techniques.

Please supply a letter of interest, curriculum vitae or resume, and the names and contact information of two individuals who can supply reference letters.

Learn more about the Duke University Marine Laboratory: <http://nicholas.duke.edu/marinelab/> For more information on this job opportunity, please contact Dr. Eric Palkovacs: [eric.palkovacs@duke.edu](mailto:eric.palkovacs@duke.edu)

To apply for this position, please go to the Duke University Human Resources website (<http://www.hr.duke.edu/jobs/index.php>) and search for ALL jobs in Beaufort.

The requisition for this job is 400427660. Please submit your resume and supporting materials online.

Eric Palkovacs <[eric.palkovacs@duke.edu](mailto:eric.palkovacs@duke.edu)>

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### DukeU Tech BacterialGenomeEvolution

Evolutionary genomics of bacteria Technician position (Lab Analyst II) Wernegreen lab, Duke University, Durham NC

If interested, please contact Jen Wernegreen at [j.wernegreen@duke.edu](mailto:j.wernegreen@duke.edu). Please note: requirements include four years of prior research experience (or two years of research plus a master's degree).

DESCRIPTION: Im looking for a molecular biology technician to contribute to our studies of bacterial genome evolution. Much of our work focuses on comparative genomics, population dynamics, and functional analysis of bacterial endosymbionts associated with insect hosts, particularly ants. In addition, we

are exploring the evolution of gene content and DNA sequence variation in mutualistic and pathogenic bacteria more broadly. Our lab is housed within Duke's Institute for Genome Sciences and Policy (<http://www.genome.duke.edu/>).

**RESPONSIBILITIES:** Responsibilities will include DNA and RNA extractions, sample prep for library construction and next-generation sequencing, standard and quantitative real-time PCR, maintenance of live insects in the lab, as well as general lab organization, ordering, and management. Depending on skills and interests, opportunities might also include comparative genome analyses, use of public databases, molecular phylogenetics, field collection of ants and other insects, microscopy, and/or flow cytometry. We recently moved to Duke, so initially the position will include helping to set up the lab.

**REQUIREMENTS:** A bachelors or masters degree in biology or a related field is required. The position level (Lab Analyst II) also requires four years of research experience, but two of those years can be offset by having earned a research-based masters degree. Considerable experience with molecular techniques is a must. Excellent written, verbal, and interpersonal skills, attention to detail, and a superb work ethic are also essential. Applicants should have strong interests in genomics, evolution, symbiosis, and/or microbiology and possess a genuine drive to perform basic research. A working knowledge of LINUX and some experience in computer programming or script writing (particularly PERL) are big pluses.

**FOR MORE INFORMATION:** For a general description of our focal areas and recent publications, please see: <http://www.genome.duke.edu/people/faculty/wernegreen/> If interested in the position or for more information, please contact me (Jen) at [j.wernegreen@duke.edu](mailto:j.wernegreen@duke.edu).

Jen Wernegreen <[jwernegreen@gmail.com](mailto:jwernegreen@gmail.com)>

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## DuquesneU EukaryoticBiologist

Duquesne University invites applications for a tenure-track position in the Department of Biological Sciences. The successful applicant is expected to develop a vigorous independent research program involving the study of molecular, cellular, and/or organismal processes in eukaryotes. Areas of interest include, but are not lim-

ited to, molecular biology, cell biology, development, immunology, and physiology. The successful candidate will join an active department of 18 faculty with a commitment to combining externally funded research with excellence in teaching at both the graduate and undergraduate levels. Applicants must have post-doctoral experience, and are expected to mentor MS and PhD students. Preference will be given to candidates at the Assistant Professor level. However, more senior candidates may also be considered. Competitive salary and start-up packages are available. Additional information about the Department can be found at <http://www.duq.edu/biology>. To apply, send a cover letter, CV, statements of research and teaching goals, and three letters of recommendation to Chair, Biology Faculty Search Committee, Department of Biological Sciences, 201 Mellon Hall, 600 Forbes Avenue, Pittsburgh, PA 15282. Review of applications will begin October 15, 2010. Please direct inquiries about the position to [biology@duq.edu](mailto:biology@duq.edu). Motivated by its Catholic identity, Duquesne values equality of opportunity both as an educational institution and as an employer.

Michael Jensen-Seaman, PhD Department of Biological Sciences Duquesne University

[seamanm@duq.edu](mailto:seamanm@duq.edu)

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## ElmhurstCollege InvertebrateEvolution

**ASSISTANT PROFESSOR - INVERTEBRATE BIOLOGY.** Elmhurst College, a 2700- student comprehensive college, invites applications for a tenure-track position for an Assistant Professor of Biology in the area of invertebrate biology commencing August, 2011. We are particularly interested in applicants with backgrounds in evolution, entomology or parasitology. The successful candidate will have a Ph.D. in an appropriate field and outstanding potential as a professor in a liberal arts setting. Prior college-level teaching experience is required. Primary teaching responsibilities will include teaching lectures and laboratories in majors' level invertebrate zoology and core biology courses, with the opportunity to develop specialized undergraduate courses in the area of expertise. In addition, the candidate will be expected to develop a strong research program that involves undergraduate students. The well-equipped Biology Department serves 180 majors and minors, participates in the college general ed-

ucation curriculum, and supports nursing and allied health students. Send letter of interest electronically with CV, statements of teaching philosophy and research plan, copies of undergraduate and graduate transcripts (unofficial transcripts acceptable with initial application), and three letters of reference to Dr. Paul Arriola (paula@elmhurst.edu), Department of Biology, Elmhurst College, 190 Prospect Ave., Elmhurst, IL 60126. Review of credentials will begin October 15, 2010. Further information about the Biology Department is available at <http://www.elmhurst.edu/~bio/index.html>. Elmhurst College, an Equal Opportunity Employer, seeks candidates with demonstrated ability to contribute positively to a multicultural campus community.

Paul E. Arriola, PhD Professor, Department of Biology Elmhurst College 190 Prospect Ave. Elmhurst, IL 60126-3296

(630) 617-3109 <http://www.elmhurst.edu/~bio/arriola>  
paula@elmhurst.edu

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### FloridaStateU LabTech AmphibianGenomics

Organization: Florida State University

Job Location: Tallahassee, FL

Job Description: To join a laboratory group involved in developing genomic resources in amphibians, using enrichment procedures and high-throughput sequencing (i.e., Illumina). Researcher will perform bench-level molecular work to prepare samples for high-throughput sequencing, conduct microsatellite and SNP screening and genotyping, and develop novel applications for hybridization-based enrichment. Researcher will also assist with processing and analysis of genomic data (bioinformatics).

Responsibilities will include: lab management, library preparation for sequencing (e.g., barcoded library preparation, etc.), genotyping and marker development (microsatellites and SNPs), sequence enrichment, and protocol development.

Must have good troubleshooting skills, a strong background in molecular biology, experience in protocol development, good organization and leadership skills, and high efficiency. Extensive experience in collection and analysis of genomic data is also desirable. Must be able to take on a project and carry it out to completion.

Start Date: flexible (early October preferred).

Salary \$30,000 to \$45,000 per year, plus benefits, depending upon experience.

Benefits Retirement, health, sick/annual/holiday leave, other benefits

Characteristic Duties - Conducts various bench level experiments - Employs a variety of standard and non-standard molecular biology techniques to help develop protocols for library construction and sample preparation for next-generation sequencing - Prepares, orders, and maintains stocks of necessary reagents, solutions and supplies - Documents, compiles and analyzes experimental data - Provides advice to fellow lab members regarding laboratory techniques - Helps mentor undergraduate lab projects - Attends weekly meeting for experimental planning - Assists with organization of tissue collections and database - Maintains and improves technical knowledge base

Essential requirements: (1) BS, MS, or PhD degree with either graduate experience or a minimum of two years of professional experience with genomic sequencing technologies and analysis. (2) Strong background in molecular biology techniques (e.g., extraction of RNA, DNA, real-time QPCR, sequencing) (3) Solid computer skills and good knowledge of public domain biological databases. Advanced computer skills (genomics data processing and analysis, databases, etc.) are preferred. (4) Excellent organizational, time management, and communication skills required; must be able to work independently, solve problems, and interact with lab members.

Contact Information: [alemmon@evotutor.org](mailto:alemmon@evotutor.org)

About Our Organization: The researcher selected will become part of the integrative laboratory groups of Alan Lemmon and Emily Moriarty Lemmon at Florida State University, in Tallahassee, Florida. For more information, see our websites: <http://www.evotutor.org/LemmonLab/> <http://www.bio.fsu.edu/chorusfrog/index.html> <http://www.bio.fsu.edu/faculty-moriarty-lemmon.php> Alan R. Lemmon Assistant Professor Florida State University

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### GeorgiaSouthernU EvoDevo

GEORGIA SOUTHERN UNIVERSITY University  
System of Georgia Developmental Biology Search #



59282 College of Science and Technology Department of Biology

The Department of Biology in the College of Science and Technology invites applications for the position of Developmental Biologist at the Assistant Professor rank. Georgia Southern University (<http://www.georgiasouthern.edu>), a member institution of the University System of Georgia and a Carnegie Doctoral/Research University, is one of Georgia's premier universities. A residential university serving over 19,000 students in fall 2010, Georgia Southern is recognized for providing all of the benefits of a major university with the feeling of a much smaller college. Founded in 1906, the University offers more than 100 campus-based and online degree programs at the baccalaureate, master's, and doctoral levels through eight colleges. The nearly 700 acre park-like campus is located in Statesboro, a classic Main Street community near historic Savannah and Hilton Head Island.

**Position Description.** The Department of Biology is comprised of 35 faculty members, 1050 majors, and 45 graduate students and has a strong emphasis in ecological and evolutionary biology. The Assistant Professor position requires teaching, research, and service responsibilities as well as a terminal degree. The successful candidate will teach undergraduate and graduate level courses including Developmental Biology. Applicants whose research focuses on animal developmental biology using an integrative or evolutionary approach are encouraged to apply. Research that can complement an integrative program exploring the biology of the Southeastern coastal plain is especially welcome. The 9-month, tenure-track appointment begins 1 August 2011. Salary is competitive and commensurate with qualifications and experience.

**Qualifications.** Candidates must have a Ph.D. by 31 Dec. 2010; post-doctoral experience is preferred. The successful candidate will have demonstrated excellence in research, will be expected to attract extramural funding, and will contribute to teaching needs at the undergraduate and graduate levels.

**Application Process.** Applicants must submit hard copies of a letter of application, curriculum vitae, and statements of research and teaching interests. Applications must also include three letters of reference, which may be sent via email in PDF format. Postmark applications by 22 Oct. 2010, and submit all materials to the search chair:

Dr. Sophie B. George Search Chair, Search # 59282  
Department of Biology Georgia Southern University P.  
O. Box 8042 Statesboro GA 30460

**Contact Information:** [developmentalbiology-search@georgiasouthern.edu](mailto:developmentalbiology-search@georgiasouthern.edu) Georgia Southern University seeks to recruit individuals who are committed to working in diverse academic and professional communities. More information about the university, college and department is available at the following web sites: <http://www.georgiasouthern.edu>, <http://cost.georgiasouthern.edu/>; <http://www.bio.georgiasouthern.edu/searches>. Georgia Southern University is an AA/EO institution and seeks individuals who are committed to excellence in teaching, scholarship, and professional service within the University and beyond. Finalists will be required to submit to a background investigation. Georgia is an Open Records state. Individuals who need reasonable accommodations under the ADA to participate in the search process should contact the Associate Provost.

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Johanne M. Lewis, Ph.D Assistant Professor Department of Biology Georgia Southern University Statesboro, GA 30460-8042

[jmlewis@georgiasouthern.edu](mailto:jmlewis@georgiasouthern.edu)

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## HongKong ConservationBiology

Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Senior Officer in Environmental and Ecological Statistics

**JOB SUMMARY** To assist in the planning and execution of the conservation work undertaken by the Flora Conservation Department at Kadoorie Farm and Botanical Garden Hong Kong, focusing on the application of environmental and ecological statistics and GIS based methods. Your work will play a key role in helping to protect Hong Kong and South Chinas natural environments. Staying one step ahead of the latest technology, you'll provide essential analytical and technical support to our regional and area teams, to solve challenging spatial problems that arise in our projects. We seek an exceptional individual with preferably a PhD and postdoctoral experience relevant to computational biology, including a degree in areas of biology, computer science, mathematics, and/or statistics with fundamental GIS and ecological and environmental modelling experience. Daily duties will include spatial image preparation and processing (e.g. rectification, resampling), digitisation, spatial data management using GIS, cli-

mate and vegetation modelling. Applicants must be enthusiastic and have excellent communication skills, as they will be an integral part of a small and dynamic team.

#### Major Responsibilities

To assist in the execution of habitat and species conservation projects, through the planning and application of experimental computational techniques

To technically support and if necessary to participate in field work to survey habitats and species distributions

To help maintain and review inventory systems including the management of the KFBG database

Plan and manage land and vegetation surveys using up to date GIS and remote sensing technologies

Model vegetation, potential species distributions and habitats using climate envelopes

Run predictive analysis on the influence of climate change on vegetation, habitat and species distributions

Produce vegetation, habitat and species distribution maps

To handle general administrative duties and daily operations towards the development of capacity within the Flora Conservation Department

As assigned from time to time

#### Requirements

You should be passionate about biodiversity and its conservation

Preferably PhD degree holder with postdoctoral experience in one of the following disciplines: computational biology, computer science, mathematics, and statistics

Experience in statistical computing using R

Experience in GIS analysis using ArcGIS software suite (ArcMap, ArcCatalog, ArcToolbox) and/or GRASS GIS

Experience in different remote sensing satellite and air-photo methodologies and techniques using adequate software suites (ENVI, ERDAS, Definiens etc.)

Experience in spatial data management using preferably Open Source technologies

Naturally, you'll have superb IT skills

The following attributes are desirable, but non-essential:

Previous programming or GIS customization experience, including writing customized R packages using the R/S and/or C/C++ or Fortran languages

Field work experience using GPS technology preferable Trimble or Topcon

Application Method Interested parties should send a detailed CV, expected salary, and a short essay (describing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: [gfisher@kfbg.org](mailto:gfisher@kfbg.org)

or

Human Resources Manager, Kadoorie Farm & Botanic Garden Corporation, Lam Kam Road, Tai Po, New Territories, Hong Kong Email to [kfjobs@kfbg.org](mailto:kfjobs@kfbg.org)

Gunter Fischer <[gfisher@kfbg.org](mailto:gfisher@kfbg.org)>

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## JamesCookU 3 EvolutionaryBiol

Lecturer/Senior Lecturer V Biology (3 positions): School of Marine & Tropical Biology, James Cook University, Queensland, Australia

Full-time on a continuing basis subject to a probationary period.

Closing date: 29 October 2010

Reference No.: 10191

Further information: <http://www-public.jcu.edu.au/-jobs/searchjobs/JCUPRD1-064376> The School of Marine and Tropical Biology has an enviable international research reputation, and is a leading global University in the ISI field of Ecology and Environment. We are seeking to appoint up to three Lecturers in the Discipline of Zoology and Tropical Ecology, to contribute to and complement our current teaching and research profile. The appointee(s) will have a strong interest in teaching and research in whole animal biology in the tropics. He/she will have demonstrated experience and success in tertiary teaching, student supervision and research. The appointee(s) will be required to teach in appropriate areas of zoology, ecology and/or quantitative biology, including their area of special expertise. Preference may be given to applicants with interests in one or more of the following: wildlife biology, conservation, terrestrial vertebrate ecology, and/or behaviour, terrestrial invertebrate biology, genetics, freshwater biology.

Zoology and Tropical Ecology is one of the top three disciplines in James Cook University for winning competitive research grants, and belongs to JCU's flagship research School. JCU is an excellent base for research in tropical zoology and ecology because: it has excellent infrastructure; there is ready access to a wide array of environments (rainforest, savanna, streams, wetlands, mountains and islands); there is a rich intellectual environment in the region, including CSIRO (on campus), Wet Tropics Management Authority, Australian Institute of Marine Science, Great Barrier Reef Marine Park Authority, several government departments and successful cognate disciplines of JCU; and it has the all the attributes of a western-style university in a safe political and healthy environment.

Associate Professor Simon KA Robson

Deputy Head of School

School of Marine and Tropical Biology Faculty of Science and Engineering James Cook University Townsville, Australia QLD 4811

ph 61 (0) 7 4781 5466 FAX 61 (0) 7 4781 5511

<http://www.jcu.edu.au/mtb/> CRICOS Provider Code 00117 J ABN 4625321195

Simon Robson <simon.robson@jcu.edu.au>

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## MichiganStateU BEACON DiversityDirector

Diversity Director - BEACON Center for the Study of Evolution in Action

Fixed-Term, 12-month basis, 100% time. Salary commensurate with degree and experience.

**\*DUTIES\*:** BEACON is a newly established NSF Science and Technology Center, funded at \$5 million/year for five years, renewable to ten years. BEACON is recruiting a person with at least a Master's degree, preferably in biological or physical sciences or computer science or engineering, a record of accomplishment in working with-and designing and conducting programs for-members of underrepresented groups at the faculty, post-doc, graduate student, undergraduate student, and/or K-12 levels; and a professional interest in diversifying participation in the STEM disciplines to serve as the Diversity Director. The position is primarily managerial and administrative, dealing with recruiting and retention of students, establishment of pro-

grams resulting in increased diversity in BEACON, etc. The Diversity Director should have an understanding of how assessment guides the development of effective diversity programs. S/he should provide strong leadership in developing, implementing, and continually updating strategic plans for diversity in collaboration with the education and research communities. The Diversity Director is a member of the management team of the BEACON Center, reporting directly to the BEACON Director. S/he is a member of the Diversity Steering Committee and the Education and Human Resource Development (EHRD) Steering Committee and works with those committees to assure that BEACON efforts involving faculty members, postdoctorals, graduate students, undergraduate researchers, K-12 students and teachers, and public outreach are designed and implemented to attract and include diverse participants-specifically underrepresented minorities, women in engineering, and persons with disabilities. The Diversity Director coordinates specific diversifying efforts among the five BEACON universities as appropriate and oversees the assessment of diversity. The Diversity Director is responsible for preparing materials related to diversity activities and outcomes to be submitted for use in any and all BEACON reports. **SPECIFIC DUTIES AND RESPONSIBILITIES:** Work closely with the BEACON Director, the Diversity Steering Committee, and the EHRD Steering Committee to help define mission priorities, especially regarding diversity. Initiate specific diversity programs to be funded by the center, in collaboration with other BEACON personnel. Oversee BEACON's diversity efforts at all levels and track outcomes of those efforts. Design and implement procedures for more general tracking of diversity of participants in BEACON programs and outreach. Serve as BEACON's ambassador to specific community constituencies, including undergraduate and master's programs, professional conferences, media, corporations, and foundations. Provide advice and support to the BEACON Director in all matters relating to diversity. Embrace and articulate the mission of BEACON and possess a working knowledge of all of its programs and themes.

**\*QUALIFICATIONS\*:** Master's degree; doctorate preferred. Qualifications other than degree: Doctorate or Master's degree plus at least three years of highly relevant job experience in academia; a commitment to evolution research and education in a research-intensive university setting; a record of successful administrative experience, such as in leadership of an academic or co-curricular program; exceptional leadership, organizational and interpersonal skills, and the ability to work collegially, and with integrity within a goal-oriented

academic organization; excellent communication skills; the ability to work efficiently on multiple assignments involving administrators, faculty, staff, students at all levels, and the public. **PREFERRED QUALIFICATIONS:** Evidence of scholarship regarding diversity in STEM disciplines; background in biological sciences, engineering or computer science; expertise in evolution; a demonstrated ability to design and assess successful programs to increase diversity in K-12, public, undergraduate and/or graduate programs.

**\*APPLICATIONS\*:** Due October 1, 2010. Late submissions will be considered if a suitable candidate pool is not identified by the deadline. MSU is an affirmative-action, equal-opportunity employer. MSU is committed to achieving excellence through cultural diversity. The university actively encourages applications and/or nominations of women, persons of color, veterans and persons with disabilities. Any questions should be addressed to Percy Pierre, Chair of the BEACON Diversity Director Search Committee, at pierre@egr.msu.edu <mailto:pierre@egr.msu.edu>, with "BEACON Diversity Director" in the subject line. Applications should be emailed to jamesc@msu.edu <mailto:jamesc@msu.edu>, with "BEACON

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## MichiganStateU MuseumLearning

**\*Position Posting: Informal Learning Specialist**

\*The Michigan State University Museum seeks an informal learning specialist to strengthen the Museum as a vibrant learning laboratory for all ages and to develop it as a portal for connecting audiences to the university's research activities. The MSU Museum is the cultural and natural science museum of Michigan State University, the land grant, research intensive university located in East Lansing, Michigan. The Museum is accredited by the American Association of Museums and is a Smithsonian Affiliate.

**Duties:** ∅ Develop informal educational products for diverse audiences including university students, elementary and high school students, and the general public ∅ Develop and manage MSU MuseumPOR-

TAL, a blended learning program that connects audiences to contemporary research through exhibits, digital applications and outreach learning ∅ Develop educational content of exhibits, teleconferenced virtual field trips, and digital domains (working with cross-university teams, content specialists, exhibition staff and digital programmers) ∅ Ensure that educational products incorporate and are grounded in the latest understanding of informal learning ∅ Conduct active research on learning through museum products and work with evaluators to evaluate the effectiveness of the educational programs in enhancing learning ∅ Secure grant and foundation support to enhance the Museum as a 'learning laboratory' ∅ Communicate the results of research on learning to professional and popular audiences, including publications and conference papers ∅ Build the Museum's educational capacities through productive relationships with faculty, university students, and education and museum sectors ∅ Manage projects and work teams of staff, students, contractors and partners

**Job requirements**

**Qualifications:** Ph.D. in education or museology, with a strong emphasis on informal learning, preferably in STEM disciplines. A Ph.D. in a STEM discipline will be considered if the candidate has extremely strong informal educational experience and achievements.

**Experience/personal qualities:** ∅ 5 years experience in developing and delivering educational programs in an informal learning setting, such as a museum, science center, zoo, or similar organization; experience with STEM disciplines will be highly regarded ∅ Experience in developing educational content through diverse media, for exhibits and via digital products (online, mobile) ∅ A profound understanding of informal learning theory, and of methods for linking informal and formal education streams ∅ Experience and publication record in research on informal learning, preferably with an emphasis on STEM fields ∅ Experience in assessment of learning and evaluation of educational products in informal education ∅ Demonstrated project management skills and experience in managing budgets and multidisciplinary teams of staff, students and partners ∅ Excellent interpersonal skills, and written and oral communication skills; the ability to work with diverse partners including researchers/faculty, designers, exhibit preparators, students ∅ Demonstrated ability to capture extramural funding for educational programs from granting agencies, sponsors and other sources

This is a renewable annual appointment position in the academic specialist system. Starting salary is \$50-55,000 per year.

The MSU Museum is an affirmative action, equal opportunity employer. MSU is committed to achieving excellence through cultural diversity.

Submit cover letter addressing the above job requirements, resume, and three professional references to email [morgang@msu.edu](mailto:morgang@msu.edu) or post to Education Specialist Recruitment, Michigan State University Museum, Room 103, West Circle Drive, East Lansing, MI 48824. Applications are due by 30 September 2010.

Danielle J. Whittaker, Ph.D. Managing Director BEACON Center for the Study of Evolution in Action 1441 Biomedical and Physical Sciences Building Michigan State University East Lansing, MI 48824 (517) 884-2561 [djwhitta@msu.edu](mailto:djwhitta@msu.edu)

[djwhitta@msu.edu](mailto:djwhitta@msu.edu)

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### MichiganStateU ResTech SticklebackEvolution

I am looking for a lab technician. My lab studies sexual selection and speciation in stickleback fish, and we combine behavioral work with genetics, morphology and evolution. The position is split between fish husbandry and research support. Applications must be made through the MSU Human Resources website for job posting # 4087. <https://jobs.msu.edu/applicants/jsp/shared/-frameset/Frameset.jsp?time=1283375322611> Informal inquiries can be made to Jenny Boughman, [boughman@msu.edu](mailto:boughman@msu.edu).

Job description: Research Technician I – Department of Zoology, Michigan State University

Minimum requirements: A Bachelor's degree in biology or related field with knowledge of animal behavior, ecology, and evolution. Several months experience with husbandry of fish or amphibians, including care of adult and juvenile fish and embryos, and of setting up and maintaining large numbers of aquariums for freshwater fish and/or amphibians. Some experience and good ability for training and supervising assistants in care of fish and colony maintenance. Excellent organizational and communication skills. Must be dependable. Week-end and holiday work required.

Desired qualifications: Ability to take charge and oversee animal husbandry and lab procedures. Understanding of campus animal care policy and procedures. Experience with the use of spreadsheet software (e.g., excel

etc) and introductory statistics. Ability to learn new software programs.

Job summary: Primary responsibility for maintaining large colony of stickleback fish, including caring for fish, keeping aquaria and lab clean. Provide support for ongoing experiments, including collection and analysis of morphological, genetic, and behavioral data on three-spine sticklebacks. Supervise and train undergraduate assistants in fish husbandry and lab maintenance tasks. Order equipment, supplies, and materials and oversee maintaining supplies necessary for fish care and experiments in the lab. Maintain animal care records and lab records of animal and maintenance protocols, genetic crosses, supplies, orders, and maintain lab website and computer network. Some animal care experience required.

Position to begin immediately. Salary \$30,846

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Jenny Boughman Associate Professor Zoology Michigan State University 203 Natural Science Bldg East Lansing MI 48824 517.353.8636 [boughman@msu.edu](mailto:boughman@msu.edu) <http://www.zoology.msu.edu/all-faculty/janette-boughman.html> Jenny Boughman <[boughman@msu.edu](mailto:boughman@msu.edu)>

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### NorthCarolinaStateU BeeEvolution

\*GRADUATE/POSTGRADUATE RESEARCH POSITIONS IN HONEY BEE GENETICS, NORTH CAROLINA, USA\*

North Carolina State University (Raleigh, NC) & University of North Carolina (Greensboro, NC)

We are looking for one or more individuals to join our collaborative research team on a project studying the genetics of honey bee stress resistance and lifespan between Dr. Olav Rueppell (UNC-Greensboro), Dr. David Tarp (NC State), and Dr. Micheline Strand (Research Triangle Park). The level of these positions is flexible, and we will consider applications for graduate students (PhD level) and/or postgraduate researchers (postdoctoral or research technician).

The project will address genetic and environmental variation in stress resistance and its relation to life expectancy in worker honey bees. The applicants should have molecular research experience, be willing to travel, and be comfortable working with live honey bees. The

project is funded for 5 years, and salaries will depend on qualifications.

Please send inquiries and applications until 15th October 2010 to [olav\\_rueppell@uncg.edu](mailto:olav_rueppell@uncg.edu). Applications should be electronic and comprise a CV, contact information of three professional references, and a short (<one-page) description of why you are interested in joining our team.

Review of applicants will begin immediately and will continue until the position is filled.

\*Distributed in furtherance of the acts of Congress of May 8 and June 30, 1914. North Carolina State University and North Carolina A&T State University commit themselves to positive action to secure equal opportunity regardless of race, color, creed, national origin, religion, sex, age, or disability. In addition, the two Universities welcome all persons without regard to sexual orientation. Dr. David Tarpy [\\*\\*david.tarpy@ncsu.edu\\*\\*](mailto:david.tarpy@ncsu.edu), 919.515.1660\*

Dr. Olav Rueppell Associate Professor Department of Biology Univ. North Carolina at Greensboro 312 Eberhart Bldg. Greensboro, NC 27403, USA Tel.: (1) 336-256-2591 Fax: (1) 336-334-5839

[orueppell@gmail.com](mailto:orueppell@gmail.com)

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## OhioStateU PollinatorBiologist

Assistant Professor: Honey Bee / Pollinator Biologist  
Department of Entomology The Ohio State University  
Ohio Agricultural Research and Development Center  
Wooster, OH

LOCATION: Department of Entomology, The Ohio State University, Ohio Agricultural Research and Development Center (OARDC), Wooster, Ohio (<http://entomology.osu.edu/>, <http://oardc.ohio-state.edu>).

QUALIFICATIONS: Ph.D. in Entomology, Zoology, or related field with focus on biology, genetics, and ecology of honey bees or other insect pollinators, including but not limited to, functional genomics, metabolomics, neurophysiology, behavior, pathology, or toxicology. Experience with pollinating insects is required, and applicants with prior experience relevant to honey bees will be strongly considered. Other qualifications include excellent oral and written communication skills, evidence of scholarly research and productivity, demonstrated potential for quality teaching, and willingness

to collaborate. Desired qualifications include teaching and post-doctoral experience, and experience with extramural funding opportunities.

POSITION DESCRIPTION: Assistant Professor, 9-month tenure-track appointment focusing on honey bees and/or other pollinating insects, 80% research / 20% teaching.

For four decades, the Department of Entomology at The Ohio State University led research in honey bee genetics. At the forefront of these efforts was Dr. Walter Rothenbuhler, the preeminent honey bee geneticist in the country who made significant contributions to our understanding of honey bee biology and their importance to modern agriculture. Currently, 30% of Ohio crops depend on bees and other insects for pollination. The Department of Entomology at The Ohio State University wishes to reclaim the Rothenbuhler legacy and regain our ability to perform world-class research on pollinators. With the sequencing of the honey bee genome, we believe that molecular biology will make important contributions to understanding honey bee physiology and ecology, including their interactions with the pesticides, pathogens, and arthropod pests that impact the health of hives. Current methods in physiology, proteomics, metabolomics and structural and functional genomics-including recent second-generation sequencing technologies-hold great promise for significant advances in biology and ecology of the insects that provide critical pollination services to support agricultural production. This position is central to addressing these vital issues and to fulfill the OARDC's mission to enhance the well-being of the people of Ohio, the nation and world through research on food, agriculture, family and environment.

Research (80%): The successful applicant is expected to develop an internationally renowned research program focused on insect pollinators relevant to food production. Research areas include but are not limited to: - molecular biology and functional genomics; - neurophysiology, learning, and behavior; - health of honey bee and other pollinators including interactions with pathogens, arthropod pests and pesticides; - ecology of honey bees and other pollinator populations in agricultural and urban ecosystems; - pollinator services to economically important plants.

Teaching (20%): The successful applicant will contribute to innovative undergraduate and graduate level curricula in entomology and related disciplines. Additional responsibilities include graduate seminar courses and the advising of graduate students.

OARDC/OSU COLLABORATION: We encourage close collaborations with existing teaching, extension,

and research programs within the Department of Entomology including a world-class extension program in apiculture, research programs in functional genomics, population genetics, physiology, behavior, chemical ecology, plant-insect interactions, biological control, modeling, landscape ecology, and ecosystem management. Strong candidates would show interest and abilities in building intra-departmental expertise on projects to scale understanding of insect biology from genes to ecosystems. Opportunities also exist for collaboration with departments across the OSU campuses including Horticulture and Crop Science, Plant Pathology, and Evolution, Ecology, and Organismal Biology, as well as interdisciplinary programs in Molecular, Cellular, & Developmental Biology, Agroecosystem Management, Organic Food and Farm Educational Research, and Urban Landscape Ecology. There exists potential to interact with the highly active Wooster Area Molecular Biology Association (WAMBA) that builds partnerships among departments on the OARDC campus and inter-institutional collaborations with molecular biologists at the College of Wooster.

**FACILITY SUPPORT:** The successful applicant will have access to existing bee hives and apiculture facilities, as well as ample greenhouse space and land

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## Paris Orsay PopulationDynamics

Dear colleagues,

the University of Paris South (Orsay, France) invites applications for a tenured academic position (Assistant Professor) in Biological Conservation/Population Dynamics, with a research focus on invasion biology in a context of climate change.

The drawbacks of such French positions, is that the teaching load is quite heavy (192h/year). Hence the importance of having a group backing you up when you are A. Prof., which will be the case here. There is also a need to at least show you are willing to be able to teach most of your classes in French in the coming years. Otherwise, we work in English in the lab.

The good sides, beside working with a great group

in a great lab on a great campus, obviously, is that these positions are tenured, with ample liberty on research themes. And croissants for every breakfast for life... Deadline for administrative applications is October 28th, deadline for scientific application is December 17th.

Contact me for more info. Thanks you to spread around Franck

Franck Courchamp

Lab ESE, UMR CNRS 8079

Univ Paris-Sud Tel (0033/0) 1 69 15 56 85

Bat 362 Fax (0033/0) 1 69 15 56 96

F-91405 Orsay Cedex FRANCE

<http://www.es.e.u-psud.fr/epc/conservation/pages/-Franck/homepage.html>

Franck Courchamp <franck.courchamp@u-psud.fr>

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## PennStateU Genomics

Systems & Computational Genomics: Faculty Cluster Hiring

The Pennsylvania State University is embarking on a comprehensive and transformative investment in systems genomics, complex traits and biological variation. This cross-college endeavor coordinates faculty recruitments and team-building efforts to address critical problems in life sciences affecting agriculture, energy production and healthcare. Development of computational and informatics systems for the analysis of genomic data is an integral part of the strategic plan. The PSU Systems Genomics Initiative is a concerted effort to bring predictive power to our understanding of biological systems and realize the potential of biology-based tools.

We seek to appoint multiple tenure-track professors at all levels from Assistant and Associate Professor through to Full Professors and Endowed Chairs who will further Penn States leadership role in the fields of Systems Genomics and Bioinformatics. We seek faculty interested in analyzing genomic data, undertaking systems and functional genomics and in applying these results to a broad range of biological problems. These will include Computer and Information Scientists, Social Scientists, Life Scientists, Physicists, Mathematicians, Statisticians and Biomedical researchers. Ap-

pointments will be made both at the main campus at University Park in Central Pennsylvania and also in the College of Medicine, located at the Penn State Medical Center in Hershey, PA. We seek interactive faculty who can work across disciplines and in a team to provide novel insights into current and future issues. We anticipate that many candidates will have joint appointments and join one of our centers of excellence in genomics, such as the Center for Comparative Genomics and Bioinformatics (<http://www.bx.psu.edu/>) or Center for Medical Genomics (<http://www.huck.psu.edu/-institutes-and-centers/medical-genomics>).

These positions feature outstanding research space and competitive start-up packages and state-of-the-art shared instrumentation for sequencing (<http://www.huck.psu.edu/>) and computational analysis (<http://www.ics.psu.edu/>). Penn State has achieved great successes in the field of genomics and bioinformatics with an impressive collection of publications and analysis software, including Galaxy (<http://galaxy.psu.edu/>), a universal platform that can continuously adapt and gain new capabilities to serve the needs of experimental and computational scientists.

Please electronically submit a cover letter, including future research plans, curriculum vitae and contact information of three references to L. Scott Boor at [lsb6@psu.edu](mailto:lsb6@psu.edu).

Review will start in August and continue until multiple positions have been filled. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

Kateryna Makova, Ph.D. Associate Professor Department of Biology 305 Wartik Lab Penn State University University Park, PA 16802 Tel: 814-863-1619 Fax: 814-865-9131 E-mail: [kmakova@bx.psu.edu](mailto:kmakova@bx.psu.edu) Web: [http://www.bx.psu.edu/makova\\_lab/](http://www.bx.psu.edu/makova_lab/) Kateryna Makova <[kmakova@bx.psu.edu](mailto:kmakova@bx.psu.edu)>

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## PortlandStateU PlantEvolution

TENURE TRACK POSITION IN BIOLOGY The Department of Biology at Portland State University invites applications for a faculty position at the rank of Assistant or Associate Professor. We seek applicants addressing fundamental questions on biotic interactions in plant systems, including but not limited to plant-microbe and plant-insect interactions at any scale of organization or integration. We encourage applications

from individuals whose interests complement existing departmental strengths in ecology, evolution, physiology, genetics and our Center for Life in Extreme Environments (see the departmental web site: <http://www.bio.pdx.edu/>). A PhD and postdoctoral experience are required. Priority will be given to candidates who have demonstrated success in developing a research program through publications and extramural funding. The successful candidate will be expected to develop an externally funded research program, be effective in teaching at the undergraduate and graduate levels, and participate in the training of graduate students in our masters and PhD programs. This is a tenure track, 9 month appointment to begin in the fall of 2011. Review of applications will begin 15 October, 2010, and will continue until the position is filled. The level of appointment will be commensurate with qualifications and experience. Curriculum vitae, statement of current and future research interests, and three letters of reference should be sent to: [plantbio@pdx.edu](mailto:plantbio@pdx.edu).

/Portland State University is an Affirmative Action, Equal Opportunity institution and, in keeping with the President's diversity initiative, welcomes applications from diverse candidates and candidates who support diversity./

Portland State University is located in downtown Portland, the major urban center of Oregon. The University is centered on the tree-lined South Park Blocks, an extensive greenway through the center of the city, and is surrounded by numerous cafes, pubs, and restaurants. PSU's Portland Business Accelerator is located near the south side of campus, part of an emerging biotechnology research cluster centered in the new South Waterfront Development. Adjacent to and within walking distance of the University is the Portland cultural district, home to the Portland Symphony, the Portland Center for the Performing Arts, the Portland Art Museum, the Northwest Film Center, and the museum of The Oregon Historical Society. The city is known for its extensive park system, highlighted by Forest Park, the largest urban park (> 5000 acres) in the United States. Extensive hiking and biking trails are found within the city and surrounding region, and hiking, biking, skiing, windsurfing, and kayaking are popular outdoor activities that are widely available. The rugged Cascade and Coast mountain ranges, and beautiful Pacific coast are all located within a 90 minute drive.

[cruzan@pdx.edu](mailto:cruzan@pdx.edu)



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## RiceU Programmer

A programmer, or research scientist, is needed for a project on developing a software tool for reconciling gene trees, and inferring species phylogenies from gene trees. JAVA programming skills is a requirement, and for the current status of the tool, interested applicants can check out <http://bioinfo.cs.rice.edu/phyloNet>. If you are interested, please contact Prof. Luay Nakhleh at [nakhleh@cs.rice.edu](mailto:nakhleh@cs.rice.edu).

Best regards, Luay

Luay Nakhleh <http://www.cs.rice.edu/~nakhleh>  
[nakhleh@rice.edu](mailto:nakhleh@rice.edu)

Luay Nakhleh <[nakhleh@rice.edu](mailto:nakhleh@rice.edu)>

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## Rutgers ResAssoc MosquitoEvolution

### POSITION ANNOUNCEMENT

Research Associate (non-tenure faculty position)

The Center for Vector Biology is looking for a Research Associate to fill in the growing need for research integrated in a USDA area-wide project to suppress the Asian tiger mosquito (ATM). We are developing a multidisciplinary large-scale strategy to suppress the ATM. Our approach is supported by an economic analysis and incorporates extensive public education and involvement with focused application of established biological and chemical control interventions. This position will support the assessment of the metapopulation structure of the ATM by using high-resolution population genetics. Qualified applicants must have a doctorate degree in population genetics, medical entomology, evolutionary ecology, or evolution. A strong background in conceptual ecology/evolution is needed. Experience with microsatellites, SNPs, and NextGen sequencing platforms are essential, as well as proficiency with standard and innovative population genetic analyses software. Ability to work collaboratively in a goal-oriented team environment is required. Excellent written and verbal communication skills are important and strong

analytical skills are preferred. Position will be available December 15, 2010. Salary will be commensurate with experience and complemented by full health and salary benefits (\$40,000 to \$55,000). Send inquiries to Prof. Dina Fonseca at [dinafons@rci.rutgers.edu](mailto:dinafons@rci.rutgers.edu) and applications consisting of curriculum vitae, a short statement of research interests, and contact information for three references to Carol Terry at [terry@aesop.rutgers.edu](mailto:terry@aesop.rutgers.edu). Applications will be reviewed as they arrive.

Rutgers University is an Equal Opportunity/Affirmative Action Employer.

– Dina M. Fonseca, PhD Associate Professor

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

“Dina M. Fonseca” <[dinafons@rci.rutgers.edu](mailto:dinafons@rci.rutgers.edu)>

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## RutgersU ComputationalGenetics

Faculty Position in Computational Genetics

The Department of Genetics in the School of Arts and Sciences at Rutgers, The State University of New Jersey seeks an outstanding scientist to complement the existing faculty in computational genetics, moving our program into exciting new areas and expanding our existing strengths. Tenure-track or tenured appointment will be made at the Assistant, Associate, or Full Professor level. Areas of interest include, but are not limited to, bioinformatics, statistical genetics, theoretical or experimental genomics, population or evolutionary genetics, and analysis of complex genetic diseases. Appropriate candidates will also be considered for appointment to the Human Genetics Institute of New Jersey. Core resources and startup funds will be provided. Research space, including wet lab if needed, will be provided in the newly constructed Life Sciences Building.

The Department of Genetics is home to nearly 30 faculty with diverse interests and numerous well-funded research programs, and is part of a vibrant life sciences and computational community. Our computational group collaborates with other Department of Genetics faculty and Rutgers scientists within the Division of Life Sciences, the Departments of Computer Science and Statistics, the Waksman Institute, the Center for Advanced Biotechnology and Medicine, the Robert Wood Johnson Medical School, the BioMaPS Institute

for Quantitative Biology, and the Center for Discrete Mathematics and Theoretical Computer Science (DIMACS). The New Brunswick/Piscataway campus is located in suburban central New Jersey, close to New York City, Philadelphia, beaches, and countryside. For more information on the Department and Rutgers see: <http://genetics.rutgers.edu/recruitment> . Candidates must have a Ph.D. and/or M.D., demonstrated record of significant research, the potential to make substantial contributions as an independent investigator, and have a commitment to teaching undergraduate and graduate students. Applicants should submit a CV, a detailed statement of research interests, a teaching statement, and full contact information for three individuals willing to provide letters of reference. Applications should be submitted electronically at <http://genetics-facsearch.rutgers.edu/applycompgen> and inquiries made to Ms. Sheri Lumpkin, [lumpkin@dls.rutgers.edu](mailto:lumpkin@dls.rutgers.edu). Review of applications will begin October 15, 2010 and continue until the position is filled.

Rutgers University is an equal opportunity/affirmative action employer committed to diversity. Women, minorities, and members of under-represented groups are encouraged to apply.

“Hey, Jody” <[Hey@Biology.Rutgers.Edu](mailto:Hey@Biology.Rutgers.Edu)>

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### SouthAmerica FieldAssist

Field assistant to study a cooperative breeding system in South America

We are looking for a highly motivated field assistant to join us working on the breeding system of the endangered El Oro parakeet (*Pyrrhura orcesi*). The apparently cooperative breeding system is studied for the first time in this species. Until now cooperative behaviour has been seldom observed in parakeets and our work focuses on the factors underlying the development of delayed dispersal and cooperative breeding. More details about the project can be looked up at: [www.biologie.uni-freiburg.de/data/bio1/schaefer/](http://www.biologie.uni-freiburg.de/data/bio1/schaefer/)

Fieldwork will take place at Buena Ventura reserve ([www.fjocotoco.org](http://www.fjocotoco.org)) near Pinas, southwest Ecuador. Fieldwork includes capturing birds with mist nets and inside artificial nest boxes, taking morphometric measurements and blood samples, banding of birds and field observation of parakeet flocks. The parakeet flocks are distributed throughout the whole reserve and adjacent

areas, therefore long and exhausting daily treks across the foothills of the Andes are unavoidable. Fieldwork will be done during rainy season. Moreover, batteries (~3kg) for nest cameras have to be changed every two days. The project will cover the costs for flight and accommodation at the reserve. If required, a letter of recommendation will be drawn up. The position is available from January until April 2011.

If interested please send an email with a short CV and application letter (why you are interested) to: [nadine.klauke@biologie.uni-freiburg.de](mailto:nadine.klauke@biologie.uni-freiburg.de)

Nadine Klauke PhD student Evolutionary Biology and Ecology University of Freiburg Hauptstraße 1 79104 Freiburg

Nadine Klauke <[nadine.klauke@biologie.uni-freiburg.de](mailto:nadine.klauke@biologie.uni-freiburg.de)>

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### UAkron EvolutionaryMicrobiol

The University of Akron's Department of Biology is currently running a search for a Microbiologist (Assistant Professor rank) to join our Integrated Bioscience Program. We have a strong group in evolutionary genetics and we have identified microbial ecology and/or microbial physiology, as areas where we would like to build a strong core as well. We encourage cross-disciplinary interactions amongst our faculty and our PhD training program spans numerous departments and colleges. We are the third largest campus in Ohio and are recognized as a regional leader in STEM disciplines.

We have advertised the position broadly and we are not restricted to hire any particular area of microbiology (you can see the ad on ASM website [http://www.asmcareerconnections.org/c/-job.cfm?vnet=0&str=26&site\\_id=756&jb=7108714](http://www.asmcareerconnections.org/c/-job.cfm?vnet=0&str=26&site_id=756&jb=7108714)). Please ignore the portion of the ASM ad that identifies the job as a microbial education position. We are a research-oriented department and it is research and not education that is the focus of the position.

Application review will begin on October 1st and will continue until the position is filled.

Our official job ad follows: The Biology Department at the University of Akron invites applications for a tenure-track position at the rank of Assistant Professor to begin Fall 2011. We seek a microbiologist with a strong background in research and teaching. The suc-

successful candidate will be expected to develop an externally funded research program and to form collaborations both within biology and across disciplines. Research areas of interest include, but are not limited to, microbial physiology and genetics of quorum sensing, microbial community genomics or ecological genetics of disease. Teaching responsibilities include an upper level microbiology course with lab and a graduate course in the applicant's area of specialization. Substantial start-up funds are available.

Paco Moore

Dr. Francisco B.-G. Moore

Program in Integrated Bioscience University of Akron  
Akron, OH 44325-3908

moore@uakron.edu

(330)972-2572

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## UAmsterdam Evolutionary Microbiology

ASSOCIATE PROFESSOR IN MICROBIAL ECOLOGY

Vacancy number: 10-1064

UNIVERSITY OF AMSTERDAM

The Universiteit van Amsterdam (UvA) is a university with an internationally acclaimed profile, located at the heart of the Dutch capital. As well as a world centre for business and research, Amsterdam is a hub of cultural and media activities. The Institute of Biodiversity and Ecosystem Dynamics (IBED) is one of the 10 research institutes of the Faculty of Science of the University of Amsterdam. Our scientific studies aim at a better understanding of the dynamics of ecosystems at all relevant levels, from genes to ecosystems, using a truly multidisciplinary approach.

### TASKS

We look for a microbial ecologist, with a strong interest to develop and apply new systems-biology approaches to the evolutionary ecology and population dynamics of aquatic microbial communities. He/she should be experienced in functional analyses of gene expression data and have a keen interest in the evolutionary ecology of species interactions, with the ambition to combine laboratory and/or field studies with mathematical models and bio-informatics. Depending on the candidate, po-

tential research topics might include experimental evolution of multispecies interactions or metagenomics approaches to aquatic food webs.

What we have to offer: The Associate Professor will play an important role in the Systems Biology initiative of the Faculty of Science, and will cover the integration between Systems Biology and Ecology. The position will be embedded in the existing IBED-research group of Aquatic Microbiology [led by prof.dr. Jef Huisman]. This research group has a prominent international position in the field of aquatic microbial ecology, with strongholds in the mathematical analysis of species interactions, laboratory chemostat experiments, and field work on plankton communities of lakes and oceans. Many experimental facilities are available, such as climate rooms and laboratory chemostats, molecular-biology laboratories, a microarray department, and extensive facilities for chemical analyses of nutrients and organic molecules. University funding will be provided for an attractive start-up package (for instance for hiring a PhD student/postdoc, or investment in lab facilities).

### REQUIREMENTS

- Strong publication record (given the timepoint in the career) in Microbial Ecology, as demonstrated by publications in first-rank scientific journals;
- Proven expertise with the application of systems-biology approaches;
- Proven success in research grant applications;
- Expertise with freshwater and/or marine microorganisms is highly recommended;
- Broad interest in the general fields of Biodiversity & Ecosystem Dynamics as well as Systems Biology;
- Inspiring teacher with excellent communication skills;
- Team player with proven organizational skills.

We would also welcome applications from promising young scientists for this position, provided that they fit the scientific profile and have demonstrated excellent scientific performance (in terms of publications) during several years of postdoctoral research. Such an early-career scientist will start as Assistant Professor in a tenure-track position, with the perspective to become Associate Professor after a successful performance in research and teaching in the first 5 years of appointment.

### FURTHER INFORMATION

Our institute's website: <http://www.science.uva.nl/-ibed> For more information, please contact: Prof.dr. Jef Huisman (Aquatic Microbiology, UvA), +31 20 525

7085, J.Huisman@uva.nl.

#### APPOINTMENT

We offer a position in a highly stimulating academic environment and a dynamic international atmosphere. The appointment will be initially on a temporary basis for a maximum period of two years. If the appointee proves him-/herself to be qualified for the position, a permanent appointment will be offered. The salary is in accordance with the university regulations for academic personnel (Collective Labour Agreement Dutch Universities) and will range from EUR 4,428.- up to EUR 5,390.- gross per month based on a full-time appointment.

An early career scientist starts as an Assistant Professor in a tenure track with a salary that ranges from EUR 3,195.- up to EUR 4,374.- gross per month, based on a full-time appointment. A permanent appointment will be offered after five years if he/she meets the criteria for Associate Professor.

The annual salary will be increased with 8 % holiday allowance and 8.3 % end-of-year bonus.

#### JOB APPLICATION

Applications should include a detailed CV including a list of publications, a motivation letter, and the names and contact addresses of two references from which information can be obtained. Applications should be sent by e-mail to [application-science@uva.nl](mailto:application-science@uva.nl). Please quote the vacancy number 10-1064 in the subject field. The deadline for applications is

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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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### UArizona ResTech PlantParasiteInteractions

A Research Specialist position is available in the laboratory of Dr. Noah Whiteman in the Department of Ecology and Evolutionary Biology at The University of Arizona (<http://www.eebweb.arizona.edu/Faculty/Bios/whiteman.html>). Research in the Whiteman Laboratory focuses on co-evolutionary interactions between host plants and parasitism including herbivorous insects and microbial pathogens. More specifically, the

research aims to identify the molecular basis and genomic architecture of host resistance and parasite virulence mechanisms using *Arabidopsis*, herbivores and bacteria. We are also developing a genomic model chewing herbivore of the reference plant *Arabidopsis thaliana*. This herbivore is a *Drosophila* species that mines the leaves of this plant and so we seek to leverage genomic tools to study the plant-insect interaction from both sides of the host and parasite equation. Finally, we are developing a co-evolutionary genomics model for studying plant-herbivore-pathogen interactions in the field and greenhouse.

Duties and responsibilities include:

- \*Maintaining an organized genomics research laboratory.
- \* Procuring supplies and purchasing equipment.
- \* Creating and maintaining laboratory protocols.
- \* Leading molecular genetic experiments in collaboration with the principal investigator.
- \* Helping to mentor undergraduate and graduate students and laboratory visitors.
- \* Conducting growth chamber and greenhouse experiments on plants, flies and bacteria.

Arizona Board of Regents Minimum Qualifications:

Bachelor's degree in a field appropriate to the area of assignment AND two years related research experience; OR,

Six years research experience appropriate to the area of assignment; OR,

Any equivalent combination of experience, training and/or education.

Salary will be \$31,125 - \$38,443 DOE

Outstanding UA benefits include health, dental, vision, and life insurance; paid vacation, sick leave, and holidays; UA/ASU/NAU tuition reduction for the employee and qualified family members; state retirement; access to UA recreation and cultural activities; and more!

Please apply through this website:

<https://www.uacareertrack.com/applicants/jsp/-shared/frameset/Frameset.jsp?time=1284594628835>

Best wishes, Noah

Noah K. Whiteman, Ph.D. Assistant Professor Department of Ecology & Evolutionary Biology Center for Insect Science The University of Arizona 424 BioSciences West, Tucson, AZ 85721 office: 520-626-3950, lab: 520-626-9315 email: [whiteman@email.arizona.edu](mailto:whiteman@email.arizona.edu) web: [www.eebweb.arizona.edu/Faculty/Whiteman/](http://www.eebweb.arizona.edu/Faculty/Whiteman/) "Noah K. Whiteman" <[whiteman@email.arizona.edu](mailto:whiteman@email.arizona.edu)>

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**UCaliforniaBerkeley**  
**AdaptationBiology**

\*ASSISTANT PROFESSOR OF GLOBAL CHANGE ORGANISMAL BIOLOGY\* University of California, Berkeley

The Division of Organisms and Environment, Department of Environment Science Policy and Management (<http://espm.berkeley.edu>), invites applications for a tenure-track, nine-month (academic year) appointment at the Assistant Professor level in the area of Global Change Organismal Biology, starting 1 July 2011. The position includes a joint appointment in the California Agricultural Experiment Station. The successful applicant must have a PhD in the biological or related sciences, an excellent record of scientific accomplishment, a strong commitment to undergraduate and graduate teaching, and a demonstrated interest in being part of a community of environmental biologists. The department seeks candidates whose research, teaching, or service has prepared them to contribute to our commitment to diversity and inclusion in higher education.

Applicants should submit the following documents electronically as pdf files labeled as follows: "LAST-NAME\_FirstName\_Document Number" with numbers as following): 1. Letter of application containing a list of referees who have been asked to email letters [globalchange@berkeley.edu](mailto:globalchange@berkeley.edu), 2. Current curriculum vitae, 3. Statement of research interests, 4. Statement of teaching interests and experience, 5A-C. pdf copies of 3 recent publications.

Submit application materials online at: <http://ecnr.berkeley.edu:80/sReg.php?i=166> . Refer potential reviewers to the UC Berkeley Statement of Confidentiality found at <http://apo.chance.berkeley.edu/evalltr.html>. The closing date for applications is 25 October 2010.

The University of California is an Equal Opportunity Affirmative Action Employer.

– Jessica Knowlton Academic Affairs Analyst Department of Environmental Science, Policy, and Management 135 Mulford Hall, # 3114 Berkeley, CA 94720-3114 Tel: (510) 643-9405

Jessica Knowlton <[jknowlton@berkeley.edu](mailto:jknowlton@berkeley.edu)>

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**UCaliforniaLosAngeles**  
**ConservationBiol****Open Conservation Biologist/Director Position**

The University of California, Los Angeles (UCLA) Department of Ecology and Evolutionary Biology and Institute of the Environment and Sustainability (IoES) seeks to fill a joint, open-rank (tenure track or tenured) faculty position in conservation biology. We are interested in all subfields within conservation biology but especially research utilizing approaches to address fundamental issues in the field. Candidates with strong interests in cross-disciplinary approaches to conservation science and climate change are especially encouraged to apply. The successful candidate is expected to establish a strong and externally funded research program and will assume faculty directorship of the recently established UCLA La Kretz Center for California Conservation Science.

Applicants should submit application materials online to [conservationbiologyposition@ioe.ucla.edu](mailto:conservationbiologyposition@ioe.ucla.edu), including a cover letter, curriculum vitae, statements of research, teaching and interdisciplinary interests, and the names and contact information of four references by December 1, 2010. Please use job number: 0830-1011-01 in all correspondence. Additional information about the Institute and the Department may be found at [www.environment.ucla.edu](http://www.environment.ucla.edu) and [www.eeb.ucla.edu](http://www.eeb.ucla.edu), respectively. Inquiries regarding the position should be directed to Search Chair, Professor Thomas B. Smith ([tbsmith@ucla.edu](mailto:tbsmith@ucla.edu)). As a campus with a diverse student body, individuals with a history of mentoring under-represented minorities in the sciences are encouraged to discuss their activities in their cover letter. Women and minority applicants are encouraged to apply. UCLA is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of faculty and staff diversity. I look forward to finding out how we can post this open position on your site.

Thanks in advance for your help with this.

Sincerely yours,

Karen A. Lefkowitz Communications Officer UCLA Institute of the Environment (310) 794-4908 <http://www.environment.ucla.edu/> "Lefkowitz, Karen A." <[karen@ioe.ucla.edu](mailto:karen@ioe.ucla.edu)>

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## UCyprus Biodiversity

Associate or Full Professor in Biodiversity and Ecology

The Department of Biological Sciences at the University of Cyprus seeks to fill a position at the rank of associate or full professor in the field of biodiversity and ecology. Candidates with a research focus in ecology, organismal or evolutionary biology are desired, whether in terrestrial or marine systems. Individuals with expertise in conservation of biodiversity are encouraged to apply. The successful candidate will have a Ph.D. in a related field and a strong publication record.

The Department of Biological Sciences at the University of Cyprus is dedicated to building research and education in ecology and evolutionary biology, and the successful candidate will be expected to take a leadership role in this process, mentoring students at undergraduate, Master's and doctoral levels. More information about the Department of Biological Sciences and its research can be found at: <http://www.ucy.ac.cy/goto/biosci/en-US/HOME.aspx> The official languages of the University are Greek and/or Turkish. For the above positions knowledge of Greek is necessary. Holding a citizenship of the Republic of Cyprus is not a requirement.

Interested individuals must submit their application both in printed form (two hardcopies) AND in electronic form (stored on two CDs, without security protection so that they can be copied) by Wednesday 13th of October 2010. The application must include the following items:

A letter stating the academic rank or ranks for which the applicant is interested in, the field of study and the date when he/she may be able to assume duties in case of selection.

Curriculum Vitae.

A brief summary of previous work and a statement of plans for future research (up to 1500 words).

A list of publications.

Copies of the three most representative publications.

Certificates copies of degree should be scanned and included in the CDs.

In addition, the applicants must ask for reference letters from three Professors to be sent directly to the Univer-

sity. The names and addresses of these referees must also be submitted with the application since additional confidential information may be sought. The recommendation letters must be received by the University by Wednesday 13th of October 2010.

The Curriculum Vitae and the statement of previous work and plans should be written in Greek or Turkish AND in English.

Applications and other documents submitted in the past will not be considered and must be re-submitted. Incomplete applications will not be considered.

All application materials should be submitted to:

Human Resources Service University of Cyprus Council/Senate Anastasios G Leventis Building P.O. Box 20537 1678 Nicosia, Cyprus Tel. 22894155/4158

by Wednesday 13th of October 2010, 2:00 p.m., by hand or to be sent by post (stamped by the post office by the 13th of October 2010 the latest). Applications will be considered valid provided that they are received by the Human Resources Service by the 18th of October 2010 at the the latest. The sole responsibility will be upon the interested applicant.

For more information contact Human Resource Service (tel.: +357 22894158) or Athena Sofokleous at the Department of Biological Sciences Tel: +357 22892880, email: [sofokleous.athina@ucy.ac.cy](mailto:sofokleous.athina@ucy.ac.cy).

Dr. Alexander N.G. Kirschel Dept. of Biological Sciences University of Cyprus PO Box 20537 Nicosia 1678 Cyprus Tel: +357 22 892660 Fax: +357 22 892881

and

Senior Research Fellow Center for Tropical Research University of California Los Angeles 621 Charles E. Young Dr. South Los Angeles, CA 90095 <http://taylor0.biology.ucla.edu/~kirschel/Site/Home.html>

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## UCyprus Biodiversity 2

Associate or Full Professor in Biodiversity and Ecology

The Department of Biological Sciences at the University of Cyprus seeks to fill a position at the rank of associate or full professor in the field of biodiversity and ecology. Candidates with a research focus in ecology, organismal or evolutionary biology are desired, whether in terrestrial or marine systems. Individuals with expertise in conservation of biodiversity are encouraged

to apply. The successful candidate will have a Ph.D. in a related field and a strong publication record.

The Department of Biological Sciences at the University of Cyprus is dedicated to building research and education in ecology and evolutionary biology, and the successful candidate will be expected to take a leadership role in this process, mentoring students at undergraduate, Master's and doctoral levels. More information about the Department of Biological Sciences and its research can be found at: <http://www.ucy.ac.cy/-goto/biosci/en-US/HOME.aspx> The official languages of the University are Greek and/or Turkish. For the above positions knowledge of Greek is necessary. Holding a citizenship of the Republic of Cyprus is not a requirement.

The annual gross salary for these positions (including the 13th salary) is:

Professor (Scale Á15-Á16) 67,668.77 - 87,959.69

Associate Professor (Scale Á14-Á15) 59,680.92 - 81,364.92

Assistant Professor (Scale Á13-Á14) 55,688.36 - 75,105.68

Lecturer (Scale Á12-Á13) 47,029.58 - 68,877.77

Én addition, the University Council may approve an annual bonus of up to 11.960,21 per year for persons appointed as Professors and up to 6.834,41 for academics appointed as Associate Professors.

Interested individuals must submit their application both in printed form (two hardcopies) AND in electronic form (stored on two CDs, without security protection so that they can be copied) by Wednesday 13th of October 2010. The application must include the following items:

A letter stating the academic rank or ranks for which the applicant is interested in, the field of study and the date when he/she may be able to assume duties in case of selection.

Curriculum Vitae.

A brief summary of previous work and a statement of plans for future research (up to 1500 words).

A list of publications.

Copies of the three most representative publications.

Certificates copies of degree should be scanned and included in the CDs.

In addition, the applicants must ask for reference letters from three Professors to be sent directly to the University. The names and addresses of these referees must also be submitted with the application since additional

confidential information may be sought. The recommendation letters must be received by the University by Wednesday 13th of October 2010.

The Curriculum Vitae and the statement of previous work and plans should be written in Greek or Turkish AND in English.

Applications and other documents submitted in the past will not be considered and must be re-submitted. Incomplete applications will not be considered.

All application materials should be submitted to:

Human Resources Service University of Cyprus Council/Senate Anastasios G Leventis Building P.O. Box 20537 1678 Nicosia, Cyprus Tel. 22894155/4158

by Wednesday 13th of October 2010, 2:00 p.m., by hand or to be sent by post (stamped by the post office by the 13th of October 2010 the latest). Applications will be considered valid provided that they are received by the Human Resources Service by the 18th of October 2010 at the the latest. The sole responsibility will be upon the interested applicant.

For more information contact Human Resource Service (tel.: +357 22894158) or Athena Sofokleous at the Department of Biological Sciences Tel: +357 22892880, email: [sofokleous.athina@ucy.ac.cy](mailto:sofokleous.athina@ucy.ac.cy).

Alex Kirschel <[kirschel@ucla.edu](mailto:kirschel@ucla.edu)>

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## UDenver EvolutionaryBiol

Evolutionary Biologist

The Department of Biological Sciences, University of Denver, invites applications for a tenure-track position at the Assistant Professor level to begin September 1, 2011. Candidates with expertise in any area of Evolutionary Biology are sought; individuals with expertise in either evolutionary-developmental biology or evolutionary ecology are encouraged to apply. The successful candidate will have a Ph.D. and post-doctoral experience in appropriate fields, will develop an extramurally funded research program, will supervise undergraduate research projects and M.S. and Ph.D. students, and will teach undergraduate and graduate courses in evolutionary biology and specific areas of specialty. All candidates must submit their application through <https://www.dujobs.org> < <https://www.dujobs.org/> > . The online application should include: curriculum vitae, statements of teaching philosophy and research

interests and two recent publications. Under separate cover have three letters of recommendation to Dr. Todd Blankenship, Chair, Evolutionary Biologist Search Committee, Department of Biological Sciences, University of Denver, Denver, CO 80208. Review of applications will begin October 15, 2010. The University of Denver is committed to enhancing the diversity of its faculty and staff and encourages applications from women, minorities, people with disabilities and veterans. DU is an EEO/AA employer.

Shannon.M.Murphy@du.edu

## UGothenburg EvolutionaryEcol

LECTURESHIP, the field of animal terrestrial evolutionary ecology

Senior Lecturer in Animal Ecology

at the Department of Zoology, Univ of Gothenburg (Göteborg), Sweden

Research in Animal Ecology at the Department deals with basic ecological and evolutionary questions as well as applied ecology, including biodiversity and environmental aspects in terrestrial and aquatic environments. We combine ecological theory and modelling with field observations and experiments to generate and address hypotheses where the focus is to understand the ecology of animals as a result of natural selection and other evolutionary processes. This approach increases the understanding of animal populations and communities, and provides background knowledge for biodiversity and other applied work. The open position should be integrated with, and enhance, the development of this successful activity at the Department.

Responsibilities The successful candidate is expected to conduct research, supervise Ph.D. students and actively apply for external research funding within the field of animal terrestrial evolutionary ecology. Other important responsibilities are to support and develop our research and teaching activities in molecular ecology and conservation ecology. Further, the successful candidate is expected to plan, teach, lead and develop courses at the basic and advanced levels, especially in animal evolutionary ecology. The position as Senior Lecturer may also include various leadership- and/or administrative responsibilities.

Qualification requirements A Ph.D. in animal ecology or related subjects is required. The qualifications re-

quirements as stated in the Higher Education Ordinance are applied for the position. The position also requires an ability to teach in Swedish and English. The successful applicant is expected to be able to teach in Swedish within two years.

Assessment grounds Scientific and pedagogical proficiency are considered to be equally important for the assessment of the applicants. When assessing scientific proficiency, special weight is given to documented competence in the field of animal terrestrial evolutionary ecology with high-quality publications in internationally renowned journals. A background in evolutionary ecology, molecular ecology and conservation biology is meriting, as is experience of leading research groups. When assessing pedagogical proficiency weight is given to successful supervision of Ph.D. students, and documented experience of teaching in animal ecology and related subjects. Experience of course leadership, development and organization is meriting, including documented experience of teaching administration. After scientific and pedagogic proficiency, as described above, documented ability to attract research grants from research councils and other external sources is the second most important basis for the assessment of candidates. Finally, the ability to interact with society and inform about research and other developmental projects is the third most important basis for the assessment.

Further information Further information about the position is provided by Prof. Lars Förllin, Head of Department, Department of Zoology, phone: +46 (0)31 786 3676, email: lars.forlin@zool.gu.se. For more information about the Department of Zoology, please visit our website at: <http://www.zool.gu.se>. Union representatives: SACO Martin Björkman, phone +46 (0)31 786 3608, FR/S Astrid Igerud, phone +46 (0)31 786 11 67, SEKO Lennart Olsson, phone +46 (0)31 786 11 73.

Selection process - The selection process will include evaluation by external reviewers, interviews, guest lectures, and/or research seminars.

Application - The application should be written in English and addressed to the Dean of the Faculty of Science. The application should include:

• CV, including publication list, employer references and other documents that the applicant wants to be considered. Documentation of teaching merits should include information about the extent and level of teaching and evaluations of its quality. Obtained research funding should be clearly stated, including the amount of funding received.

• A short summary describing the applicant's history of



research, teaching, and interactions with society (max 5 pages).

â A description of current and planned research as well as other planned activities relevant to the position (max 5 pages).

â A maximum of 10 scientific papers, including a motivation for choosing these.

A complete copy of the application must be sent electronically to the University through the following website: <http://www.science.gu.se/english/-application/e324546509> Here applicants will find further instructions for how to submit their applications electronically. Also, a complete hardcopy of the application must be

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## UIdaho DirectorFacilities IBEST

The IBEST (Initiative for Bioinformatics and Evolutionary Studies) group at the University of Idaho is looking for a Director of IBEST Core Facilities. We have three cores: bioinformatics core, sequencing core, and imaging core.

MAJOR FUNCTION: Management of IBEST research core facilities, which include the DNA Sequence Analysis Core, Bioinformatics Core, and Optical Imaging Core. This individual will provide strategic and technical management of core facilities and guidance to the core facility user community. Responsibilities include the development of procedures and policies of facility use, financial oversight of operations, employee supervision, and funding procurement activities. The director will ensure compliance with federal, state, and local agencies regulations and guidelines. This position is an integral part of the IBEST administrative management team.

Details are here: [https://www.sites.uidaho.edu/AppTrack/Agency/Applicant/-ViewAnnouncement.asp?announcement\\_no=16904058981](https://www.sites.uidaho.edu/AppTrack/Agency/Applicant/-ViewAnnouncement.asp?announcement_no=16904058981)  
 “James A. Foster”  
 <jamesafoster@mac.com>

## UMainz BehavioralEvolution 2

Closing date for application approaching\*

Job announcement

University of Mainz

\*Assistant professor / wissenschaftlicher Assistant - Behavioral / Evolutionary Biology \*

\*(non-tenure track, 6 years - extendable up to 10 years)\*

\* \*

Closing date: 30.09.2010

We invite applications for three open \*Assistant professor / wissenschaftlicher Assistent \*positions in the newly established evolutionary biology group at the Institute of Zoology at the Johannes Gutenberg University of Mainz, Germany.

We are seeking highly motivated researchers with a PhD and Postdoctoral Experience and a background in behavioral or evolutionary biology. Three new junior research groups will be established associated to the new evolutionary biology group of Prof. Susanne Foitzik, who recently moved from Munich. Successful candidates should work in related research areas, for example on the behavior or ecology of (social) insects, host-parasite coevolution, population genetics, chemical ecology, genomics, life history or experimental evolution or theoretical evolutionary biology. Information on Prof. Susanne Foitzik's research can be found at [http://ecology.bio.lmu.de/etho\\_e/index.htm](http://ecology.bio.lmu.de/etho_e/index.htm), or by directly contacting her: foitzik@biologie.uni-muenchen.de. Excellent research conditions will be found at the newly renovated and well equipped behavioral, genetic and chemical laboratories in Mainz. Furthermore, new climate chambers are available for animal maintenance.

Successful candidates should have an excellent publication record. Experience with grant acquisition and teaching is advantageous. The candidates should set-up independent research labs and are encouraged to apply for grants in Germany or abroad (e.g., DFG, EU). The positions come with a teaching requirement of 4h per week during the semester. Some basic zoology classes have to be taught in German. Therefore, willingness to learn the German language is required. The candidates have the option to acquire a “Habilitation”. Working

language of the lab is English.

The Johannes Gutenberg-Universität Mainz is interested to increase the number of women in Science. Applications from female scientists are strongly encouraged. Similarly qualified candidates with disabilities will be preferred.

The university of Mainz hosts many excellent scientific institutions <http://www.uni-mainz.de/eng/> and Mainz is a historic city located at the river Rhine with many students and a rich social and cultural life (<http://www.mainz.de/WGAPublisher/online/html/default/hpkr-5nkek8.en.html>).

Interested candidates should send applications as a single e-mail attachment containing a CV, a list of publications (including reprints of the three most important publications), a research and teaching statement and the addresses of two potential referees to:

Prof. Dr. Susanne Foitzik Evolutionary Biology

Institute of Zoology Johannes-v.- Müller-Weg 6 55128 Mainz

Germany foitzik@biologie.uni-muenchen.de

\*Closing date for application is September 30th, 2010\*

Starting date for the positions is Winter – Spring 2011

Prof. Dr. Susanne Foitzik Department Biologie II Behavioral Ecology (Verhaltensökologie) Ludwig-Maximilians-Universität München Großhaderner Str. 2 D - 82152 Planegg / Martinsried Germany

Phone: + 49 89 / 2180 74 209 Fax: + 49 89 / 2180 74 221 e-mail: foitzik@biologie.uni-muenchen.de [http://ecology.bio.lmu.de/etho\\_e/index.htm](http://ecology.bio.lmu.de/etho_e/index.htm) Susanne Foitzik <foitzik@zi.biologie.uni-muenchen.de>

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## UMississippi PopulationGenetics

UMississippi.2.Genetics

The University of Mississippi Two Assistant Professor Positions in Genetics

The Department of Biology at the University of Mississippi invites applications for two Assistant Professor positions (tenure-track) in genetics. The appointments require a Ph.D. in a biological science. The incumbents will be expected to establish extramurally funded research programs involving graduate and undergraduate training. Both will be expected to teach an introduc-

tory genetics course, as well as courses in their area of specialization. The opportunity also exists to be involved with our freshman biology program and with upper division core courses.

Position 1 - Molecular Geneticist. We seek a biologist investigating molecular genetic processes using animal, plant, or microbial model systems. Position 2 - Population Geneticist. We seek a biologist with strong quantitative skills, who uses contemporary techniques in the study of population genetics. This person will also be expected to teach population genetics.

The Department of Biology consists of 16 faculty and educates 800 undergraduate biology majors and 37 graduate students (M.S. and Ph.D.). Current departmental interests span all levels of organization from the cell to the ecosystem. Recent hires include faculty in the areas of cell physiology, conservation biology, evolutionary genetics and phylogeography, microbial ecology, neurobiology, and symbiotic systems. More detailed information concerning the department is available at <http://olemiss.edu/depts/biology>. The University of Mississippi is located in Oxford, Mississippi, one of the top college towns in the U.S., and a community known for outstanding educational and cultural opportunities. Recently, the University was rated a “best college to work for” and \$B!H(Bmost appealing college\$B!I(B by the Chronicle of Higher Education.

To apply, please visit our Online Employment Service at [jobs.olemiss.edu](http://jobs.olemiss.edu). Applications should include: (1) cover letter outlining interest and suitability for the position, (2) curriculum vitae, (3) statement of research interests, (4) one-page statement of teaching experience and interests, including a list of potential graduate and undergraduate courses, (5) reprints of up to 5 recent publications or submitted papers, and (6) three letters of reference. Reference letters should be addressed to either Dr. Brad Jones (position 1) or Dr. Tamar Goulet (position 2). Review of applications will begin November 1 and continue until the position is filled or an adequate applicant pool is established. The University of Mississippi is an EEO/AA/TITLE VI/TITLE IX/SECTION 504/ADA/ADEA EMPLOYER.

Brice Noonan

The University of Mississippi Department of Biology, Box 1848 University, MS 38677 Ph: 662-915-6705 Fax: 662-915-5144

<http://bnoonan.org> bnoonan@olemiss.edu

Brice Noonan <bnoonan@olemiss.edu>

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## UNotreDame 2 SystemsBiology

Faculty Positions, University of Notre Dame. Statisticians in statistical genetics and systems biology

The newly formed Department of Applied and Computational Mathematics and Statistics (ACMS) will initialize a group in statistics with a search for three statistics faculty. The University of Notre Dame has approved positions at both the tenured and tenure-track level. Preference will be given to applicants whose statistical research is complemented with collaborations in genetics, systems biology, ecology or the social sciences. The Department of Applied and Computational Mathematics and Statistics was formed in 2010 within Notre Dame's College of Science. The founding members, who transferred from the Department of Mathematics have research activities in mathematical biology, scientific computing, numerical analysis, and statistical bioinformatics. The successful applicants must have a doctorate in statistics, biostatistics or a closely related field, and a record of success in both research and teaching. The evaluation of associate professor candidates will begin immediately, and the evaluation of assistant professor candidates will begin December 1, 2010. Applications, including a curriculum vitae and research and teaching statements, should be filed through MathJobs ([www.MathJobs.org](http://www.MathJobs.org)). Applicants should also arrange for at least three letters of recommendation to be submitted through the MathJobs systems. For additional information about the position or ACMS, please contact the Department Chair, Steven Buechler, at [buechler.1@nd.edu](mailto:buechler.1@nd.edu). Notre Dame is an equal opportunity employer, and we particularly welcome applications from women and minority candidates.

Faculty position, University of Notre Dame. Biological Networks

The Department of Physics together with the Interdisciplinary Center for Network Science and Applications (ICENSA) at the University of Notre Dame invites applications for a faculty position in Network Science with emphasis on biological-networks. This position is open to all ranks, including endowed chair. The main appointment will be in the Department of Physics, although joint appointments with other departments will be explored, in particular with the Department of Applied and Computational Mathematics and Statistics. Successful candidates are expected to have a strong

record of research accomplishments, to embrace collaborations across disciplines, and an interest in excellence in both undergraduate and graduate education. Senior applicants should have a record of national and international distinction. Information about the Physics department, ICENSA and the College of Science can be found at <http://physics.nd.edu>, <http://icensa.nd.edu>, and <http://science.nd.edu> respectively. Applicants should submit a curriculum vitae, a list of publications, detailed research plans, and a statement of teaching interests. Junior candidates must arrange for at least three letters of recommendation, while senior applicants can apply in confidence. Applications will be reviewed beginning November 1st, and on a continuing basis until the position is filled. All materials should be either uploaded at <https://academicjobsonline.org/ajo/jobs/446> or post-mailed to Network Science Search Committee, Department of Physics, 225 Nieuwland Science Hall, University of Notre Dame, Notre Dame, IN 46556. Notre Dame is an equal opportunity employer, and we particularly welcome applications from women and minority candidates.

Mike Ferdig <[mferdig@nd.edu](mailto:mferdig@nd.edu)>

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## UOklahoma BiologicalDiversity

The University of Oklahoma is seeking a new faculty member who works at the intersection of climate change and biological diversity to fill a 12-month, tenure-track position as an Assistant Professor jointly appointed between the Oklahoma Biological Survey and the Department of Botany and Microbiology, beginning 1 July 2011. We seek researchers who use modern tools to understand how changing climate patterns influence plant biodiversity and ecosystem function. The University of Oklahoma provides an ideal setting for addressing this question because of the sharp, east-west climate gradient across the southern Plains, the diversity of ecoregions and habitats, excellent infrastructure including world-class climate and genomics facilities, and strong faculty expertise in Meteorology, Climate, Molecular and Organismal Biology, and Ecology and Environmental Science. Responsibilities will include developing an externally funded research program and teaching one course per year in the candidate's area of expertise. A Ph.D. is required; postdoctoral experience is preferred. The successful applicant must demonstrate research productivity, the potential to attract external funding, and teaching skills. Screening will begin 15 December

2010 and continue until the position is filled. Please send curriculum vitae, up to five sample reprints, and full contact information for four references to Michael A. Patten, Search Committee Chair, Oklahoma Biological Survey, University of Oklahoma, 111 East Chesapeake Street, Norman, Oklahoma 73019. For additional information on programs at the Oklahoma Biological Survey and Department of Botany and Microbiology, please visit <http://www.biosurvey.ou.edu/> and <http://www.ou.edu/cas/botany-micro/>. For information on the university's climate resources, see <http://www.ocs.ou.edu/>. The University is an equal opportunity and affirmative action employer. Woman and minorities are encouraged to apply.

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

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## UOxford Evolutionary Biol

University Lecturer in Evolutionary Biology

Department of Zoology

University of Oxford

The Department of Zoology proposes to appoint a University Lecturer in the broad area of Evolutionary Biology with effect from 1 January 2011 or as soon as possible thereafter. The post is associated with a Tutorial Fellowship at Magdalen College, under arrangements described in the further particulars. The combined University and College salary will be on a scale up to £57,201 per annum, and an additional College housing allowance of £10,250 per annum is available if the successful candidate chooses not to reside in College. Other allowances are detailed in the further particulars.

Preference will be given to applicants with a strong background in Evolutionary Biology. The successful candidate will be expected to lead a research programme and research group in Evolutionary Biology, to give undergraduate lectures and tutorials, to supervise graduate students and to carry out examining and administrative duties in the Department and the College.//

Further particulars, containing details of the application procedure and of the duties, may be obtained from [paul.harvey@zoo.ox.ac.uk](mailto:paul.harvey@zoo.ox.ac.uk) or by visiting <http://www.zoo.ox.ac.uk/jobs>. The closing date for applications is noon on 25 October 2010.

Applications are particularly welcome from women and black and minority ethnic candidates, who are under-represented in academic posts in Oxford.

The University is committed to equality and valuing diversity. Detailed information about the Department of Zoology may be found at <http://www.zoo.ox.ac.uk/>. The Department of Zoology is the country's foremost Department researching whole organism biology from an evolutionary perspective. Research focuses on aspects of behaviour, development, disease, ecology and evolution, though most members of the Department work at the interface of two or more of those topics. The Department incorporates three research Institutes: The James Martin Biodiversity Institute, The Edward Grey Institute of Field Ornithology and the Wildlife Conservation Research Unit (WildCRU). The main Department is located in the Tinbergen Building in the University's Science Area. The Department also runs the John Krebs Field Station in Wytham Woods and Tubney House, which houses WildCRU. Linked to the Tinbergen Building is the multi-disciplinary Peter Medawar Building for Pathogen Research with high-grade containment facilities.

The Department is unusual in having about the same number of independently funded Research Fellows as Faculty. 58 members of the Department were included in the 2008 Research Assessment Exercise, resulting in a year-on-year increase in funding of 42% from that source.

In 2010 the Department was given an Athena Swan Silver award in recognition of its success at promoting the careers of women.

Evolutionary biology has been an historical strength of the Department (W.D. Hamilton and Richard Dawkins were former members). In addition to the continued presence of Professor Alan Grafen and Professor Paul Harvey CBE FRS, its research presence has been strengthened in recent years by several new faculty appointments (for example Professor Charles Godfray FRS, Professor Peter Holland FRS, Dr Judith Mank, Dr Oliver Pybus, Professor Stuart West and Professor Kathy Willis), the recruitment of many research fellows (for example Drs Tom Bell, Craig MacLean, Andy Gardner, Ashleigh Griffith, and Stuart Wigby), increased grant income (particularly from the ERC), and continued investment in sequencing facilities. Taken together, there are many potential collaborators in the Department who might assist the development of the successful applicant's own research group. Outside the Department, many Departments and research groups in the Medical Sciences Division offer further opportunities for collaboration and access to facilities.

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Judith Mank Department of Zoology University of Oxford  
South Parks Road Oxford OX1 3PS

+44 (1865) 281 312

judith.mank@zoo.ox.ac.uk

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## UParis PierreMarieCurie HumanGenomics

Professorship position in human genomics - University  
Paris 6 Pierre et Marie Curie

A full permanent position of professor of genetics/genomics is opened for 2011-2012 at University Paris 6 “Pierre and Marie Curie”, located in the center of Paris (<http://www.upmc.fr/>). Duties associated with this professorship position include both teaching (in the genetic division of UPMC, <http://genetique.snv.jussieu.fr/>) and research activities in the INSERM (French National Institute for Research in Health and Medicine, <http://www.inserm.fr/>)-UPMC UMRS 937 laboratory.

Teaching activities will cover any aspects of human genomics that could include genetics of complex diseases, transcriptomics, epigenetics and statistical genomics in License and Master but also molecular biology in License. Fluent French language is not totally compulsory at the beginning as it will be possible to teach in English in Master degrees but will become necessary in the following years to teach in License. The post-holder will conduct his/her own research activities in the field of health genomics (cardiovascular diseases, metabolic disorders, immunity-related diseases, oncology, ...) in connection with the groups of Laurence Tiret ([Laurence.tiret@upmc.fr](mailto:Laurence.tiret@upmc.fr)), David Tregouet ([david.tregouet@upmc.fr](mailto:david.tregouet@upmc.fr)) and François Cambien ([francois.cambien@upmc.fr](mailto:francois.cambien@upmc.fr)) within the Unit of Cardiovascular Genomics, INSERM UMRS 937 located at the Pitié-Salpêtrière Hospital near the University Pierre and Marie Curie. A large panel of research facilities will be available including the Pitié-Salpêtrière Illumina post-genomic platform (P3S, <http://www.p3s.chups.jussieu.fr/>), a powerful computer cluster, important bio-resources as well as connections with clinical departments.

To apply to the professorship position the candidate has to be qualified by the French ministry of national education (the qualification campaign will start during

September 2010) and have an HDR (authorization of the French national education ministry to direct PhD students) or any equivalent foreign diploma. Candidates are invited to send their CV and application letter to Francois Cambien ([francois.cambien@upmc.fr](mailto:francois.cambien@upmc.fr)) and Sophie Garnier ([sophie.garnier@upmc.fr](mailto:sophie.garnier@upmc.fr)).

Lluis Quintana-Murci <[lluis.quintana-murci@pasteur.fr](mailto:lluis.quintana-murci@pasteur.fr)>

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## UPittsburgh EvolutionaryBiol

### TWO FACULTY POSITIONS

#### Ecology and Evolution

The Department of Biological Sciences at the University of Pittsburgh invites applications for two full-time tenure-track faculty appointments, one in Ecology and one in Evolution, pending budgetary approval. Appointments are anticipated to begin in September 2011 continuing our goal of establishing a broad-based interactive community of scientific researchers. We encourage all candidates working on cutting edge questions incorporating the topics of ecology, evolution, or behavior and using animal, plant or microbial systems.

We anticipate making both appointments at the ASSISTANT PROFESSOR level. The successful candidates must have a Ph.D. and extensive postdoctoral experience and will be expected to establish extramurally funded research programs, train graduate students, and actively participate in undergraduate education and research. To ensure full consideration, applications should be received by November 1, 2010. Applicants should email a single PDF document identifying the position they would like to be considered for in the subject line and containing a curriculum vitae, a statement of research accomplishments and goals, and a brief description of teaching interests to [biojobs@pitt.edu](mailto:biojobs@pitt.edu). In addition, applicants should arrange to have at least three letters of reference sent to [biojobs@pitt.edu](mailto:biojobs@pitt.edu) as a PDF document with signature.

Further information on the Department of Biological Sciences and the Pymatuning Laboratory of Ecology is available at: <http://www.pitt.edu/~biology>. The University of Pittsburgh is an Affirmative Action, Equal Opportunity Employer. Women and members of minority groups under-represented in academia are especially encouraged to apply.

Tia-Lynn Ashman Professor Department of Biologi-

cal Sciences 4249 Fifth Ave. & Ruskin University of Pittsburgh Pittsburgh, PA 15260-3929 phone: 412-624-0984 fax: 412-624-4759 web: <http://www.pitt.edu/~biohome/Dept/Frame/Faculty/ashman.htm> “Ashman, Tia-Lynn” <tial@pitt.edu>

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## URhodeIsland Evolution GlobalChange

Subject line: Tenure-track position: effect of global change on population-level evolutionary processes

Body of message: We are seeking a tenure-track Assistant Professor in the Department of Biological Sciences, College of Environment and Life Sciences (CELS) with research interests in the effects of global change on population-level evolutionary processes. The anticipated appointment is August 1, 2011. Visit website: <https://jobs.uri.edu> to view complete details for job posting #6000230. Position is open until filled, with review of applications to begin October 1, 2010. Only electronic applications will be accepted. Documents to attach in PDF format to your letter of application: curriculum vitae which, through your record of experience, education, publications, research plan, and statement of teaching philosophy, demonstrates your potential for excellence in teaching and for developing a high quality, nationally recognized and externally-funded research program. Additionally, send copies of up to three published papers and arrange to have three letters of reference sent by October 1, 2010 to: Dr. Brad A. Seibel, Associate Professor, CELS-Bio, Center Biotech Life Science, University of Rhode Island, Kingston, RI 02881. Visit the department website: <http://www.uri.edu/cels/bio/> for additional information. The University of Rhode Island is an Affirmative Action/Equal Employment Opportunity Employer and values diversity. URI is an E-Verify Employer.

Evan Preisser, Assistant Professor

Dept. of Biological Sciences, University of Rhode Island

9 E. Alumni Ave., Kingston RI 02881 USA

401 874-2120; [preisser@uri.edu](mailto:preisser@uri.edu); <http://cels.uri.edu/preisserlab/>

Evan Preisser <[preisser@uri.edu](mailto:preisser@uri.edu)>

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## USalzburg PlantEvolEcol

Full Professor in Plant Ecology: Department of Organismic Biology, Paris Lodron-University, Salzburg, Austria

Closing date: 31 October 2010

Reference No: GZ B 0016/1-2010

Further information: [http://www.uni-salzburg.at/-portal/page?\\_pageid=786,254475&.dad=portal&.schema=PORTAL](http://www.uni-salzburg.at/-portal/page?_pageid=786,254475&.dad=portal&.schema=PORTAL)

Applications are invited for the position of Full Professor of Plant Ecology at the University of Salzburg (Austria) in the Dept. of Organismic Biology/working group “Ecology and Diversity of Plants”. The working group has interdisciplinary teaching and research interests in plant morphology, molecular biology and ecology. The appointee should have broad background in plant ecology, both in teaching and research.

The applicant should be an established scientist, demonstrating outstanding international qualifications in experimental plant ecology, with strengths in one or more of the following categories: population biology, community or ecosystem ecology, evolutionary ecology, ecophysiology and/or conservation ecology. Given the location of Salzburg, interest and experience in alpine ecology would be an advantage, but not a requirement.

It is expected that the appointee would be able and willing to collaborate with the existing working groups in ecology and biodiversity in the Faculty of Natural Sciences.

The professorship is integrated in teaching at the Bachelor’s and Master’s level, as well as in the teacher’s training program in environmental biology. It is expected that the applicant will be able to teach in all areas of ecology in these programs.

Prerequisites for this position are: A relevant university degree, a PhD, teaching skills at university level and a post-doctoral degree (Habilitation) or equivalent qualification, outstanding qualifications in research and teaching in the relevant field, several years of experience in teaching at the university level, social and administrative competence, the ability to take a leading position at a university, experience in international collaborations, experience in modern scientific management and in raising external funding for research projects.

We further expect the successful candidate to be team orientated, to participate in university committees and to have some knowledge of the German language.

The position is tenured, with full time employment according to the specifications of the "UG 2002" and the Austrian "Angestelltengesetz".

The university seeks to increase the number of female faculty members. Therefore, applications from female candidates are explicitly encouraged and women with equal qualifications will be given preference. Disabled candidates or candidates with a chronic illness with essentially equal qualifications are explicitly encouraged to apply and will be given preference.

Unfortunately, travel costs in connection with the application cannot be reimbursed by the University of Salzburg.

Please address your application including a description of your scientific goals concerning research and teaching, and standard documents such as c.v., list of publications, teaching experience, scientific projects etc. to the Head of the University of Salzburg, Univ.-Prof. Dr. Heinrich Schmidinger and send it to the department of Human Resources, Kapitelgasse 4, A - 5020 Salzburg, Austria. Please also enclose a digital version of your application on a CD.

Prof. Dr. Hans Peter Comes Deputy Head of Department of Organismic Biology Chair of Plant Evolution, Systematics, and Diversity University of Salzburg Hellbrunnerstrasse 34 A-5020 Salzburg Austria

Phone: ++43 (0)662 8044 5505 FAX: ++43 (0)662 8044 142 e-mail: peter.comes@sbg.ac.at

"Comes, Hans-Peter" <Hans-Peter.Comes@sbg.ac.at>

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## USouthernCalifornia CompBiolBioinformatics

Assistant Professor

Computational Biology and Bioinformatics

University of Southern California The Molecular & Computational Biology Section of the Department of Biological Sciences in the College of Letters, Arts & Sciences at the University of Southern California invites applications for a tenure-track Assistant Professor in all areas of Computational Biology and Bioinformatics with preference for computational population/

evolutionary genomics, beginning Fall 2011. We seek an innovative, productive scientist who is making significant contributions to the field. The successful candidate will be expected to participate in undergraduate and graduate teaching and to establish a vigorous, externally funded research program. The position will be in the Molecular and Computational Biology (MCB) Program, which is a unique collaborative environment with strong expertise in the generation and quantitative analysis of molecular biology data. The MCB Program includes an NIH Center of Excellence in Genomic Science. For additional information please visit our website <http://www.cmb.usc.edu/> Review of applications will begin immediately. Please apply through <http://www.cmb.usc.edu/> with a curriculum vitae, research plan and three reference letters, or, if necessary, Eleni Yokas, Computational Biology Search Committee, Department of Biological Sciences, RRI201, University of Southern California, Los Angeles, CA 90089-2910 by December 1. For more information, contact Fengzhu Sun (fsun@usc.edu), search committee chair. USC strongly values diversity and is committed to equal opportunity in employment. Women and men, and members of all racial and ethnic groups, are encouraged to apply.

Matt Dean <matthew.dean@usc.edu>

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## UtahStateU DirectorCenter

Interested evolutionary biologists would be welcome to apply.

Thank you, Michelle

Director, Ecology Center, Utah State University Utah State University invites nominations and applications for the Director of the Ecology Center. The Ecology Center (<http://www.usu.edu/ecology>) is a well-funded interdepartmental, cross-college organization with the mission of promoting and supporting research and graduate education in basic and applied ecology. The Director will provide vision and leadership to position the Ecology Center to be a world leader in ecology in a future increasingly emphasizing large-scale interdisciplinary research with educational, outreach, as well as scientific outputs. Duties are 50% administration and 50% research/teaching. This tenured position is open to candidates with (1) a Ph.D. (or equivalent) in ecology or related field, (2) excellent leadership and interpersonal skills, and (3) a distinguished record of

scholarly activity that includes extramurally funded research and successful mentoring of graduate students. Preference will be given to candidates who possess a sincere appreciation for the accomplishment of others, a demonstrated ability to foster interdisciplinary activities, and administrative experience. The successful candidate can choose to be tenured in any of the participating departments within the Ecology Center.

The position is available anytime after January 1, 2011 but should be filled by July 1, 2011. Application review will begin November 1, 2010 and will continue until the position is filled. Applicants should submit a cover letter describing their qualifications for the position, a current curriculum vitae, a statement regarding their vision for graduate education and research in ecological sciences, and the contact information for a minimum of five references. To apply, go to <http://jobs.usu.edu/applicants/Central?quickFind=55396>.

Nominations and inquiries should be sent to:

Michelle A. Baker, Chair Ecology Center Director Search Committee Department of Biology 5305 Old Main Hill Utah State University Logan, Utah 84322-5305 Telephone: 435-797-7131 E-mail: [michelle.baker@usu.edu](mailto:michelle.baker@usu.edu)

Utah State University is located in the city of Logan in northern Utah's beautiful Cache Valley and is within a day's driving distance of six national parks. The surrounding Wasatch Mountains, including ski resorts, trails, lakes and rivers, locates Utah State University in one of the finest recreational environments in the nation. The university is a place of diverse thought, where first-rate cultural offerings by local and visiting artists benefit thousands of students and members of the community. Logan is an attractive, affordable, and safe mountain west community that provides an outstanding living-learning lifestyle.

Utah State University offers competitive salaries and outstanding medical, retirement, and professional benefits that were recently ranked second among land grant universities in the nation. Women, minority, and veteran candidates as well as candidates with disabilities are encouraged to apply. Utah State is sensitive to the needs of dual-career couples, is an affirmative action/equal opportunity employer, and has a National Science Foundation ADVANCE Gender Equity program committed to increasing diversity among students, faculty, and all participants in university life.

Michelle Baker <[michelle.baker@usu.edu](mailto:michelle.baker@usu.edu)>

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## UTexasArlington 2 GeneticsGenomics

Two tenure-track faculty positions: Genetics/Genomics Ecosystem Ecology The University of Texas Arlington

The Department of Biology invites applications for two tenure-track positions at the rank of Assistant Professor. The successful candidates will be expected to establish a vigorous, innovative and extramurally funded research program and to participate in both undergraduate and graduate education. Salary and startup for the positions are highly competitive.

**Ecosystem Ecologist:** We seek applicants working on ecological problems above the level of the population. The individuals specific research emphasis is less important than his/her demonstrated accomplishments and future potential. The successful candidate will occupy recently remodeled laboratory facilities, and join a faculty with strengths in aquatic ecology, community ecology, evolutionary ecology, microbial ecology and herpetology. Interactions are also possible with faculty in genomics, computer science, environmental science, geology and mathematics. Additional details can be found at [http://biology.uta.edu/ecology\\_group/index.htm](http://biology.uta.edu/ecology_group/index.htm).

**Genetics/Genomics:** We seek applicants whose research addresses fundamental biological questions using genetic, genomic, and/or computational approaches. Areas of interests include, but are not limited to, evolutionary genomics, genetic variation, gene regulation, epigenetics, cancer and genome integrity, development, host-microbe interactions, and metagenomics. Research space will be available in a new 234,000 sq. ft. building housing a multi-disciplinary group of researchers in genomics, computer sciences and bioengineering. The successful candidate will also have access to our state-of-the-art Genomics Core Facility [http://gcf.uta.edu/Core\\_Facility/Main.html](http://gcf.uta.edu/Core_Facility/Main.html) including next-generation sequencing technology. Additional details can be obtained from [http://biology.uta.edu/genome\\_group](http://biology.uta.edu/genome_group). The University of Texas Arlington is a comprehensive university offering a wide range of undergraduate and graduate degree programs. Current enrollment at the university exceeds 30,000. UT Arlington is part of the University of Texas System and is located in the heart of the Dallas-Fort Worth metropolitan area.

Applicants must have a Ph.D. and a demonstrated



record of research productivity. Applicants should submit electronically a curriculum vitae; statements of research and teaching interests; names, and e-mail addresses of four persons who can provide letters of reference. Send application to Linda Taylor, lktaylor@uta.edu Department of Biology, University of Texas at Arlington, Box 19498, Arlington, TX 76019-0498. Review of completed applications will begin 1 November 2010 and will continue until the position is filled. Hiring will be contingent on completion of a satisfactory criminal background investigation for security sensitive positions.

Effective August 1, 2011, the use of tobacco products (including cigarettes, cigars, pipes, smokeless tobacco and other tobacco products) by students, faculty, staff, and visitors are prohibited on all UT Arlington properties.

UT Arlington is an Equal Opportunity/Affirmative Action Employer. The University of Texas at Arlington does not discriminate on the basis of race, color, national origin, sex, religion, age, disability, veteran status or sexual orientation in employment or in the provision of services.

Cedric Feschotte, Ph.D Associate Professor Department of Biology UT Arlington Box 19498 - TX 76019 Phone: 817 272-2426 <http://www3.uta.edu/faculty/-cedric> Cedric Feschotte <cedric@uta.edu>

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## UVermont PlantEvoDevo

Assistant Professor in Plant Development and Evolution

The Department of Plant Biology at the University of Vermont is seeking applications for a plant evolutionary developmental biologist to join a diverse group of active scholars in the department. The position is for a tenure-track assistant professor, beginning in the fall of 2011. The successful candidate will show evidence of ability to implement a productive research program, consistently attract extramural funding, and develop a strong teaching record. Teaching will be in introductory biology for majors as well as in an area of the candidate's expertise. A Ph.D. and postdoc in a relevant area are required. Preference will be given to candidates whose research addresses evolutionary explanations of plant form and/or function especially within the context of environmental signals. The University of Vermont recently identified three "Spires of Excel-

lence" in which it will strategically focus institutional investments and growth over the next several years. One of these spires is Complex Systems (original proposal may be viewed at <http://www.uvm.edu/~ovpr/-CSYS.pdf>). Candidates whose research, scholarship, and/or creative work interests align or intersect with Complex Systems are especially encouraged to apply.

Applicants should apply online at [www.uvmjobs.com](http://www.uvmjobs.com) (#033581). A letter of application, curriculum vitae, a research statement, and a statement of interests and vision regarding teaching should all be attached electronically to the online application. In addition, applicants should enter in the application names and email addresses for three individuals who will provide letters of reference. The University is especially interested in candidates who can contribute to the diversity and excellence of the academic community through their research, teaching, and/or service. Applicants are requested to include in their cover letter information about how they will further this goal. Review of applications will begin on October 1, 2010, and will continue until the position is filled. Questions may be directed to Dr. Jeanne Harris, search chair, at [Jeanne.Harris@uvm.edu](mailto:Jeanne.Harris@uvm.edu).

The University of Vermont is an Affirmative Action/Equal Opportunity employer. The Department of Plant Biology is committed to increasing faculty diversity and welcomes applications from women and under-represented ethnic, racial and cultural groups and from people with disabilities.

[Donald.Stratton@uvm.edu](mailto:Donald.Stratton@uvm.edu)

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## WashingtonU Evolutionary Anthropology

We invite applications for a tenure-track appointment in Physical or Biological Anthropology at the level of Assistant Professor to begin in Fall 2011.

We seek an anthropologist with a research specialization in human physiology (energetics, nutrition, endocrinology, development and related areas), who examines human adaptations in a comparative primate and evolutionary context. An active field work program is essential. The candidate is expected to work with graduate students in developing research projects, and have a strong commitment to undergraduate and graduate teaching. Duties include teaching courses, advising students, conducting research and

writing for publication, and university service. Applications should consist of a curriculum vitae and a cover letter describing current research and teaching interests, and names of three referees. Applicants must have a Ph.D. in hand by time of appointment. All materials from candidates and referees should be sent as MSWord files or PDFs via e-mail with "Physical Anthropology Search" in the subject line to: [coguin@artsci.wustl.edu](mailto:coguin@artsci.wustl.edu). Applications are due by December 10th. Washington University is an equal opportunity/affirmative action employer. Applications from women and other members of under-represented groups are especially encouraged. This employer prohibits discrimination on the basis of sexual orientation/preference and gender identity/expression. Employment eligibility verification required upon hire.

Thank you, Erik Trinkaus

Erik Trinkaus Mary Tileston Hemenway Professor of Anthropology Department of Anthropology Washington University Saint Louis MO 63130, USA Email: [trinkaus@artsci.wustl.edu](mailto:trinkaus@artsci.wustl.edu) Tel: 1-314-935-5207 Webpage: <http://artsci.wustl.edu/~trinkaus/trinkaus.html> [trinkaus@artsci.wustl.edu](mailto:trinkaus@artsci.wustl.edu)

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### YorkU AlternateStreamFaculty EvolutionaryBiology

The Department of Biology invites applications for a tenure-track alternate-stream appointment at the Assistant Lecturer level, to commence July 1, 2011. The alternate stream at York is a special category of tenured faculty whose expertise and duties focus on undergraduate teaching and programming. Therefore, applicants should be interested in a career that is teaching-centred, with strong motivation, dedication to and interest in in-

novative, effective evidence-based approaches to teaching science at the university level.

The successful candidate must have a PhD in biology or a related scientific field, and have demonstrated experience in teaching life sciences at the post-secondary level. Experience in developing and directing undergraduate laboratories and training TAs would be an asset. Interest in pedagogical research would also be valuable. The successful candidate will be expected to develop and teach courses and direct/coordinate laboratories at the undergraduate level, including Natural Science courses for non-majors, and may be called upon to assist with student advising and undergraduate program administration.

Further information about the Undergraduate Biology program can be found on our website at:

<http://www.science.yorku.ca/Schools-Departments/-Biology/> Applications must be received by November 30, 2010. Applicants should forward (in hard copy) a curriculum vitae, a teaching dossier (including a statement of teaching philosophy and preference), a summary of publications, a summary of relevant activities and arrange for three references to be sent to:

Chair, Alternate Stream Lecturer Search Committee, Department of Biology, Room 247 Farquharson Building, York University, 4700 Keele Street, Toronto, Ontario, Canada M3J 1P3. Fax: 416-736-5698

All York University appointments are subject to budgetary approval.

York University is an Affirmative Action Employer. The Affirmative Action Program can be found on York's website at [www.yorku.ca/acadjobs](http://www.yorku.ca/acadjobs) or a copy can be obtained by calling the affirmative action office at 416-736-5713. All qualified candidates are encouraged to apply; however, Canadian citizens and Permanent Residents will be given priority.

[lepuszenicus@gmail.com](mailto:lepuszenicus@gmail.com)

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## AFLP multiplexing

Hello,

In an old posting from Evoldir I found someone pointing out that multiplexing dyes for AFLPs was problematic because of interference between dyes. I would like to get some feedback from anyone who might have experienced the same problems or who maybe have found a solution around this.

Thank you,

gruberloo2@yahoo.com

karlgruber@daad-alumni.de

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## AMOVA Bootstrap

Dear community,

does anyone know of a way to get confidence-intervals for the variance explained by an AMOVA ? Arlequin and GenAlEx do both only permutations, i.e. permute geno/haplotypes among groups. I am looking for a way to bootstrap my character matrix and to do many AMOVAS to estimate a CI for the variance a particular grouping explains. Unfortunately my R skills are very very limited.

Any help is highly appreciated,

regards,

Matthias

– Matthias Felix Geiger Bavarian State Collection of Zoology DNA Bank Network Münchhausenstraße 21 81247 Munich Germany Tel. +49 (0)89 - 8107 124 Fax +49 (0)89 - 8107 300 Mob. 0177 / 7989588

geiger@daad-alumni.de

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## Are ML distances Euclidean

Dear Evoldir community,

Could anyone tell me whether Maximum Likelihood distances between taxa exported from PAUP (e.g. based on a GTR+Gamma+I model of sequence evolution) are Euclidean or Euclidean Squared distances?

Thanks for you help. Katja –

Dr. Katja T.C.A. Peijnenburg Institute for Biodiversity and Ecosystem Dynamics University of Amsterdam visiting: Sciencepark 904, Room C3.209 1098 XH Amsterdam mailing: P.O. Box 94240 1090 GE Amsterdam The Netherlands +31 20 5257856 K.T.C.A.Peijnenburg@uva.nl

Katja Peijnenburg <K.T.C.A.Peijnenburg@uva.nl>

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## Biodiversity survey

Dear colleague:

The team listed below is charged by the Global Biodiversity Information Facility (GBIF, <http://gbif.org>) with developing a position paper about its future needs for Knowledge Organization Systems (KOS), a rubric which includes thesauri, controlled vocabularies, ontologies, gazetteers, linked data, and other such resources. The paper will cover tools, impediments to deployment, training requirements, etc. After we draft it, the position paper will be put forth for a period of public comment before final recommendations to GBIF.

In order to put together the position paper, we solicit your opinions, experiences, needs, and information on resources you already in place about Knowledge Organization for biodiversity research. Please go to <http://surveymonkey.com/GBIFKOSurvey> to participate in the survey.

We especially value your input about points you feel the survey doesn't cover.

Please feel free to forward this invitation to mailing lists or colleagues you feel appropriate, hopefully to people who may not have seen it already.

Thanks GBIF KOS position paper team Bob Morris, Convenor. Terry Catapano, Donald Hobern, Hilmar Lapp, Norman Morrison, Natasha Noy, Mark Schildhauer, Dave Thau

hlapp@nescent.org

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## Chakraborty Neutrality Test for Dominant Markers

Hello, I am interested in performing Chakraborty's neutrality test for my dominant data (ISSRs). I would appreciate for any suggestion about the computer program that can perform the test using dominant data. Kind regards,

Madhav

madhav.pandey@ttu.edu

---

## DNA extraction insect cuticles answers

Hi folks,

Many thanks to those of you who responded to my query about extracting DNA from molted insect cuticles. Below is a summary of the answers I received. A colleague also referred me to this publication:

<http://ddr.nal.usda.gov/bitstream/10113/39588/1/-IND43638893.pdf> Thanks again,

Rob

Dr Rob Cruickshank Lecturer in Entomology

Department of Ecology Burns Building, Room B522 PO Box 84 Lincoln University Lincoln 7647 Christchurch, New Zealand

p +64 3 321 8355 | f +64 3 325 3844 e Rob.Cruickshank@lincoln.ac.nz | w [www.lincoln.ac.nz](http://www.lincoln.ac.nz) Lincoln University, Te Whare Wanaka o Aoraki New Zealand's Specialist Land Based University

Original query:

I would be interested to know whether anyone has tried extracting DNA from molted insect cuticles.

Responses:

I have done it a few times, with variable success. The main issue is to keep PCR analyses restricted to short fragments, at least at first until you prove it works! I tend to put the whole cuticle in a suitable volume of the following buffer (enough to cover)

10mM Tris

10mM NaCl

5mM CaCl

2.5mM EDTA

10% final volume Prot K solution (may be overkill to use this much) 40mM DTT 2% final volume SDS

Then incubate for some hours/overnight at 55C. The cuticle won't dissolve, but should yield some DNA.

I then purify the liquid using something like a Qiaquick PCR clean up kit (you just pretend the buffer is a PCR....) and elute into a small amount of EB (say 50ul).

>

Many years ago we did some tests on molted butterfly cuticles (I don't even remember the species) using a Guanidium/silica particles method by Gerloff et. al. (I guess this is the primary reference).

Results were very good, but we tested just a few samples. I would definitely do some more test if I was on such a project.

>

We have had OK DNA from larval butterfly head capsules, and from Onychophoran shed skins.

>

Try searching google scholar for "exuviae DNA". Extraction protocols have been developed for many different arthropods/insects.

>

My lab has tremendous success in getting mitochondrial sequences from empty fly puparia from various families. Getting nuclear genes appears to be more difficult, as you might expect, and we haven't yet done much. We are in the final stages of manuscript preparation on the mitochondrial data.

>

I have successfully extracted DNA from the pupal exuviae of bees. I had hoped to use these for non-destructive genotyping at microsatellite loci. However, I find that the genotyping results are highly inconsistent - I was getting different allele calls on each separate run. I did not invest too much energy in troubleshoot-

ing before giving up. You might be able to get better consistency with more replicates, as is standard for mammalian fecal samples. Best of luck!

>

I was getting good yields from tarantula exuvia. Here is the paper\*. It has been a while but I can try to answer any questions you might have.

\*The paper that was sent can be found at <http://dx.doi.org/10.1007/s10592-006-9173-2> "The contents of this e-mail (including any attachments) may be confidential and/or subject to copyright. Any unauthorised use, distribution, or copying of the contents is expressly prohibited. If you have received this e-mail in error, please advise the sender by return e-mail or telephone and then delete this e-mail together with all attachments from your system."

Robert.Cruickshank@lincoln.ac.nz

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## DNA from FormalinFixedBone answers

Dear list:

My request for protocols for getting DNA out of bone and formalin-fixed generated lots of response. Thanks for your time and information! Below is a collection of all the responses so far. I can't comment on the efficacy of any one of them yet, but I'm working on it.

Thanks, Steve

\*\*

If you are not having success I suspect your problems are one/some of the below

a) There is absolutely no DNA in the samples - in particular if the material was in formalin for more than ca. 12-24 hours it will have been heavily crosslinked, and even fragmented if it was in unbuffered formalin

b) There is DNA but the primers you are using are targeting too big a fragment.

How old are the samples and how long were the fixed ones fixed, and how long ago where they fixed?

In general, a simply and effective bone protocol is that by Rohland et al, attached. If that doesn't work, and you are using really short PCRs (ca 100bp) my guess is it won't work.

For formalin, I once did a lot of work on it. Please see

the extremely tedious paper that I wrote as a result. As you will gather from it, heat + alkali can help matters (the Shi 2004 paper I cite), but in general by increasing yield only. If there is no DNA...it won't do much.

Happy to help with any specific questions.

\*\*

Hi Steve,

Dealing with formalin-fixed material is not an easy task, as you might already know. We recently published a paper using a new method based on Tetramethylsilane (TMS)-Chelex to reduce costs compared with Fang et al. (2002). Most importantly, we observed that neither an indigestible matrix of cross-linked protein nor soluble PCR inhibitors impede PCR success when dealing with formalin-fixed material. Instead, amplification success from formalin-fixed tissue appears to depend on the presence of unmodified DNA in the extracted sample. We were not able to get DNA sequences out of every sample, but we provide a 'test' to check if DNA will be useful for PCR. You can obtain a pdf of our paper at <http://www.icm.csic.es/scimar/index.php/secId/6/-IdArt/3907/> I hope this helps. Cheers,

\*\*

Dear Steve, Take a look on this article ( <http://www.pnas.org/content/105/40/15464.figures-only>).

The authors extracted DNA from museum specimens (mostly bones) of the giant tortoises of Galapagos. Take care

\*\*

Hi Steve,

I think you're wasting your time with formalin-fixed tissues, as this issue has appeared on EvolDir about twice or thrice a year for fifteen years...but you should be able to get DNA from the carapace. For ideas, see

Biotechniques. 1999 Jun;26(6):1086-8. Microsatellite locus amplification using deer antler DNA. O'Connell A, Denome RM. PMID: 10376147 [PubMed - indexed for MEDLINE]

also

[http://oldwww.wii.gov.in/ars/2006/imran\\_khan.htm](http://oldwww.wii.gov.in/ars/2006/imran_khan.htm)

\*\*

< [http://oldwww.wii.gov.in/ars/2006/-imran\\_khan.htm](http://oldwww.wii.gov.in/ars/2006/-imran_khan.htm) >If you are interested in using a kit to do the extraction, there is an excellent protocol on the Qiagen website for extraction of DNA from bone. It is called "Purification of total DNA from compact animal bone using the DNeasy Blood and Tissue Kit". I recently used it to extract over 40

toe bone specimens from a mouse species with a lot of success. If not I also have a standard ethanol precipitation method that I have used with success in bones as well.

Let me know if you would like that.

\*\*

I would suggest you post your message on the ancient DNA forum at: <https://www.jiscmail.ac.uk/cgi-bin/webadmin?A0=ancient-dna> Several people worked on Museum specimen. I work on bones so let me know if you want a few protocols. Usually the one from Hofreiter & Rohland is the one most aDNA people use.

\*\*

Steve,

I saw your message this morning on EvolDir. Coincidentally, I am working on a very similar problem with the goal of extracting DNA from turtle claws. We have had success with fresh tissue and we have been able to amplify a 630 bp fragment from the mtDNA control region of painted turtles. During the past month, we have been conducting experiments where we expose claws to buffered formalin for 48 hours followed by 4-5 days in 70% EtOH (modeling museum protocol), and then attempting extraction using a modified protocol from the Qiagen blood and tissue kit (basically the addition of DTT, additional proteinase K, and longer digestion times). So far the results are not too encouraging but we are actively trying some different things and have some claws from specimens of different collection date from the Field Museum that we will test once we're confident in a protocol.

\*\*

Dear Steve, There are many methods that can be used for extraction and almost all of

— / —

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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## DNA from molted insect cuticles

Hi folks,

I would be interested to know whether anyone has tried extracting DNA from molted insect cuticles.

Many thanks,

Dr Rob Cruickshank Lecturer in Entomology

Department of Ecology Burns Building, Room  
B522 PO Box 84 Lincoln University Lincoln 7647  
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Robert.Cruickshank@lincoln.ac.nz

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### DNA RNA ratio

Dear Evoldir

I am interesting to know about new spectrophotometric method for determining RNA:DNA ratio as a growth indicator in fishes. I would be appreciated if I receiving the protocols. Kind regards Mahtab

mahtab yarmohammadi  
<mahtab\_yarmohammadi@yahoo.com>

---

### Dominant Handedness

Greetings,

I am interested in evolutionary explanations for handedness dominance in humans and other primates. If anyone can suggest references on this subject, it would be much appreciated.

Sam Zeveloff

Dr. Sam Zeveloff Chair, Department of Zoology Presidential Distinguished Professor Weber State University Ogden, UT 84408-2505 U.S.A.

tel.: 801 626-6655 fax: 801 626-7445 email: szeveloff@weber.edu

Sam ZEVELOFF <szeveloff@weber.edu>

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### Drosophila nigrosparsa samples

Dear All, Does anyone of you have an inbred Drosophila

nigrosparsa line and would be willing to share living individuals of that line, or does anyone know someone else who has such a line?

Any help with this would be much appreciated, warmest, Birgit

Birgit Schlick-Steiner

Birgit C. Schlick-Steiner Professor of Molecular Ecology

Institute of Ecology University of Innsbruck Technikerstr. 25 A-6020 Innsbruck, Austria Phone: +43 512 507-6120 Fax: +43 512 507-6190 [http://www.uibk.ac.at/ecology/forschung/molecular\\_ecology.html](http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html)

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### EBI survey

Dear All,

The EBI is a major international supplier of data and data services in molecular biology. We are currently conducting a survey (<http://www.surveymonkey.com/s/EMBL-EBI>) with the aim of learning how to improve the scope and useability of our website. I have been asked to forward this to the list to request your help. There is a prize draw for participants!

Apologies to those who get multiple copies of this from multiple mailing lists.

Nick Goldman

//

Dear Friend,

We are writing to ask you to complete the European Bioinformatics Institute (EBI) Survey at: <http://www.surveymonkey.com/s/EMBL-EBI> - It should take 10-15 minutes. - There are no compulsory questions. - You can be entered into a prize draw where you could win an iPad.

This survey is collecting input from users and potential users of the EBI services. We really value this input for development of our services, and want as many responses as possible. We apologise if, in our enthusiasm, we have included you inappropriately (or even more than once). Please delete the message and forgive us!

Otherwise, please visit <http://www.surveymonkey.com/s/EMBL-EBI> and complete the questions relevant to you. We will be collecting data until the end of September.

Thank you for your help.

Graham Cameron

Associate Director, EMBL-EBI

If you have technical problems with the survey please let us know at <http://www.ebi.ac.uk/support> Nick Goldman <goldman@ebi.ac.uk>

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## EncycloOfLife RubensteinFellowshipDeadline

Dear All,

Encyclopedia of Life has recently announced a deadline extension for the 2011 EOL Rubenstein Fellows competition through September 30, 2010.

Please send all application materials to fellows\_program@eol.org by midnight on September 30, 2010. If you have previously submitted an application and would like to use this time to revise it, please feel free. Simply submit updated materials by September 30. We encourage all applicants to download our revised application form (online since August 22) from <http://www.eol.org/content/page/fellows>. Please direct any additional questions you may have to fellows\_program@eol.org and feel free to pass this update along to any colleagues or contacts who may be interested.

Leo Shapiro EOL Species Pages Group

Leo Shapiro <lshapiro@eol.org>

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## Euglenozoa primers

Dear all,

I am looking for non-18S primers suitable for Bodonidae (Euglenozoa). They need not be very specific, but they should preferably be known to amplify something not too far from Bodonidae. I aim to look upon supposedly closely related species from mostly pure cultures.

I am aware of this paper

<http://mbe.oxfordjournals.org.ep.fjernadgang.kb.dk/-content/23/3/615.full.pdf+html?sidja3816f-d6a8-4f7e-be1d-fc913173354f> which presents some slow-evolving

loci (a-tubulin, b-tubulin, elongation factor 1a (EF-1a), elongation factor 2 (EF-2), cytosolic heat shock protein 70 (HSP70), and cytosolic heat shock protein 90 (HSP90)) for one Bodonidae species (*Rhynchomonas nasuta*) found with degenerate primers.

However, I would like to hear any good suggestions for more rapidly evolving loci and/or useful nondegenerate primers, too. Any suggestions or direction towards useful literature on the subject would be greatly appreciated.

Best regards,

Christoffer Bugge Harder, PhD Student, Dep of biology, Uni Kopenhagen

cbharder@bio.ku.dk

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## EvoDevo funding

Dear Colleague,

This email is to announce a new funding and networking opportunity for researchers in evolutionary and ecological developmental biology: a National Science Foundation Research Coordination Evo-Devo-Eco Network called EDEN (<http://edenrcn.com/>).

The major aims of EDEN are the following: To fund research exchange grants allowing active interchange of tools and techniques among labs working on emerging model systems. To fund undergraduate internships in the field of Evo-Devo-Eco with an emphasis on emerging model systems. To document the tools and techniques being used and developed in these organisms and make them publicly available for future users. To promote interactions across the Evo-Devo-Eco community through conference funding and the sponsorship of workshops. EDEN's first deadline for funding applications is October 31, 2010. You can read about the funding available at <http://edenrcn.com/funding/>. If you are working at the interface of the fields of development, evolution, and ecology, and/or with non-traditional model organisms, you have probably found yourself developing new techniques and tools. Perhaps you have used well-established protocols from traditional model organisms as a starting point, but have had to modify these protocols by painstaking trial and error, without the benefit of a large research community to support work on your organism.

If you are working with well-established model organ-



isms, perhaps you would like to add an evolutionary or comparative dimension to your work, but have not worked with other organisms before.

With the support of the National Science Foundation, we have developed a new research coordination network called EDEN (Evo-Devo-Eco Network) to help address these challenges. You can read about EDEN's activities and opportunities at <http://edenrcn.com/>. Please consider "joining" EDEN by filling out a brief survey about your lab's areas of expertise. You can complete the survey on our website at

<http://edenrcn.com/join/> or by clicking here

<http://www.surveymonkey.com/s/JoinEDEN> This survey will allow your lab to be added to a searchable database of scientists, organisms and techniques that will soon be available on the EDEN website. With this database, other researchers in development, evolution and ecology will be able to learn about your work, hopefully facilitating new and useful networks and collaborations.

We encourage you to go to EDEN's website to read more about it, and to check back frequently for future calls for applications, protocols, and workshop and symposia announcements.

Please feel free to email us at [edenrcn@fas.harvard.edu](mailto:edenrcn@fas.harvard.edu) with questions about the program, and forward this email to colleagues who you think would be interested in EDEN.

Best wishes,

Cassandra Extavour

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

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Cassandra Extavour <[cextavour@oeb.harvard.edu](mailto:cextavour@oeb.harvard.edu)>

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## Evolution Rap Music in London

Something slightly different....

Baba Brinkman will be performing songs from "The Rap Guide to Evolution" and "The Rap Guide to Human Nature" at The Boston Music Room in Tufnell Park, London on Saturday Oct 2nd (doors open 7pm, £5 on the door). Also performing will be Frank-adelic, a weird and wonderful band, which contains a few editors from some of the leading science journals. They play a selection of covers with an interesting scientific theme...could be a good night out...

Adam Eyre-Walker

Adam Eyre-Walker <[a.c.eyre-walker@sussex.ac.uk](mailto:a.c.eyre-walker@sussex.ac.uk)>

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## Evolution textbook Nonmajors

Hello all!

I am teaching a non-majors evolution course (<http://www.christopherxjjensen.com/teaching/courses/-evolution/>) and have been using the McGraw-Hill textbook "An Introduction to Biological Evolution" by Kenneth Kardong. This book is working but I am considering a switch to a different book.

For those of you who teach non-majors evolution, what textbook are you using? Do you like this textbook? What are its strengths and weaknesses?

Also, I am curious if anyone has thought about using the newly-released book by Carl Zimmer "The Tangled Bank". It's not exactly a textbook, but seems fairly accessible to non-majors.

Finally, if anyone knows of an analogous list for evolutionary biology where I might post this, let me know that as well.

Looking forward to and also very grateful for any help you can give.

Thanks, Chris <http://www.christopherxjjensen.com/> [cjensen@pratt.edu](mailto:cjensen@pratt.edu)

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## Fecal DNA degradation

Hello all.

I appreciate all the replies. It seems other have similar issues, and protocols have been adapted to circumvent the problem, but no one has pinpointed why this would happen. Does the DNA actually degrade? Or, does something that co-extracts modify the DNA so it becomes inaccessible to PCR?

I have also contacted QIAGEN technical support on the matter, but they have not given me an answer yet.

I pasted below the responses.

Cheers.

Anders.

–

Hi Anders,

Here in the lab we have had the same problem with primate fecal DNA. We collect fecal samples in RNA later (1:1 ratio) but I suspect that post-extraction degradation will be similar regardless of the conservation method. We also use the QIAamp Stool Kit.

I'm not aware of any reagent you can add to the DNA eluate to delay DNA degradation and not prevent (e.g. EDTA) downstream enzymatic reactions.

Here is what I usually do in order to get the most from my DNA extractions.

I do my final eluate in two elution steps of 75 ul (AE buffer) to collect a final volume of 150 ul of DNA (the two 75 ul aliquots are mixed together in the same tube so as to have a homogeneous eluate). I follow Morin et al. (2001), so I quantify the DNA with a qPCR to determine how many repetitions will be necessary for microsatellite genotyping. I then split the eluate in either one 50 ul + one 100ul aliquots or three 50 ul aliquots. I keep the first 50 ul aliquot in the fridge to run PCRs. The other aliquots (one 100-ul or two of 50-ul) is kept frozen to be used after the first aliquot is gone. I also try to run as many loci as possible (with repetitions) within the first week of extraction. With these precautions I avoid too many freeze and thaw cycles, which seems to increase DNA degradation. At the bench, I also keep the DNA extracts on ice.

Finally, if I have, say 200 poop samples, I usually work on small batches (multiples of 8 - e.g. 16 or 24 - because it fits well the 96-well plates) from DNA extraction to result. Thus my DNA extracts will not be kept frozen for several weeks before PCRs.

I hope this helps, Abraço. Paulo.

PS: We collect fresh scats and keep them at -20 oC.

Morin, P.A., K.E. Chambers, C. Boesch, and L. Vigilant (2001) Quantitative PCR analysis of DNA from

noninvasive samples for accurate microsatellite genotyping of wild chimpanzees (*Pan troglodytes*). *Molecular Ecology* 10: 1835-1844. - Show quoted text -

–

HI, Anders,

I have a student working on Asiatic black bear and encountered similar problem. DNA stopped working after a few months, but not a few days. She is now drying DNA on PCR plate once they passed the DNA quality test, to prevent further degradation.

Thanks!

Shu-Jin Luo

–

Hi Anders, Before extraction, the best is to put the faeces in alcohol for max. 24 h. and then to transfer in silica until extraction. this will enhance the quality of the extract. then it depends what you are doing with the sample: If the goal is to assess the herbivore's diet look at the mat & meth of the valentini (*MolEcol-Res* 2009) and Pegard (*JAFC* 2009) papers for DNA extraction. if your goal is to got the herbivore's genotype look at the Naderi (*PNAS* 2008) and Rezaei (*MPE* 2010) papers

good luck cheers

françois

–

On my forest elephant dung I've used longer ProtK incubation periods -even added a second dose of ProtK- and overnight lysis at 37oC.

-sergios

–

Hi Anders, I have seen degradation, but not over this short a time period. I'd suggest a couple of things:

1) In the field, I'd suggest she use Queen's College Buffer (some call it DETS) to preserve as much as she can of the cellular material she's collecting. The protocol for making 1000 ml is:

Queens College Buffer (20% DMSO, 0.25 M EDTA, 100 mM Tris, pH 7.5, saturated with NaCl):

Per Liter:

200 mL DIMETHYL SULFOXIDE (DMSO) 250 mL 1 M ETHYLENEDIAMINETETRAACETIC ACID (EDTA) 100 mL 1 M TRIS, pH 7.5

Saturate with SODIUM CHLORIDE (Salt, NaCl). Add sterile water to 900 ml and add NaCl until the solution is saturated again, then add sterile water until

you reach 1 L.

I add only enough to each sample to fully cover it. If using the buffer isn't feasible, she could try drying her samples in the field using silica gel. I only use Longmire buffer for blood or good tissue samples.

2) We start our extractions with an overnight incubation with Proteinase K - that might help.

3) How large are the fragments you're amplifying? If they're nuclear fragments over about 250 bp, I'd suggest you break them up into multiple overlapping fragments which might increase your success on new and older extractions.

4) I aliquot about 25µl of extracted DNA for PCR, and keep the rest frozen. If she's not already doing that, it might retard degradation.

5) If she's not already adding BSA to her PCR, she might add that to see if her extracts still contain some kind of inhibitors.

— / —

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

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## Fecal DNA extraction

Hello all.

I have a student working on a tropical herbivore. She collects samples in longmire buffer, and has extracted DNA using the QIAGEN Stool Kit, following the human stool protocol, with only a short 10min proteinase K incubation step. PCRs work in about 60-70% of the samples, but the DNA stops amplifying after only a few days from extraction, even while storing at -20 oC. I was wondering if anyone has had a similar experience, or ideas on how to reduce this rapid degradation.

Thank you.

Sincerely,

Anders.

andersgs@gmail.com

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## FieldMuseum Chicago Temporary Closure

The Field Museum of Natural History's Division of Insects is preparing for extensive research laboratory and collection renovations, which will integrate and compactorize its entire pinned collection in one collection room over the next several months. Starting September 15, 2010, the insect collection rooms will have to be closed to allow installation of compactors and cabinets and renovation of research labs.

>From now until May 1, 2011, please

\* contact us before scheduling any visits to determine whether we can accommodate you and \* postpone all new loan requests and specimen return shipments.

If our reopening date becomes significantly earlier or later than that, we will circulate an update. Our newly renovated collection and research areas will better serve the entomological community and our training efforts by providing additional work space, better access to the collection and research facilities, and enhanced long-term collection expansion space.

Thank you for your cooperation and patience during this construction phase. We apologize for the lack of advance notice, but we got short notice of the final approval of the funding.

Margaret K. Thayer, Ph.D. [mthayer@fieldmuseum.org](mailto:mthayer@fieldmuseum.org)  
Associate Curator, Zoology and Head, Division of Insects Fieldiana Associate Editor (Zoology) <http://www.fieldmuseum.org/fieldiana/> Field Museum of Natural History 1400 South Lake Shore Drive Chicago IL 60605-2496, USA PHONE: +1-312-665-7741 (direct) FAX: +1-312-665-7754 FMNH personal web page: <http://tinyurl.com/4g4zz> Austral Staphylinidae with Staphyliniformia databases: <http://tinyurl.com/3a39n7> Beetle Tree of Life project: <http://tinyurl.com/38yryf> Division of Insects collection database: <http://tinyurl.com/2mnc9j> [mthayer@fieldmuseum.org](mailto:mthayer@fieldmuseum.org)

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## GenomicResources ExchangeGrants

GENOMIC-RESOURCES - Exchange Grants - Call for Applications

“Advances in Farm Animal Genomic Resources” (GENOMIC-RESOURCES) is a project (<http://www.esf.org/genomic-resources>) funded by the European Science Foundation (ESF) to contribute to the education of a new generation of scientists in cutting edge approaches to the characterization, socio-economic evaluation, management, exploitation and conservation of Farm Animal Genetic Resources (FAnGR). Target researchers will learn and work with novel tools and methods made available by recent advances in molecular technologies, statistical and socio-economic approaches, GIScience and integrated data analysis.

GENOMIC-RESOURCES offers funding for a number of Exchange Grants (from 2 weeks up to 3 months) related to the scientific objectives of the programme, to take place between February and July 2011.

Applications from all scientists are welcome, but priority will be given to those early in their career and to applicants who come from and intend to visit countries that financially support the programme (Austria, Belgium, Finland, Germany, Netherlands, Norway, Sweden, Switzerland and United Kingdom).

Exchange Grants are reimbursed on the basis of an allowance of 400 EUR per week. In addition, travel expenses are reimbursed up to a maximum of 500 EUR. The grants DO NOT cover health insurance, taxes, or retirement scheme contributions.

All Exchange Grant applications should be submitted using the online APPLICATION FORM at the bottom of the following web page: <http://www.esf.org/genomic-resources> Detailed conditions of eligibility and application procedure are described on the same page.

The deadline for submission for applications is 18 November 2010, 17:00 CET..

Please spread this msg to all interested persons.

The GENOMIC-RESOURCES Steering Committee

Murelli Elena <[elena.murelli@unicatt.it](mailto:elena.murelli@unicatt.it)>

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## Genotyping DNAsample preparation

Hello all,

I am graduate student preparing DNA samples to be genotyped for about 6 SNPs using TaqMan. I'm

having trouble quantifying the samples using a Nano drop. These samples were extracted from saliva, whole genome amplified, and stored at -80 for about 2 years. I took them out this summer and stored them in a normal freezer. My attempts to determine the concentration of the samples using a Nanodrop have failed as some of the samples have a white residue at the bottom of the tubes and Nanodrop readings indicate a substantial amount of impurities and give really low conc. These samples worked fine two years ago, I'm not sure what the problem is now.

I'm trying to figure out ways to clean the samples. I heard that heating the samples to 95C could dissolve the residue. I am limited by amount for each sample, roughly 25ul. If any of you have any suggestions on how to clean the samples, I would be most grateful.

Thanks,

Tamar

[tecarter2@gmail.com](mailto:tecarter2@gmail.com)

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## George Williams 1926-2010

Hi all. George C. Williams died on Wednesday, September 8th. I and many others would say that at the time of his death, he was the greatest living evolutionary biologist. His 1966 book “Adaptation and natural selection” is a cornerstone of contemporary behavioural ecology, evolutionary psychology, and much else, and is still very much worth reading. Below is a lovely autobiographical piece that George wrote a few years ago (lifted from Edge; I didn't just give the link 'cuz there's a lot of blather to wade through before this gem, but if you want the link it's < [www.edge.org/documents/-williams\\_index.html](http://www.edge.org/documents/-williams_index.html) >. George was extremely self-effacing. Don't be fooled by this! Gather ye rosebuds while ye may. Martin

---

My interest in evolution started in the summer of 1947, when I spent six weeks in the Painted Desert with a paleontologist named Sam Welles, who had a group of students there, officially in a summer course, but we spent most of the time swinging picks and shovels, digging fossils, as part of Welles' research project. He was a specialist in Triassic amphibians. Evenings were spent sitting around the campfire talking about things like evolution. For the first time in my life, people - real biologists, real scholars - were willing to sit and listen

to my opinions. I was twenty one years old. I certainly became interested in many aspects of evolution then, and shortly after that I signed up at the University of California at Berkeley for a course in evolution with Ledyard Stebbins, who at the time, and for quite a while thereafter, was the world's primary expert in evolution with respect to things botanical. Stebbins' course introduced me to Theodosius Dobzhansky's *Genetics and The Origin of Species*. Stebbins was great, but Dobzhansky's book was what got me interested in natural selection as a process.

At the University of Chicago, my job was strictly teaching. I was in their early-entrant undergraduate program - taught freshmen and sophomores biology. They had a great-books approach. We read Darwin, Mendel, and others. Also I attended seminars by people such as Alfred Emerson, the termite specialist and recognized authority on things evolutionary. I found his ideas absolutely unacceptable. That motivated me to do something. If it was biology Emerson was discussing, I would be better off selling insurance.

I remember especially his lecture on the role of death in evolution. He was all in favor of death, and said that the reason we grow old and die is to make room for successors, so that they can have a chance. This seemed so totally impossible, given that evolution proceeds by natural selection. There was absolutely no logical way you could reconcile his ideas with Darwinism, even though he claimed to be a Darwinist.

This initiated my first theoretical obsession: the evolution of senescence - the decline in adaptive performance with age. You can't run as fast at sixty as you could at thirty. On the way home that evening, talking about the problem with my wife, I independently came up with an idea that Peter Medawar is chiefly responsible for and published in 1952, although he may have published something that foreshadowed it in the 1940s - and that is that the effectiveness of selection in maintaining adaptation is essentially the product of reproductive value and survival.

The survival factor is easier to appreciate. If you're more likely to be alive at thirty than at sixty, then selection will be more effective at maintaining adaptation at thirty than at sixty. At an age you'd be extremely unlikely to survive to, such as one hundred years old, adaptation would be a lost cause, and selection wouldn't be concerned with it.

As the effectiveness of selection declines, the effectiveness of its products declines. This explains the rising mortality rate that comes with age. It seemed to me at the time, and still does, that this is an inevitable conclusion, arising from just the simple fact of mortality. If

there's any possibility of dying, at any age, then you're less likely to be alive at a later age than you are at an earlier age.

Another one of Alfred Emerson's ideas was that evolution is much more concerned with cooperation than with competition. It seemed to me to be very much the other way around, and that there was something very special about the social insects which accounted for their extreme cooperativeness. That special thing was their kinship - high levels of kinship within the colony. This was the focus of a theoretical paper I published in 1957. It was a model of natural selection between families; now I think that's a silly way to do it, but at the time I wasn't smart enough to think of the kin-selection idea, which was some years later worked out by William D. Hamilton. In extreme models, this kind of selection can lead to things like forgoing reproduction, if in

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## George Williams death

George C. Williams, 1926-2010

George C. Williams, a renowned evolutionary biologist and Professor Emeritus of Ecology and Evolution at Stony Brook University in Stony Brook, New York, passed away on September 8, 2010.

Professor Williams is widely regarded by peers in his field as one of the most influential and incisive evolutionary theorists of the twentieth century, internationally respected for having shaped conceptual progress and new fields of research in evolutionary biology. He advocated and helped to build a "science of adaptation" that addresses the evolution of animal and human behaviors, organisms' life histories, and other complex features. Together with Randolph Nesse, professor of psychiatry at the University of Michigan, he launched the field of "Darwinian medicine," an evolutionary approach to human health and disease.

The study of evolution in the 1950's was based on advances in the previous two decades that had established a powerful, very general theory of evolution by natural selection, cast in terms of genetic change of species. It applied to organisms' features in the abstract; what was

lacking, for the most part, was analysis of the causes of evolution of various puzzling features that vary among species. Why, for example, do some organisms reproduce sexually and others asexually? Why do some species have a short life span, whereas tortoises and redwoods can live for more than a century? How do we account for cooperation in social animals, when natural selection is based on selfish, individual advantage? To the extent that biologists addressed such questions, they generally supposed that these traits benefit the species as a whole, even if they are harmful to the individual. Senescence and death, for example, were thought to provide space and resources for a vigorous new generation, and so promote the species' welfare.

Although Williams's research area was the ecology and life history of fishes, he started to address such questions in 1957, when he published a theory to account for the evolution of senescence and short life span; this paper is now recognized in all major biological works on gerontology as a foundation for understanding the genetic and evolutionary bases of the age distribution of mortality. In the same year, he and his wife Doris were among the first to advance the modern theory for the evolution of cooperative behavior that is harmful to the cooperating individual but beneficial to the group. Williams, adhering to Darwin's conception of natural selection, sought explanations based on the reproductive success of individual organisms and their genes, and rejected hypotheses based on "group selection" that promotes the "good of the species." He developed these ideas at length in *Adaptation and Natural Selection: A Critique of Some Current Evolutionary Thought* (1966), which had enormous influence and immediately established his reputation as one of the most original, incisive thinkers in evolutionary biology. In this book, in other publications, and in conversation, Williams had a gift for clear thinking about complex problems, and for explaining them in disarmingly simple terms.

Although much of evolutionary theory takes the form of mathematical models, Williams made sparing use of math, and developed almost entirely verbal theory. Nonetheless, he helped to establish the foundations for new subdisciplines within modern evolutionary biology, including behavioral ecology and sociobiology, sexual selection, and the evolution of sexual reproduction and reproductive systems, to which Williams devoted another book (*Sex and Evolution*, 1975). Richard Dawkins and others credit Williams with pioneering a reductionist approach to evolution, by analyzing how mutational changes in a characteristic would affect the reproductive success (fitness) of an individual organism or of the gene itself (i.e., the "selfish gene" paradigm).

Despite some controversy, this approach is widely considered to have enhanced the explanatory power of evolutionary theory. Williams published five other books, including *Why We Get Sick: The New Science of Darwinian Medicine*, with Randolph Nesse (1994), that shows why an understanding of evolution is helpful and even necessary in the health sciences. Since then, Darwinian medicine has been the subject of numerous books and symposia, and is beginning to influence some medical school curricula.

Williams was born on May 12, 1926. After serving in the U.S. Army, he enrolled in the University of California at Berkeley and received a B.A. in zoology in 1949. He received his M. A. (1952) and Ph.D. (1955) at UCLA, held a postdoctoral fellowship at the University of Chicago for one year, and became an Assistant Professor at Michigan State University in 1955. In 1960 he moved to the nascent State University of New York at Stony Brook as

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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>

## Goat Sheep hair DNAExtraction

Dear colleagues,

Does anybody knows a good protocol for DNA extraction from goat and sheep hair? (commercial or preferentially home made). I have some samples collected from different animals and I'd like to use them in genetic diversity studies. The samples have been collected from the animals' tails. In addition, Id like to know if anybody could suggest me the best way of storing these kind of material. I'll appreciate any information on this topic.

Thanks a lot, Fbio B. Britto Universidade Federal do Piau (UFPI) - Federal University of Piau Campus Universitrio Profa. Cinobelina Elvas BR 135, Km 03, Planalto Horizonte Cep 64900-000 Bom Jesus, PI

Brasil (Brazil)

Fabio Britto <fbritto@yahoo.com>

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## Homalopsid snake samples

Hi all,

I am trying to get hold of (sequencable) tissue samples for two homalopsid snake species; *Cerberus australis* (the Australian Bockadam - occurring across the north coast of Australia) and *Fordonia leucobalia* (White Belled or Crab Eating Mangrove Snake occurring in Australia and throughout Asia). If you know of any, or can direct me towards someone who might please let me know.

Many Thanks

Emma Francis PhD Candidate Charles Darwin University +618 8946 6863

Emma.Francis@cdu.edu.au

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## How to break crosslinks

Dear evoldir members,

Last month Steve Kimble posted a message entitled "Other: Extraction of genomic DNA from bone and formalin-fixed". Steve kindly posted all the responses he had received. One of them mentioned ways to break crosslinks. Here is the exact response: "The other form of damage is cross-links which can occur between the DNA and other molecules like metals and proteins (amongst others). There has been some research to develop methods of cleaving these cross-links off to allow the DNA to be analyzed".

I don't know if this referred to using heat or enzymatic treatments but I am curious to know if members here have any idea on how to break cross-links without damaging nucleic acids any further.

Thank you

Odile Loreille

Odile.loreille@us.army.mil

"Loreille, Odile CONTR" <odile.loreille@us.army.mil>

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## Microsatellite size standards

To experienced ABI 3730XL users,

I am requesting some guidance regarding the use of internal size standards for microsatellite genotyping on the ABI 3730XL.

In our lab we have been using two different size standards (McLab500 and Applied biosystem's, GeneScan600). When creating bin sets for markers there seems to be around a 2bp difference between these size standards (has anyone else noticed this?). We can easily get around this problem by setting up two separate, standardised bin sets.

We would prefer however, if we could just stick to using the McLab500 alone (because it is much cheaper), but we are unsure if this size standard is accurate enough. In the 3730xl the 250bp fragment within size standards is inaccurately called and so it is recommended that it be excluded when analyzing samples. This means that there is a 100bp jump from the 200 to the 300bp fragment. Is this an acceptable distance between reference fragments for accurate allele calls? We also have some alleles that occur beyond 500bp (up to 590bp). The results from an in-house test suggest that there is nothing to worry about as alleles are accurately called within established bins for controls, but this has only been assessed for a small number of individuals.

Any input would be greatly appreciated

Sincerely, Kevin Keenan kkeen02@qub.ac.uk QUB

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## Multiplexing fluorophores

Has anyone used IDT's MAX fluorophore in multiplex with AB's LIZ size standard? I can't find data on the abs/emission spectra for LIZ. VIC (538/554) is compatible with LIZ, but IDT doesn't offer VIC, and recommend either HEX (538/555), JOE (529/555), or MAX (524/557), instead. The Yale sequencing center says that while HEX is not compatible with LIZ, JOE is; this is perplexing given that HEX and VIC have nearly identical spectral characteristics. I'd prefer to buy HEX or

MAX because they're considerably cheaper than JOE. Anyone want to weigh in on this? Thanks, Bob Marra

Robert E. Marra, Ph.D. Forest Pathologist Department of Plant Pathology and Ecology Connecticut Agricultural Experiment Station 123 Huntington Street, P.O. Box 1106 New Haven CT 06504-1106

<http://www.ct.gov/caes/cwp/view.asp?a=3D2812&q=3D394858> E-mail: robert.marra@ct.gov  
Phone: (203) 974-8508 Fax: (203) 974-8502

Robert.Marra@ct.gov

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### New *Drosophila* stocks

The *Drosophila*/ Species Stock Center has recently added new wild-type and mutant stocks of *D. pseudoobscura*/ and *D. persimilis*/:

14 wild-type strains of *D. pseudoobscura bogotana*/ (from WW Anderson); stock numbers 14011-0121.174 through 14011-0121.189  
4 mutant strains of *D. pseudoobscura pseudoobscura*/; (from WW Anderson); stock numbers 14011-0121.190 through 14011-0121.193  
6 inbred strains of *D. pseudoobscura pseudoobscura*/ (from M. Noor); stock numbers 14011-0121.194 through 14011-0121.199

AND

4 mutant strains of *D. persimilis*/ (from WW Anderson); stock numbers 14011-0111.57 through 14011.0111.60

Details are available on the *Drosophila*/ Species Stock Center Website at <https://stockcenter.ucsd.edu/info/welcome.php> – Maxi Polihronakis, PhD *Drosophila* Species Stock Center University of California, San Diego 9500 Gilman Drive # 0116 La Jolla, California 92093-0116

Section of Cell and Developmental Biology Division of Biological Sciences Muir Biology, Rm. 2125 or 2208  
Phone: 858-246-0350

Maxi Polihronakis <mpolihronakis@ucsd.edu>

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### Old book

Hello to everyone,

I am trying to locate a copy of the book "Cytochromes C: Evolutionary, Structural and Physicochemical Aspects, by Geoffrey R. Moore and Graham W. Pettigrew (ed 1990 o 1991)" but so far no luck. Amazon seems to have run out of copies and the used ones are not shipping to Greece. Does anyone out there have an old copy that is not usefull anymore and would like to sell it? Thank you in advance.

Aris

—

ARIS PARMAKELIS, MSc., PhD. DEPARTMENT OF ECOLOGY AND TAXONOMY FACULTY OF BIOLOGY NATIONAL & KAPODISTRIAN UNIVERSITY OF ATHENS PANEPISTHMIOUPOLI ZOGRAFOU, GR-15784, ATHENS, GREECE Tel.: ++302107274736  
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aparmakel@biol.uoa.gr

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### Partial 454 plate

I'm new to next generation sequencing, and would like to pay for 1/8th of a 454 run. If you will soon send off a plate with left over wells, I will pay to fill it in with my samples. I've heard that 1/8th of a plate can run 1,200-1,700 \$US. I can afford that, but not much more. This is for an unfunded conservation project, so the budget is slim. Thanks for any help.

Michael Sandel University of Alabama

kwksand@yahoo.com

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### Regional Conference information

The American Naturalists Society is exploring the possibility of offering financial support to regional meetings, such as those of the Southeast Ecological Geneticists (SEEG), the Guild of Rocky Mountain Ecologists and Evolutionary Biologists (GRUMPS) or the now defunct California Population and Evolutionary Genetics



group (CalPEG). Possible venues of support might be to fund a keynote speaker, a small symposium or mixers. The challenge we face is that these societies exist as loose consortia with no fixed address or people in charge. As a first step in developing a plan, we would like to compile a list of such societies and some basic information about each of them. Who are they? When do they meet? How many undergraduates, graduate students, post-docs and faculty usually attend? We would also like to compile a short contact list for people affiliated with each society so that we can communicate with them to develop ideas for how we can enrich their conferences. If any of you can help, then please answer these questions and give us the names and e-mail addresses of possible contacts. Send this information to: David.Reznick@UCR.EDU. Please put "regional conference information" in the subject line so that I do not confuse you with spam.

Andres Lopez-Sepulcre <lopezsepulcre@gmail.com>

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## SGS analysis inbreeding plant

Hello,

I am a PhD student working on an annual plant which is highly inbreeding and seeds are dispersed either passively or by ants. I would like to perform some fine-scale spatial genetic structure (SGS) analyses on mapped samples collected at very close distances to each other, using microsatellites, to infer 'neighbourhood size', the scale of gene flow by rare pollination events and seed dispersal, and to see if habitat changes correlate with genetic differentiation.

Could anyone recommend any software programs for such SGS analyses that do not require the species/populations to be in Hardy-Weinberg equilibrium?

Many thanks,

Rhiannon Crichton rcrichton@rbge.ac.uk

– The Royal Botanic Garden Edinburgh is a Charity registered in Scotland (No SC007983)

R.Crichton@rbge.ac.uk

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## SGS analysis inbreeding plant answers

Thank you to all who responded to my question posted last week, original question and responses below. Cheers, Rhiannon

I am a PhD student working on an annual plant which is highly inbreeding and seeds are dispersed either passively or by ants. I would like to perform some fine-scale spatial genetic structure (SGS) analyses on mapped samples collected at very close distances to each other, using microsatellites, to infer 'neighbourhood size', the scale of gene flow by rare pollination events and seed dispersal, and to see if habitat changes correlate with genetic differentiation.

Could anyone recommend any software programs for such SGS analyses that do not require the species/populations to be in Hardy-Weinberg equilibrium?

\*\*\*

Dear Crichton, I suggest to use Spagedi 1.3. (<http://ebe.ulb.ac.be/ebe/Software.html>). This is very good program and, actually all using this program. Regarding the Hardy-Weinberg equilibrium, I suggest to use the Loiselle et al. (1995) method. This method not assume HW equilibrium.

Best regards, Alexandre

\*\*\*

Dear Rhiannon,

software for analysis of spatial genetic structure by essence do not assume that the genotype frequencies correspond to Hardy-Weinberg expectations, as spatial genetic structure is a deviation from random mating, a major hypothesis of H-W model. If your markers are co-dominant, then you can use any software for SGS analysis, including Spagedi by my colleague Olivier Hardy and myself (see Vekemans & Hardy 2004 *Molecular Ecology* 13:921- for practical considerations on SGS analyses and a review of the empirical literature considering among others the effect of mating system on patterns of SGS; and Hardy & Vekemans 2002 *Mol. Ecol. Notes* 2:618- for a description of the software, available at <http://ebe.ulb.ac.be/ebe/Software.html>), but there are many others.

best regards,

Xavier Vekemans

\*\*\*

Hi,

Depending on how many plants & markers, and particularly what proportion of the (local) population you are surveying in each generation, you could presumably take a pedigree-based approach (and infer the relationships between all the sampled plants)?

For example, Masterbays:

<http://wildevolution.biology.ed.ac.uk/jhadfield/-software.html> <http://onlinelibrary.wiley.com/doi/10.1111/j.1365-294X.2006.03050.x/abstract>  
<http://onlinelibrary.wiley.com/doi/10.1111/j.1469-8137.2010.03438.x/pdf> <http://cran.r-project.org/web/packages/MasterBayes/vignettes/Tutorial.pdf> I imagine this might work if you are looking at (e.g.) all candidate parents in an area plus several seeds from each mother in that area.

Regards!

Darren

\*\*\*

I'd suggest spatial autocorrelation. It can be done on the Genalax package and has been used on lots of botanical species. It's particularly appropriate where you have individuals (rather than populations) spread across an area and want to make inferences about connectivity.

I've attached a paper I've used it on (although it's not a perfect example of it's use by any means. However, it should give you the references you need to investigate further!

Cheers,

Andrew

(Paper: Griffiths et al, Evolutionary Applications, 2009)

\*\*\*

Hi,

my software SPAGeDi should be fine for this (<http://ebe.ulb.ac.be/ebe/Software.html>).

Best,

Olivier

–

Rhiannon Crichton <R.Crichton@rbge.ac.uk>

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## Software LOSITAN version 2

Dear colleagues,

I would like to announce version 2 of LOSITAN, a free easy to use application based on the fdist (Beaumont and Nichols, 1996) Fst-outlier method to detect markers under selection.

Version 2 features are: 1. Support for large datasets 2. Support for Windows 7 3. False Discovery Rates

We are currently developing a similar free application for DOMINANT markers (AFLPs), if you are interested in using it during our beta test period, please contact us.

Lositan can be found here: <http://popgen.eu/soft/-lositan/> LOSITAN tries to make selection detection feasible to a much wider range of users, even for large population genomic datasets, by both providing an easy to use interface and essential functionality to complete the whole selection detection process. The application runs directly from the web on Windows, Mac and Linux (only a recent Java installation is required).

Best Regards, Tiago Antao

tiagoantao@gmail.com

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## Software MetaPIGA2

Dear all,

We are glad to announce the release of \*MetaPIGA2\* (BMC Bioinformatics 2010, 11: 379), a robust implementation of the Metapopulation Genetic Algorithm (metaGA) for large phylogeny inference under Maximum Likelihood (PNAS, 99: 10516-10521 (2002))

In MetaPIGA2, the metaGA is implemented together with: -Complex substitution models (including GTR), -Discrete Gamma rate heterogeneity, -The possibility to partition data.

Importantly, MetaPIGA2 will make you happy if you like using a graphical user interface (GUI) BUT it should also make you happy if you hate using a GUI. Indeed, MetaPIGA provides BOTH: - An extensive

GUI for parameters setting, following run progress, and manipulating result trees, and - High customization through manual batch files and command line processing.

Furthermore, if you need to use batch files (for example, to run them on a distant server) but hate to type the commands yourself, MetaPIGA2 allows you to generate batch files through the GUI.

MetaPIGA2 also implements the Likelihood Ratio Test (LRT), the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC) for automated selection of substitution models that best fit the data ... such that you don't need using 3 softwares before starting analyze your data.

MetaPIGA2 uses standard formats for data sets and trees, is platform independent, runs in 32 and 64-bits systems, and TAKES ADVANTAGE OF MULTIPROCESSOR & MULTICORE COMPUTERS.

MetaPIGA2 is described in: Helaers & Milinkovitch; BMC Bioinformatics 2010, 11: 379 <http://www.biomedcentral.com/content/pdf/1471-2105-11-379.pdf>

The metaGA algorithm is described in: Lemmon & Milinkovitch; PNAS, 99: 10516-10521 (2002): <http://www.pnas.org/content/99/16/10516.full.pdf> The software and its extensive manual are freely available to academics at <http://www.metapiga.org>. Best, Michel.

PS: Note that we also implemented a Simulated Annealing algorithm and a classical Genetic Algorithm for those who want to play with other stochastic heuristics.

Prof. Michel C. Milinkovitch Laboratory of Artificial & Natural Evolution Dept of Genetics & Evolution University of Geneva Sciences III, 30, Quai Ernest-Ansermet 1211 Genève 4, Switzerland

Tel +41(0)22 379 67 85 Fax +41(0)22 379 67 95

[www.lanevol.org](http://www.lanevol.org) Michel.Milinkovitch@unige.ch

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## Software SGoF MultipleTestCorrection

Dear evoldir members,

I am please to announce the free software SGoF+ that performs different multiple testing correction methods as the Sequential Bonferroni, Benjamini-Hochberg FDR, SGoF and SGoF+. The software also provides

the associated q-values allowing up to 5 different q-value estimation methods. SGoF+ is very eassy to use and can be obtained from the web page:

<http://webs.uvigo.es/acraaj/SGoF.htm> The SGoF correction method is described in the following paper: BMC Bioinformatics 10: 209 (2009). Details about the SGoF+ improvement onto SGoF and about q-value estimation can be obtained in the web page.

Sincerely,

Antonio

- Antonio Carvajal-Rodríguez Área de genética (grupo XB2) Facultad de Biología Universidad de Vigo 36310 Vigo Phone/Fax: (34) 986813828 email: [acraaj@uvigo.es](mailto:acraaj@uvigo.es) <http://webs.uvigo.es/acraaj/acraaj@uvigo.es>

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## Software TREEFINDER Update

Dear Colleagues,

It might be necessary to update my Treefinder software, to recompile it for newer computers and to develop newer installation procedures. I could also implement deeper search levels and some other extensions. But so far the academic system has been unable to offer me some adequate compensation for my work. My questions are:

1. Is there anybody interested in having updated Treefinder software?
2. If so, is there anybody willing and able to motivate me to do such updates?

According to my cultural background, an "adequate" compensation for good work would be something that enabled me to buy a nice house with a garden and raise a big family HERE AT MY HOME PLACE. A traditional permanent income. And I am not interested in working on somebody else's projects as long as I have more useful ideas of my own.

But the acedemic system selects people who are good at doing what they are told and good at migrating from place to place all the time. It selects people who accept miserable salaries that neither allow raising a big family nor buying a nice house with a garden. The academic system produces too many professors and hardly any inventors, thinkers. In the academic system one hardly has any time to THINK. The academic system

discriminates against people like me. This raises further questions:

3. Is there any advantage in selecting cheap and flexible but possibly incompetent scientists?
4. Is such an academic system useful?
5. If so, for whom?
6. If not, what are good strategies to get rid of such a system?
7. Do we need an alternative academic system that supports free scientists with own ideas?

I know that most of you are what the system has selected so far and will therefore agree with the established system in many aspects. Whereas those who would not agree have already been excluded. But I nevertheless ask.

The other point is that updating Treefinder requires several new computers, compiler software, internet services etc. that I cannot afford because somebody else gets my income.

Gangolf Jobb

Gangolf Jobb <gangolf.jobb@treefinder.de>

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## Solanaceae phylogeny

Dear Evoldirians,

I would like to find the phylogenetic relationships among some Solanaceae, which are hostplants for neotropical butterflies. I see from recent publications that there is a myriad of available markers (eg COSII gene set, various ITS, ndhF, trnLF, matK...). I need to select a combination of loci that would enable to recover both shallow and deep relationships. Most of my plants belong to the Solanum and Cestrum genera, but I also have Lycianthes, Markea, Juanulloa, Physalis, Larnax. In addition these loci should be easily amplified, because my material is old, stored in silica at room temperature and possibly degraded.

Could someone advise me on the best combination of markers?

Many thanks,

Marianne

– Marianne Elias CNRS researcher, UMR CNRS 7205 Muséum National d'Histoire Naturelle Département

Systématique et Evolution 45 Rue Buffon, CP50, 75005, Paris, France tel: +33 1 40 79 37 90 fax: +33 1 40 79 56 79 <http://heliconius.zoo.cam.ac.uk/2009/marianne-elias/> melias2008@googlemail.com

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## SouthAfrica Volunteers EvolutionSmallMammals

Volunteers needed as field assistants for the project:

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

2 open positions from January 2011 onwards

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

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

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

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

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

Costs: Students have to arrange their transport to the

field site themselves. Per month, an amount of Rand 1000 (around 110 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 135 Euro) per month applies. Students must buy their own food etc in Springbok (costs of about R 2250 or 250 Euro/month). Including extras, you should expect costs of about 400 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

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

When and how long: At the moment we are looking for two volunteers starting January 2011. The volunteer project is ongoing, i.e. positions will also be available later in 2011. Volunteers are expected to stay at least 2 months, but longer periods of up to 6 months are preferred.

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

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

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

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

Working as a field assistant in Goegap Nature Reserve  
A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

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

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

and joke about!

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

— / —

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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## Spatial autocorrelation analysis

Dear evoldir members,

We have carried out a spatial autocorrelation analysis using GenAlEx software. We have analyzed a “putative plant population” that include two clusters of separated individuals by 50 meters. When we considered all the individuals of the population the genetic structure detected was 50 meters. But, when we analyzed each group of individuals separately, the genetic structure were 5 and 7 meters, respectively. So, should we consider the whole “population” or each group separately in order to determinate the genetic structure of the species?

Thank in advance,

Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología Facultad de Ciencias del Mar Campus Universitario de Tafira Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain

Phone: (+34) 928.454.543 Fax: (+34) 928.452.922

[canariensis750@hotmail.com](mailto:canariensis750@hotmail.com)

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## Speciation Research Travel Grant Applications

Dear colleagues,

The European Research Networking Programme “Frontiers of Speciation Research”, supported by 18 National Funding Organizations in member countries of the European Science Foundation, is inviting applications for travel grants intended to foster collaborations between European researchers working on topics related to the Programme.

Support is available for short visits (up to 2 weeks) and exchange grants (up to 3 months), with preference given to junior researchers at a graduate or postdoctoral level. Applicants will want to keep in mind that, owing to the difference in costs, applications for short visits are more likely to be successful than applications for exchange grants.

Applications are reviewed quarterly after a submission deadline of 24:00 CET on 15 March, 15 June, 15 September, and 15 December. About 4-6 weeks after each deadline, the ESF will inform applicants about the outcome of evaluations.

Further information and instructions on how to apply are available at [www.iiasa.ac.at/Research/EEP/FroSpects/Travel.Grants.html](http://www.iiasa.ac.at/Research/EEP/FroSpects/Travel.Grants.html).

For general information about the FroSpects Research Networking Programme, please see [www.iiasa.ac.at/Research/EEP/FroSpects](http://www.iiasa.ac.at/Research/EEP/FroSpects).

With best wishes,

Åke Brännström & Ulf Dieckmann, on behalf of the FroSpects Steering Committee

dieckmann@iiasa.ac.at

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## SYNTHESYS Grants Madrid

Dear all,

At the Department of Biodiversity and Evolutionary Biology of the National Museum of Natural Sciences (Spanish Research Council), we encourage applica-

tions for the SYNTHESYS programme. SYNTHESYS Project funding is available to provide scientists based in European Member and Associated States (see below for eligible countries) to undertake short visits to utilize our infrastructure (namely the collections, staff expertise and analytical facilities including molecular biology facilities).

CALL 2 IS NOW OPEN. Deadline: Friday 15th October 2010 (5pm UKtime)

Award Proposals are welcomed from high calibre researchers seeking access for short-term visits. SYNTHESYS is able to meet the Users' costs for:

- Research costs\*
- International travel
- Local accommodation while based at the TAF
- A per diem to contribute towards living costs

\* Research related costs including bench fees and consumables (including molecular biology).

Eligible Countries

Austria, Belgium, Bulgaria, Cyprus, Czech Republic, Denmark (including Greenland), Estonia, Finland, France (including Guadeloupe, Martinique, Guyane, La Réunion), Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, United Kingdom. Plus the Associated Countries of the EU: Albania, Bosnia and Herzegovina, Croatia, Faroe Islands, FYR Macedonia, Iceland, Israel, Liechtenstein, Montenegro, Norway, Republic of Serbia, Switzerland and Turkey.

You can contact me for phylogenetic or phylogeographic projects ([www.vieiteslab.com](http://www.vieiteslab.com) < <http://www.vieiteslab.com/> >) or other faculty at the Department ([www.beb-mncn.es](http://www.beb-mncn.es) < <http://www.beb-mncn.es/> >).

Sincerely,

David R. Vieites

- - David R. Vieites Museo Nacional de Ciencias Naturales (MNCN) Consejo Superior de Investigaciones Científicas (CSIC). C./ José Gutiérrez Abascal no2 Madrid 28006. SPAIN Phone: +34 91 411 1328 ext 1219 e-mail: [vieites@gmail.com](mailto:vieites@gmail.com) < <http://gmail.com> > e-mail: [vieites@mncn.csic.es](mailto:vieites@mncn.csic.es) < <http://mncn.csic.es> > <http://www.vieiteslab.com> David Vieites <[vieites@mncn.csic.es](mailto:vieites@mncn.csic.es)>

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## TreeAnnotator branch problem

Dear all,

I run BEAST to construct the phylogenetic tree of 138 orthologs, with the chain length of 6E7. However, there existed some branches with 0-posterior probability in the tree generated by treeannotator, and if I run the GMYC on it, a problem will be showed as following:

```
> tree <- read.nexus("C:\\Documents and Settings\\sli\\My Documents\\phoB\\gamma_138\\138_original_freannotator.out.tree")
> test1 <- gmyc(tree,method = "single",interval=c(0,138)) node T loglik 2 -0.2634113 778.7273
```

Error in optim(c(1, 1), l.min2, method = "Nelder-Mead", control list(fnscale = -1)) : function cannot be evaluated at initial parameters

In addition: Warning messages:

- 1: In optimise(l.null, interval = interval, maximum = 1) : NA/Inf replaced by maximum positive value
- 2: In log(lik) : NaNs produced

No idea which step I did wrong.

The tree file and and the screenshot of part of the tree (demonstrated with FigureTree) are attached here.

Another question:

If I don't want such a long chain length and such a huge trees file in the end, can I just simply combine the trees file from multiple runs using Logcombiner with a shorter chain length? For example, Now I'm running BEAST on 3 computers each with the chain length 2E7. But will the ESS vaules decrease a lot after the combination of the 3 results? Is it necessary for me to choose one analysis step, e.g. "Bayesian skyline reconstruction" to combine the results?

Thanks a lot!

Shan

– Shan Li Bioinformatics UNC Charlotte

lishan989@gmail.com

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## Year EvolutionaryBiology

Announcing The Year in Evolutionary Biology 2010 (aka Annals of the New York Academy of Sciences 1206)

<http://onlinelibrary.wiley.com/doi/10.1111/nyas.2010.1206.issue-1/issuetoc>

Craig W. Benkman, Thomas L. Parchman and Eduardo T. Mezquida. 2010. Patterns of coevolution in the adaptive radiation of crossbills. *Annals of the New York Academy of Sciences* 1206: 1-16. DOI: 10.1111/j.1749-6632.2010.05702.x

Ronald D. Bassar, Andrés Lpez-Sepulcre, Matthew R. Walsh, Martin M. Turcotte, Mauricio Torres-Mejia and David N. Reznick. 2010. Bridging the gap between ecology and evolution: integrating density regulation and life-history evolution. *Annals of the New York Academy of Sciences* 1206: 17-34. DOI: 10.1111/j.1749-6632.2010.05706.x

Silvia Matesanz, Ernesto Gianoli and Fernando Valladares. 2010. Global change and the evolution of phenotypic plasticity in plants. *Annals of the New York Academy of Sciences* 1206: 35-55. DOI: 10.1111/j.1749-6632.2010.05704.x

David L. Des Marais and Thomas E. Juenger. 2010. Pleiotropy, plasticity, and the evolution of plant abiotic stress tolerance. *Annals of the New York Academy of Sciences* 1206: 56-79. DOI: 10.1111/j.1749-6632.2010.05703.x

Bernard J. Crespi. The origins and evolution of genetic disease risk in modern humans. *Annals of the New York Academy of Sciences* 1206: 80-109. DOI: 10.1111/j.1749-6632.2010.05707.x

Scott A. Pavey, Hne Collin, Patrik Nosil and Sean M. Rogers. 2 The role of gene expression in ecological speciation. *Annals of the New York Academy of Sciences* 1206: 110-129. DOI: 10.1111/j.1749-6632.2010.05765.x

Pat Monaghan. 2010. Telomeres and life histories: the long and the short of it. *Annals of the New York Academy of Sciences* 1206: 130-142. DOI: 10.1111/j.1749-6632.2010.05705.x

Kerstin Johannesson. 2010. Are we analyzing speciation without prejudice? *Annals of the New York Academy of Sciences* 1206: 143-149. DOI: 10.1111/j.1749-6632.2010.05701.x

see also the previous issues:

The Year in Evolutionary Biology 2009: <http://onlinelibrary.wiley.com/doi/10.1111/-nyas.2009.1168.issue-1/issuetoc> The Year in Evolutionary Biology 2008: <http://onlinelibrary.wiley.com/doi/10.1196/nyas.2008.1133.issue-1/issuetoc> “Schlichting, Carl” <schlicht@uconn.edu> “Schlichting, Carl” <schlicht@uconn.edu>

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## PostDocs

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PennState ComparativeEvolutionaryGenomics ...	100		
SantaFeInst EvolutionaryBiol .....	100		

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### Boston EvolutionaryGenomics

Postdoctoral position(s) are available at Harvard Medical School and Brigham and Women’s Hospital, Boston for Evolutionary Genomic studies. Our lab focuses on understanding genomic structural variation with respect to evolution, population genetics and disease as-

sociations (<http://www.chromosome.bwh.harvard.edu>) (e.g., Nat Genet. 42:400,2010; Nature 464:704, 2010).

We are looking for both computational and experimental biologists to complement ongoing projects in the laboratory. Interested individuals must have or be close to obtaining a Ph.D. degree. In addition, applicants must demonstrate a high level of research productivity demonstrated by publication in top peer-reviewed journals. Candidates should have a strong background in evolutionary/population genetics, bioinformatics, computational biology and/or biostatistics.



Experience with analyzing next generation sequencing or array-CGH data and knowledge of statistical and/or programming languages (PERL, Python) would be desirable, but not prohibitive.

Interested applicants should submit current curriculum vitae, statement of research experience and names of three individuals who can provide letters of reference electronically to: Dr. Omer Gokcumen (ogokcumen@partners.org)

gokcumen@gmail.com

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### BrownU AllelicDifferences

We have developed a novel high throughput binding assay that can detect allelic differences in protein/nucleic interactions. It is likely that about 1/3 - 1/2 of all hereditary disease are associated with missprocessing of pre-mRNA. More subtle genetic risk factors are also likely to involve missprocessing of pre-mRNA. We have been funded to identify causal variants within haplotype blocks that associate with genetic diseases. I am looking for a postdoc with basic molecular biology /biochemistry skills who wants to work this screen and learn genomics/computational biology and perhaps transition into human genetics/medical genomics. click here < <http://fairbrother.biomed.brown.edu/research.php> >to learn about my lab's research projects.

Will Fairbrother

william\_fairbrother@brown.edu

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### Buffalo CoralEvolution

Post-Doc position available in the study of the ontogeny of coral-algal symbioses

The post-doc will participate in all aspects of an NSF funded study to identify the mechanisms and selective processes that lead to the final assemblage of symbionts harbored by adult coral hosts. The work requires familiarity with techniques as DNA extraction, DNA sequencing, microarray expression analysis, next-generation sequencing, and DNA bioinformatic analysis as well as conducting physiological measurements

of coral recruits. The successful applicant will participate in field work in the Florida Keys. The postdoc will also mentor graduate and undergraduate students, write manuscripts, and oversee day-to-day management of the project.

**\*Minimum Qualifications:\*** Ph.D. with a strong background in 2 or more of the following: photobiology, population genetics, larval biology, phylogenetic, and/or genomic analyses. Knowledge in molecular DNA techniques; Excellent writing skills; Strong quantitative and statistical skills; self-starter and creative problem solver; strong communication and interpersonal skills.

**\*Preferred qualifications:\*** Extensive experience in microarray expression experimental design, genomic analyses and photobiology with skill in measuring photosynthesis. Field experience with coral spawning and rearing coral larvae. Experienced SCUBA diver.

**\*Preferred start date:\*** January 1, 2011

**\*Salary range\*** \$32-35K, depending upon experience and qualifications

All applicants must **\*apply through UBJobs\*** ([www.ubjobs.buffalo.edu](http://www.ubjobs.buffalo.edu)) and include a cover letter, contact information for three references, a research statement and a copy of your CV.

“The University at Buffalo is an Equal Opportunity/Affirmative Action Employer/Recruiter.”

Please contact me directly with any questions

Cheers, Mary Alice Coffroth

– PLEASE NOTE NEW PHONE NUMBERS Mary Alice Coffroth, PhD Professor 447 Hochstetter Hall Department of Geology Graduate Program in Evolution, Ecology and Behavior State University of New York at Buffalo Buffalo NY 14260

Phone: 716-645-4871 716-645- 4874 Fax: 716-645-3999 Email: [Coffroth@buffalo.edu](mailto:Coffroth@buffalo.edu) Web page: <http://www.nsm.buffalo.edu/Bio/burr/>

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### CedarCrestCollege Teaching EvolBiol

Postdoctoral research/teaching position Department of Biological Sciences Cedar Crest College

Cedar Crest College anticipates hiring a full-time postdoc (2/3 research, 1/3 teaching) for the 2011 calendar year. Research will be carried out in the evolutionary

genetics lab of Dr. Richard Kliman; duties will include supervision of undergraduate research students. Current projects relate to molecular evolution and population genetics/genomics of *Cryptococcus*, *Drosophila*, and queen conch. Previous molecular laboratory experience is required; experience with bioinformatics, including genomic applications, is a plus.

The individual will teach an upper-level Mendelian and population genetics course in the spring; team-teach a sophomore-level ecology, evolution and genetics course, along with one section of the associated lab, in the fall; and teach one other lab section in either the spring or the fall. Excellent oral and written communication skills are expected.

Salary range is \$40-\$45,000, depending on experience, plus benefits. Please send a cover letter and CV to [rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu). Three letters of recommendation should be sent directly by the recommenders to the same email address. Review of applications will begin immediately and continue until the position is filled.

Inquiries should be directed to: Richard Kliman [rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu) 610-606-4666 ext 3501

Richard M. Kliman Associate Professor Dept. of Biological Sciences Cedar Crest College 100 College Drive Allentown, PA 18104 (610) 606-4666, ext. 3501 [rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu) [www2.cedarcrest.edu/academic/bio/rkliman](http://www2.cedarcrest.edu/academic/bio/rkliman)

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## ColoradoStateU EvolutionaryEcol

Postdoc position in evolutionary ecology at Colorado State University

The Hufbauer lab interested in candidates for a 2 year postdoctoral position in to work on a collaborative project between CSU and CU Boulder at the interface of demography, modeling and ecological genetics.

The project focuses on the contributions of demography and genetics in the founding and spread of new populations, combining a model biological system (*Tribolium* flour beetles) and quantitative models. The main experiments will be conducted in the lab of Ruth Hufbauer at Colorado State University (<http://lamar.colostate.edu/~hufbauer/>). We will collaborate closely with mathematical biologists at CU Boulder in Brett Melbourne's lab (<http://www.colorado.edu/eeb/facultysites/melbourne/>).

Previous experience conducting lab experiments using insects or other model organisms and working with microsatellites would be helpful, and a strong background in evolutionary ecology is vital. The ability to start as early as January 2011 would be a bonus.

Please get in touch with Ruth for additional details. When you write, please send a CV.

Ruth A. Hufbauer Associate Professor BSPM, GDPE  
Colorado State University 1177 Campus Mail Fort Collins, CO 80523-1177 USA

office: C147 Plant Sciences (970) 491-6945 lab: E113/115 Plant Sciences (970) 491-5984 fax: (970) 491-3862 email: [hufbauer@lamar.colostate.edu](mailto:hufbauer@lamar.colostate.edu)  
<http://lamar.colostate.edu/~hufbauer/> <http://www.invasionsrcn.org/> [hufbauer@lamar.colostate.edu](mailto:hufbauer@lamar.colostate.edu)

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## ColumbiaU 2 ComputationalBiol Bioinformatics

Two Postdoctoral Research Scientist positions are available (one full-time for 11 months and other full-time for 10 months). We are looking for young scholars with experience in the areas of computational biology. The position will involve maintaining a database of annotations of protein subcellular localization and the development of novel machine-learning based prediction methods. Candidates should have a PhD in Computational Biology or Bioinformatics; We specifically encourage applications from recent PhD graduates. Strong programming skills are essential for these positions, as well as, some familiarity with the major bioinformatics tools and databases. Experience in machine learning algorithms is preferred. The candidates may have to develop and maintain applications using Perl, CGI, PHP and MySQL. The candidates should be fluent in spoken and written English and should be able to communicate ideas and results to colleagues from all the diversity of life sciences. The ability to work in a team is as essential as that to complete a project without constant supervision. The positions may involve spending significant portions of time at Rutgers University, New Brunswick and/or at the Technical University of Munich, Germany.

Education: A PhD degree in Computational Biology or Bioinformatics is required.

Interested persons should e-mail a cover letter and C.V. to: Ed Johnson (EG), Columbia University, Depart-

ment of Biochemistry and Molecular Biophysics, NY, NY e-mail: etj1@columbia.edu

Contact Dr. Yana Bromberg (bromberg@rostlab.org) for more information. Additional information is also available at the web site: <http://biochemistry.hs.columbia.edu> Columbia University takes affirmative action to ensure equal opportunity.  
yana.bromberg@gmail.com

competitive salary. Applicants for this position MUST be U.S. permanent residents or citizens.

Please email your current CV to sjm336@cornell.edu

Sara Miller Administrator, Buckler Lab Institute for Genomic Diversity Cornell University 607.255.1809 sjm336@cornell.edu

sara.miller@cornell.edu

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## CornellU GrassBioinformatics

Buckler Lab for Maize Genetics and Diversity A USDA-ARS Lab with Cornell's Institute for Genomic Diversity

Job Description

Postdoc in Grass Bioinformatics

Position Overview:

Postdoc will process and analyze next generation sequencing data from *Tripsacum dactyloides*, maize's perennial relative, and switchgrass, a potential perennial biofuel grass. They will conduct analysis and develop software for an ongoing research program focused on the natural variation inherent in perennial grass genomes for the dissection of complex traits. The research will focus specifically on (1) identifying the novel genes in perennial grasses that are lacking in maize, (2) identify the alleles involved in adaptation of perennial grasses to North American environments. Our longer term goal is to support the development of high performance perennial grass crops.

Responsibilities:

\* Develop the analysis pipelines for genotype by sequencing without the aid of a reference genome, using next generation sequencing libraries from *Tripsacum* and switchgrass. \* Construct high density genetic, diversity, and QTL maps of *Tripsacum* and switchgrass to facilitate the identification of key genes. \* Develop analytic approaches for combining next generation sequencing with higher ploidy organisms.

Qualifications:

Applicant must have Ph.D. in statistical genetics, population genetics, bioinformatics or a related field and demonstrated skills in bioinformatics, programming and the analysis of next generation DNA sequence data. Knowledge of PERL, Java, and C required.

This is position is a two year appointment at a highly

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## Dalhousie MicrobeDiversity

The Doolittle, Bielawski and Beiko labs at Dalhousie University, in collaboration with Olga Zhaxybayeva (West Virginia) and Marc Ereshefsky (Calgary) are looking for several PhD students and postdocs to join the project "Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes", recently funded by the Canadian Institutes of Health Research as part of the Canadian Microbiome Initiative. The main aim of this project is to understand human-associated microbial communities not only in terms of who is there, but also in terms of what key genetic and metabolic processes are characteristic of different clinical scenarios. This purely bioinformatic project involves the analysis of large genomic and metagenomic datasets from public repositories and from several collaborating research groups.

Key elements of the project include

(i) Analysis of publicly available microbial genomic and metagenomic datasets to delineate appropriate units of diversity. To what extent is it useful to consider microbial species and speciation as key determinants of a microbiome? (ii) Uncovering the determinants of phenotype for microbes and microbial communities. What important genes, metabolic and evolutionary processes (particularly neutral evolution, adaptation, recombination, and lateral gene transfer) are characteristic of complex individual and community phenotypes (pathogen vs. commensal, healthy vs. diseased)? (iii) Development and deployment of software. We will build a modular suite of software tools that incorporates insights gained from (i) and (ii), and from other sources. The main software framework and graphical interface will be implemented in Python, but management and analysis of large data sets will require certain modules to be written in C/C++.

Individuals with backgrounds in population genetics, microbial genomics, molecular evolution, phylogenetic

ics, bioinformatics, computer science, mathematics or statistics are encouraged to apply. Applications will be considered on an ongoing basis, with positions beginning immediately. Successful applicants will join a thriving multidisciplinary team that is already developing and applying bioinformatics software (see <http://kiwi.cs.dal.ca/Software> for examples), and will have access to several high-performance computing clusters as well as conference travel opportunities, and be active participants in Dalhousie's Centre for Comparative Genomics and Evolutionary Bioinformatics (<http://cgeb.dal.ca/>).

Interested and qualified applicants should send a curriculum vitae and a one-page statement of interest to [microbiome@lists.dal.ca](mailto:microbiome@lists.dal.ca).

[beiko@cs.dal.ca](mailto:beiko@cs.dal.ca)

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## DukeU EvolutionaryGenetics

Duke University, Biology Department, Associate in Research/Postdoctoral Associate:

Associate in Research/Postdoctoral Associate wanted to participate in research in evolutionary ecology and genetics of plants. Research of this lab combines work in the field, laboratory, and greenhouse to study genotype-environment interaction. This position requires technical skills in RNA extraction, qRT-PCR, transcriptome analysis, and other methods of quantifying gene expression and regulation. Available immediately. Currently for one year. Competitive salary and full Duke benefits. Duke University is an Equal Opportunity/Affirmative Action employer.

Please send CV and names of references to Kathleen Donohue: [k.donohue@duke.edu](mailto:k.donohue@duke.edu)

DEADLINE FOR CONSIDERATION: OCTOBER 1, 2010

– Kathleen Donohue Associate Professor Department of Biology Duke University Box 90338 Durham, NC 27708 USA

Office: 919 613-7467 Lab: 919 613-7468 Fax: 919-660-7293 [k.donohue@duke.edu](mailto:k.donohue@duke.edu)

Kathleen Donohue <[k.donohue@duke.edu](mailto:k.donohue@duke.edu)>

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## ETH Zurich GeneticDiversity

ETH Zurich.VeluxFellowship

Genetic diversity is a key characteristic of biological systems. Diversity allows populations to adapt to changing environments, or, for example, to evolve resistance to parasitic infections. Technological advances have made the measurement and analysis of genetic diversity faster and more efficient. The Genetic Diversity Centre (GDC) at ETH Zürich provides a technology, knowledge, and education platform that meets the needs of researchers from many different fields. The GDC fosters an academic community where students and peers from various academic institutions meet, work, and discuss their results and ideas. To strengthen these activities the Velux Foundation offers stays at the GDC as:

Velux Foundation Fellow at the Genetic Diversity Centre (GDC) ETH Zürich

The Fellow will have the opportunity to work freely at GDC on topics of mutual interest and can benefit from the academic environment of ETH and the University of Zurich. Work can either be empirical, theoretical, or conceptual. Possible topics are in the broader field of genetic diversity studies, including various extensions such as expression study, proteomics, or community genomics. The Fellow will receive official guest researcher status at ETH Zürich and financial support for travel, working expenses, and a modest honorarium during his/her stay. The fellow will be expected to support GDC's training and education activities by sharing the expertise in his/her field. Post-graduate researchers at all levels are eligible for this fellowship. It can cover time periods from one month to a maximum of one year. The fellowship program is available starting from January 2011.

Applications can be made at any time. Please send your CV, publication list, and a short statement (1-2 pages) on your planned activities at GDC to the: Director (Prof. P. Schmid-Hempel), Genetic Diversity Centre (GDC), ETH Zürich CHN E55, Universitätsstrasse 16, CH-8092 Zürich, Switzerland. Electronic applications preferred (send email with application material to: [psh@env.ethz.ch](mailto:psh@env.ethz.ch), or: [Aria.Minder@env.ethz.ch](mailto:Aria.Minder@env.ethz.ch)). Applications will be reviewed continuously.

For further information, email the Director, or see the webpages: Genetic Diversity Centre: [www.gdc.ethz.ch](http://www.gdc.ethz.ch)

Dept. of Environmental Sciences: [www.env.ethz.ch](http://www.env.ethz.ch)  
 Velux Foundation (in German): [www.veluxstiftung.ch](http://www.veluxstiftung.ch)  
 Prof. Paul Schmid-Hempel ETH Zurich Institute  
 of Integrative Biology (IBZ) (Experimental Ecology)  
 ETH-Zentrum CHN K11 Universitätsstrasse 16 CH-  
 8092 Zurich

ph: + 41 44 633 6048 / 6033 fax: +41 44 632 1271  
 psh@env.ethz.ch [www.eco.ethz.ch](http://www.eco.ethz.ch)

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## ETH Zurich PopBiol GeneticsInfectiousDiseases

### PHD AND POSTDOC POSITIONS IN POPULATION BIOLOGY AND GENETICS OF INFECTIOUS DISEASES AT THE ETH ZURICH

Positions for two PhD student, a junior and a senior postdoc are available in the groups of Sebastian Bonhoeffer and Roland Regoes at the ETH Zurich. In our groups we study the population biology and genetics of infectious diseases. For more information on our groups see [www.tb.ethz.ch](http://www.tb.ethz.ch). One of the PhD students and the senior postdoc would work in the group of Sebastian Bonhoeffer. The broad research area of these two positions will be the theoretical population genetics of infectious disease (see [www.tb.ethz.ch/research/-Bonhoeffer](http://www.tb.ethz.ch/research/-Bonhoeffer)). Applicants for the PhD position should have strong quantitative skills. We therefore encourage people with a background in mathematics, biostatistics, bioinformatics or physics to apply. For applicants for the senior postdoc position a track-record in studying the emergence and the control of drug-resistance is an advantage. The postdoc position comes with a high degree of independence, and it would be great if you developed your own projects, possibly also involving the more junior members of the group. A strong background in mathematical modelling and computation is required for this position.

The other PhD student and the junior postdoc would work with Roland Regoes, studying the population biology of immune responses against viruses. In the last years Roland Regoes and his group members studied the dynamics of cytotoxic T lymphocyte killing in vivo, and the neutralization of HIV by antibodies (see [www.tb.ethz.ch/research/Regoes](http://www.tb.ethz.ch/research/Regoes)), and the PhD student and the postdoc could work on some of these topics initially. While our research is conducted in close collaboration with experimental immunology and virology laboratories (eg Annette Oxenius and Alexandra

Trkola), we are seeking candidates with strong quantitative skills (for example, trained mathematicians, biostatisticians, or physicists).

The starting dates of these positions are fairly flexible. We envisage some time at the end of this year.

Our groups are strongly linked with the experimental ecology group of Paul Schmid-Hempel, and the microbial evolution group of Martin Ackermann at the Institute of Integrative Biology of the ETH Zurich (see <http://www.ibz.ethz.ch/> for more details).

Zurich is a great place to live and to do research. It is the home of two big universities (the University of Zurich and the ETH), and is an attractive city in beautiful surroundings with a multinational population and many educational and recreational opportunities.

To apply send a letter describing your interest in this position, a CV and the names and contact addresses of two referees by email to our secretary Rita Jenny: [rita.jenny@env.ethz.ch](mailto:rita.jenny@env.ethz.ch). Please write "Application for postdoc/PhD position with Sebastian Bonhoeffer/Roland Regoes" into the subject line of your email. The deadline of the application is October 31, 2010. Informal enquires to [roland.regoes@env.ethz.ch](mailto:roland.regoes@env.ethz.ch) or [sebastian.bonhoeffer@env.ethz.ch](mailto:sebastian.bonhoeffer@env.ethz.ch) are also welcome.

Sebastian Bonhoeffer and Roland Regoes Institute of Integrative Biology, ETH Zurich [www.tb.ethz.ch](http://www.tb.ethz.ch)  
[roland.regoes@env.ethz.ch](mailto:roland.regoes@env.ethz.ch)

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## ExeterU EvolutionarySyntheticBiology

Evolutionary Synthetic Biology Postdoc Positions at Exeter University UK

Two postdoctoral positions on evolutionary projects in synthetic biology are available at the University of Exeter.

The first post (in the lab of Orkun Soyer) is part of a multi-lab project and involves development of methods for rational engineering of metabolic pathways, focusing on Mitomycin C synthesis in *Streptomyces Lavendulae*. For details, see text below. The online ad can be found here; <http://www.jobs.ac.uk/job/-ABP609/postdoctoral-research-position> The second post (in the lab of Declan Bates) is part of the project titled Synthetic integrons for continuous directed evolution of complex genetic ensembles. For details

and online ad, see here: <http://www.jobs.ac.uk/job/-ABO312/postdoctoral-researcher-synthetic-biology-mathematical-modelling/> best regards, orkun

Orkun S. Soyer, PhD Lecturer in Systems Biology Engineering, Mathematics and Physical Sciences University of Exeter Tel: +44 (0)1392 723615 URL: <http://people.exeter.ac.uk/oss203/>

Engineering biosynthetic pathways in bacterial consortia. One of the major promises of the nascent field of synthetic biology is to engineer bacteria for the production of biomolecules that are relevant for therapeutic and technological use. Currently synthetic engineering of bacterial metabolism relies heavily on intuition and experimental tweaking: we are still far from being able to rationally engineer metabolic capabilities of bacteria. Focusing on the biosynthetic pathway of Mitomycin C (in *Streptomyces Lavendulae*), this project aims to increase our ability to rationally design metabolic pathways. Our specific goals are to (i) increase Mitomycin yields in *S. Lavendulae* by rational engineering of pathway structure and enzyme regulation, (ii) improve implementation of the Mitomycin pathway in other bacteria through segmentation over several microbial subpopulations that can function as a consortium, and (iii) to explore alternative Mitomycin-producing metabolic network designs through sampling of the network space [Bar-Even, A. et al PNAS 107, 2010] and in silico evolution [Pfeiffer, T. et al PLoS Biol 3(7), 2005].

This project is part of the Engineering a Semi-Biotic Immune System, a multi-lab, integrated project funded by the EPSRC Flashlight Funding in Synthetic Biology. Our long-term goal is a semi-biotic immune device, which will detect and react to the onset of disease in its host subject. The outcomes of this advertised post will interface and feed-in to experimental work. In particular, the metabolic pathways resulting from this theoretical work will be implemented in bacterial consortia that will be housed in specifically designed microfluidic devices.

The team behind Engineering a Semi-Biotic Immune System comprises expertise in cell biology (Tavassoli Lab, University of Southampton and Huang Lab, Sheffield University), microfluidic devices (Yin Lab, University of Glasgow), functional peptides (Miller Lab, University of Manchester), antibody production (Kontoravdi Lab, Imperial College) and theoretical network analysis (Soyer Lab, University of Exeter).

We are looking for postdoctoral researcher to join this team under the mentorship of Dr. Orkun Soyer at the University of Exeter. The ideal candidate is a motivated individual with a PhD in computational biology (or a related field). Experience in network analysis, dy-

namic systems, FBA and object-oriented programming is beneficial but not necessary.

Scientific Benefits: As part of a ambitious, innovative and multi-lab endeavor, this project offers a unique career opportunity for the chosen candidate. S/he will be exposed to a highly diverse set of expertise within the team and will benefit from the broader mentorship structure which includes world-renowned senior scientists. This will allow the PDRA to develop his/her own ideas both within the context of this project and that of the larger one. Duration and Salary: This positions is initially for one year with possible extension to 18 months. Salary will be circa 25,500. Exeter: University of Exeter is well positioned among the leading research-intensive universities in the UK. The University is undergoing a strategic development with continuing investment in excess of 40 million. Within this development, Systems and Synthetic Biology are recognised as growth areas and there are now several leading research groups at Exeter. Exeter offers excellent student living and the University is ranked number one in the UK for student satisfaction. Exeter is in the south-west of England which is considered the most beautiful part of the country and a hub for outdoor

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## FloridaStateU AmphibianGenomics

Advanced Research Technician or Postdoctoral Researcher

Organization: Florida State University

Job Location: Tallahassee, FL

Job Description: To join a laboratory group involved in developing genomic resources in amphibians, using enrichment procedures and high-throughput sequencing (i.e., Illumina). Researcher will perform bench-level molecular work to prepare samples for high-throughput sequencing, conduct microsatellite and SNP screening and genotyping, and develop novel applications for hybridization-based enrichment. Researcher will also assist with processing and analysis of genomic data (bioinformatics).

Responsibilities will include: lab management, library preparation for sequencing (e.g., barcoded library preparation, etc.), genotyping and marker development (microsatellites and SNPs), sequence enrichment, and protocol development.

Must have good troubleshooting skills, a strong background in molecular biology, experience in protocol development, good organization and leadership skills, and high efficiency. Extensive experience in collection and analysis of genomic data is also desirable. Must be able to take on a project and carry it out to completion.

Start Date: flexible (early October preferred).

Salary \$30,000 to \$45,000 per year, plus benefits, depending upon experience.

Benefits Retirement, health, sick/annual/holiday leave, other benefits

Characteristic Duties - Conducts various bench level experiments - Employs a variety of standard and non-standard molecular biology techniques to help develop protocols for library construction and sample preparation for next-generation sequencing - Prepares, orders, and maintains stocks of necessary reagents, solutions and supplies - Documents, compiles and analyzes experimental data - Provides advice to fellow lab members regarding laboratory techniques - Helps mentor undergraduate lab projects - Attends weekly meeting for experimental planning - Assists with organization of tissue collections and database - Maintains and improves technical knowledge base

Essential requirements: (1) BS, MS, or PhD degree with either graduate experience or a minimum of two years of professional experience with genomic sequencing technologies and analysis. (2) Strong background in molecular biology techniques (e.g., extraction of RNA, DNA, real-time QPCR, sequencing) (3) Solid computer skills and good knowledge of public domain biological databases. Advanced computer skills (genomics data processing and analysis, databases, etc.) are preferred. (4) Excellent organizational, time management, and communication skills required; must be able to work independently, solve problems, and interact with lab members.

Contact Information: [alemmon@evotutor.org](mailto:alemmon@evotutor.org)

About Our Organization: The researcher selected will become part of the integrative laboratory groups of Alan Lemmon and Emily Moriarty Lemmon at Florida State University, in Tallahassee, Florida. For more information, see our websites: <http://www.evotutor.org/LemmonLab/> <http://www.bio.fsu.edu/chorusfrog/index.html>

[www.bio.fsu.edu/faculty-moriarty-lemmon.php](http://www.bio.fsu.edu/faculty-moriarty-lemmon.php) – Alan R. Lemmon Assistant Professor Florida State University  
[arlemmon@gmail.com](mailto:arlemmon@gmail.com)

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## Grenoble Population Genomics

A one-year postdoctoral position in population genomics is available to work at the Laboratoire d'Ecologie Alpine, Grenoble, France.

I am looking for a highly motivated researcher interested in joining a team of PhD students and postdocs working on the development of statistical methods to make inferences about evolutionary and ecological processes influencing the population genetic structure of non-model species. The post holder will develop a statistical method to identify regions or loci of the pea aphid genome involved in differences in reproductive mode. The genome scan method will use Approximate Bayesian Computation (ABC) techniques and will be aimed at detecting outlier loci in species that can reproduce both sexually and asexually.

The postdoctoral fellow will be part of a larger project focused on pea aphids that includes research teams in Rennes (INRA) and Nantes (INSERM) and is funded by the French research agency (ANR).

The successful candidate will have strong bioinformatic skills and a solid background in population genetics.

The position is available from December 1st 2010 but starting date could be postponed until early 2011. The net salary is 2000 euros per month.

How to apply: Send BEFORE November 1st the following information by e-mail to [oscar.gaggiotti@ujf-grenoble.fr](mailto:oscar.gaggiotti@ujf-grenoble.fr):

- detailed CV - the name and e-mail addresses of two references

Contact Oscar Gaggiotti ([oscar.gaggiotti@ujf-grenoble.fr](mailto:oscar.gaggiotti@ujf-grenoble.fr)) for more details about the project, the lab, and the Grenoble area.

Oscar Gaggiotti Professor Equipe Genomique de Populations et Biodiversité LECA UMR CNRS 5553 Université Joseph Fourier BP 53 38041 GRENOBLE France Tel.: 33(0)4 76 51 44 97 Fax: 33(0)4 76 51 42 79 <http://www-leca.ujf-grenoble.fr/membres/gaggiotti.htm> <http://www-leca.ujf-grenoble.fr/>

grenoble.fr/projets/gaggiottiprojets/IMPBioFr.htm  
oscar.gaggiotti@ujf-grenoble.fr

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## MartinLutherU BeeParasiteRelations

2.5 year postdoc on bee-parasite relations

A postdoctoral researcher is sought for a newly funded project on the ecology and evolution of honey bee parasite interactions within Robert Paxton's lab at the University of Halle, Germany. The goals of the research are to understand interactions between parasites and pesticides in relation to their impact on insect health and immunity. The post-holder will contribute to the recently funded EU project BeeDoc (<http://www.bee-doc.eu/index.html>) that addresses large-scale honey bee colony losses. Research will involve lab and field-based (in the UK, Germany and Sweden) experiments as well as molecular genetic analysis of bee pathogens and host immune response. We seek a highly motivated individual with an interest and experience in host-parasite interactions or insect immunity as well as molecular genetic skills that can interact well with the pan-European BeeDoc team of researchers.

The working language of the lab is English. The neighboring group of Robin Mortiz makes for a strong profile in honeybee biology and genetics at the University of Halle. The position is available for 2.5 years and, though the start date is flexible, we seek a person to commence in autumn 2010. Halle is a delightful, historical city approximately 2 hours SW of Berlin. The salary is on the standard German postdoc scale E13, which translates to approximately Euro 35,000 per annum (dependent on experience).

Further details of the position can be obtained from Robert Paxton ([robert.paxton@zoologie.uni-halle.de](mailto:robert.paxton@zoologie.uni-halle.de)).

Please send applications as a single pdf file, to include post reference number D 167/2010, a cv, list of publications, a statement of research interests and goals (maximum 1 page), and contact details of two referees, to Robert Paxton ([robert.paxton@zoologie.uni-halle.de](mailto:robert.paxton@zoologie.uni-halle.de)) by September 20th, 2010 or by snail mail to:

Natural Sciences Faculty I  
Institute for Biology  
Zoology/General Zoology  
- Prof. Dr. R. Paxton -

Martin-Luther-Universität Halle-Wittenberg  
D-06099 Halle (Saale)  
Germany  
Robert Paxton <[robert.paxton@zoologie.uni-halle.de](mailto:robert.paxton@zoologie.uni-halle.de)>

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## MartinLutherU BeeParasiteRelations 2

2.5 year postdoc on bee-parasite relations

A postdoctoral researcher is sought for a newly funded project on the ecology and evolution of honey bee parasite interactions within Robert Paxton's lab at the University of Halle, Germany. The goals of the research are to understand interactions between parasites and pesticides in relation to their impact on insect health and immunity. The post-holder will contribute to the recently funded EU project BeeDoc (<http://www.bee-doc.eu/index.html>) that addresses large-scale honey bee colony losses. Research will involve lab and field-based (in the UK, Germany and Sweden) experiments as well as molecular genetic analysis of bee pathogens and host immune response. We seek a highly motivated individual with an interest and experience in host-parasite interactions or insect immunity as well as molecular genetic skills that can interact well with the pan-European BeeDoc team of researchers.

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Please send applications as a single pdf file, to include post reference number D 167/2010, a cv, list of publications, a statement of research interests and goals (maximum 1 page), and contact details of two referees, to Robert Paxton ([robert.paxton@zoologie.uni-halle.de](mailto:robert.paxton@zoologie.uni-halle.de)) by September 27th, 2010 or by snail mail to:

Natural Sciences Faculty I



Institute for Biology  
Zoology/General Zoology

- Prof. Dr. R. Paxton

Martin-Luther-Universität Halle-Wittenberg

D-06099 Halle (Saale)

Germany

Dr. Robert J. Paxton Professor of General Zoology  
Institute for Biology Martin-Luther-Universität Halle-  
Wittenberg Hoher Weg 8 D-06099 Halle (Saale) Ger-  
many

Tel: +49 (0)345 55 26500 FAX: +49 (0)345  
55 27152 E-mail: robert.paxton@zoologie.uni-halle.de  
<http://www2.biologie.uni-halle.de/zool/> Robert Pax-  
ton <robert.paxton@zoologie.uni-halle.de>

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### McMasterU EvolutionInfectiousDisease

Post-doctoral fellowship at McMaster University Dept.  
of Biology

We are seeking a talented, quantitatively oriented post-  
doc to work on models of the interaction of the spread  
of infectious diseases, and related beliefs and behaviors.  
The application deadline is December 1, and the start  
date is open.

Please contact Jonathan Dushoff  
dushoff@mcmaster.ca.

More information is available at [http://-  
lalashan.mcmaster.ca/theobio/public/index.php/-  
Post-doctoral\\_opportunities](http://lalashan.mcmaster.ca/theobio/public/index.php/-Post-doctoral_opportunities) . Jonathan Dushoff  
<dushoff@mcmaster.ca>

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### MissouriBotanicalGarden PlantEvolution

Postdoctoral position in plant ecology, evolution, and  
conservation

at the Center for Conservation and Sustainable Devel-  
opment, Missouri Botanical Garden

A Postdoctoral position is available at the Center for

Conservation and Sustainable Development (CCSD) of  
the Missouri Botanical Garden (MBG) to participate in  
ongoing projects about determinants of plant diversity  
(alfa, beta, and gamma diversity) and size of species  
geographic ranges, the effects of climate change on  
plants spatial distribution, and the conservation status  
of plant species. The post holder will also be expected  
to develop new projects by integrating into spatial anal-  
yses plant data contained in the MBG's herbarium and  
TROPICOS database (<http://tropicos.org/>) with other  
types of information such as quantitative local vegeta-  
tion inventories (i.e., plant plots), phylogenies, and geo-  
graphic environmental data. See website for description  
of ongoing research at CCSD ([http://www.mobot.org/-  
plantscience/ccsd/](http://www.mobot.org/-plantscience/ccsd/)) and MBG in general ([http://-  
www.mobot.org/plantscience/default.asp](http://-www.mobot.org/plantscience/default.asp)).

Applicants should have excellent writing and commu-  
nications skills as well as an eagerness to produce and  
publish scientific results. Candidates should have a  
strong background in one or more of the following fields:  
ecology, evolution, systematics, spatial analysis, infer-  
ential statistics, or bioinformatics. Applicants should  
furthermore have experience with one or more of the fol-  
lowing tools: the R statistical environment, ESRI soft-  
ware or species distribution models. Computer simula-  
tion skills are particularly desirable. Fluency in Spanish  
is a plus.

The Postdoctoral fellow will be based in St. Louis  
where a vibrant community of systematists, ecologists,  
and evolutionary biologists interact through partner-  
ships among MBG, Washington University, University  
of Missouri-St. Louis and Saint Louis University. Fund-  
ing for this position is available for two years, extend-  
able to three years subject to review after one year.  
The starting annual salary range is anticipated to be  
between \$30,000-\$34,000. The Missouri Botanical Gar-  
den offers a comprehensive benefits package.

To be considered, applicants should apply on-  
line (<http://www.mobot.org/jobs/mbgjobs.asp#J053>),  
and submit a brief statement of research interests, a  
CV, copies of relevant publications or manuscripts, and  
three letters of recommendation from people familiar  
with their research to [tracy.breckenridge@mobot.org](mailto:tracy.breckenridge@mobot.org)  
before 31st October 2010.

Iván Jiménez

Assistant Curator

Center for Conservation and Sustainable Development  
Missouri Botanical Garden

P.O. Box 299 St. Louis, MO 63166

[ivan.jimenez\[at\]mobot.org](mailto:ivan.jimenez[at]mobot.org)

<http://www.mobot.org/MOBOT/Research/curators/-jimenez.shtml>

Ivan Jimenez <Ivan.Jimenez@mobot.org>

## Montpellier Evolutionary Biology

Postdoc in Evolutionary Community Ecology and Experimental Evolution, Montpellier, France.

A postdoctoral contract of 24 months starting from January 2011 (earlier appointment is negotiable) and funded by the French National Research Agency (ANR) is available in the « Evolutionary Community Ecology » group headed by Nicolas Mouquet at the Institute of Evolutionary Sciences of Montpellier (University of Montpellier, France).

The role: The successful appointee will undertake innovative research related to mechanisms of evolutionary diversification and emerging community properties using bacteria as a model system. The main objective is to understand how evolution on simple and complex environments alters the relationship between species richness and ecosystem functioning. His work will be done in close collaboration with theoreticians and can also include modeling if the applicant wants to develop both experimental and theoretical approaches. The research will be supervised by Nicolas Mouquet and will benefit of technical helps.

The person: Applicants should possess a PhD in the area of ecology, evolutionary ecology, or microbial ecology/evolution. A strong background in conceptual ecology/evolution is needed. Experience with ecological microcosms and bacterial evolution will be appreciated. Candidates should have a working knowledge of English, good communication, teamwork and organizational skills as well as to be able to work independently.

The team: Our group associate theoretical and experimental approaches to understand the dynamics of species diversity over short (ecological) and long (evolutionary) time scales. Our approaches are multidisciplinary, mixing community and ecosystem ecology, biogeography, evolution, microbiology, conservation biology and modeling of complex systems. We use different techniques and biological material : (1) mathematical modeling, (2) experimental evolution (with two systems : *Pseudomonas fluorescens* SBW25 and its phage Phy2 and the protozoan *Paramecium caudatum* and its bacterial parasite *Holospira undulata*), (3) data anal-

yses on large-scale species distribution datasets (Birds, Fishes, Rodents and their parasites) and (4) field studies on tropical fishes *Monogenea* and marine bacteria. Our team hosts 7 permanent researchers (Vincent Devictor, Michael Hochberg, Oliver Kaltz, Sonia Kefi, Serge Morand, Nicolas Mouquet and Antoine Pariselle) one permanent Technician, several postdocs, Phd and master students.

The department: The Institute of Evolutionary Sciences of Montpellier (ISEM) is one of the strongest French institutes in the field of biodiversity. It hosts 63 permanent researchers (plus 92 technicians, engineers, post-docs and PhD), and encompasses every aspect of evolutionary biology: paleontology, systematics, phylogeny, population genetics, ecology and conservation biology. ISEM belongs to University Montpellier 2, and is deeply involved into teaching, from master to doctorate.

Remuneration: The net salary will be of at least 1800 euros including social security and medical assistance depending on the candidate experience. This is a full-time, fixed term appointment for 24 months.

Contact/Application: This job will remain open until the position is filled, but applicants are encouraged to apply by October 1, 2010. To discuss the role and/or send application contact Dr. Nicolas Mouquet [nmouquet@univ-montp2.fr](mailto:nmouquet@univ-montp2.fr)

Application materials should include: (1) Cover letter summarizing interests and qualifications. (2) Resume/Vita. (3) Names and contact information of at least two professional references

Nicolas Mouquet

Institut des Sciences de l'Évolution - CNRS UMR 5554 - Université de Montpellier II - CC 065 34095 MONTPELLIER Cedex 05

[nmouquet@univ-montp2.fr](mailto:nmouquet@univ-montp2.fr) Tel +33 4 67 14 93 57 Fax +33 4 67 14 40 61 Skype : nmouquet

<http://nicolasmouquet.free.fr/> Nicolas Mouquet <[nmouquet@univ-montp2.fr](mailto:nmouquet@univ-montp2.fr)>

## New Zealand Evolutionary Physiology

We seek a Postdoctoral Fellow with experience in evolutionary physiology, who will combine insect physiology and molecular ecology to compare the evolutionary limits of alpine-adaptation of weta populations in New

Zealand. The position is for two years, within Ecology group of the Institute of Natural Resources, Massey University, New Zealand.

The Postdoctoral Fellow will compare cold adaptation among populations of an endemic insect under the project title "What limits a weta?" We have a naturally-replicated study system that will allow us to investigate the role of gene flow in limiting or facilitating adaptation on an environmental gradient. High altitude populations of orthoptera species will be compared both in the field and laboratory. The project will combine ecology, insect physiology and population genetic tools to address a fundamental evolutionary question.

You will need a PhD in physiology, or related area of evolutionary biology and have proven research capabilities.

The salary for this position is NZ\$62,992 per annum, with two years funding.

Enquiries should be directed to Dr Mary Morgan-Richards (telephone +64 6 356 9099 extn 2043, email [m.morgan-richards@massey.ac.nz](mailto:m.morgan-richards@massey.ac.nz)) or Dr Steve Trewick (email [s.trewick@massey.ac.nz](mailto:s.trewick@massey.ac.nz)). Information about the Institute can be found at <http://inr.massey.ac.nz> and the Ecology Group at <http://ecology.massey.ac.nz> Closing date: 19th November 2010

[M.Morgan-Richards@massey.ac.nz](mailto:M.Morgan-Richards@massey.ac.nz)

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## NorthCarolinaStateU PlantSystematicsEvolution

Postdoc: Evolutionary developmental genetics of inflorescence architecture in Dogwoods

We are looking for a scientist who is interested in evolutionary developmental genetics of plant morphology. The position is available at the North Carolina State University, Raleigh, NC, USA and funded by the National Science Foundation for 2-4 years. It is open until filled.

A PhD in plant genetics, evolutionary development or molecular systematics is required, ideally with experience in working with flowering plants in the interface of the three areas. Experimental skills in plant genetic transformation, RNA in-situ hybridization, RT-PCR or qRT-PCR, and phylogenetics are desired. Excellent

written and oral communication skills in English and the interest in joining a multidisciplinary team are expected. The postdoc will be working with a team of three faculty members in the Department of Plant Biology and Department of Genetics at NCSU.

The salary is \$32,000-35,000 depending on experiences. Women and applicants in minority categories are encouraged to apply. Please send application by e-mail attachment to [jenny\\_xiang@ncsu.edu](mailto:jenny_xiang@ncsu.edu) including a letter outlining your suitability for the position, a detailed CV, and contact details of 3 referees.

Jenny Xiang

Qiu-Yun (Jenny) Xiang, Ph.D. Associate Professor Department of Plant Biology North Carolina State University Gardner Hall 2115 Raleigh, NC 27695-7612 USA Phone: 919-515-2728 Fax: 919-515-3436 Homepage: <http://www4.ncsu.edu/~qyxiang> Jenny Xiang <[jenny\\_xiang@ncsu.edu](mailto:jenny_xiang@ncsu.edu)>

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## OhioStateU ComputationalBiol

Post-doctoral positions open immediately in computational biology, bioinformatics, molecular biology and evolution in The Ohio State University Program in Pharmacogenomics (<http://pharmacogenomics.osu.edu>).

We invite applications from candidates with a Ph.D. or equivalent degrees interested in phylogenetic footprinting, detecting selection in noncoding regions, and analyses of expression (allelic expression imbalance and EQTLS)

The Program is newly funded with a U01 from NIGMS titled Expression Genetics in Drug Therapy, as part of the Pharmacogenomics Network, <http://www.nigms.nih.gov/Initiatives/PGRN>).

The Program directed by Wolfgang Sadée, is highly interactive, with multiple collaborators, affording unique opportunities for both fundamental genetics research and translation into clinical applications.

Send CV, statement of interest, names of three references and contact details to Sherry Ring, [ring.32@osu.edu](mailto:ring.32@osu.edu). The Ohio State University is an equal opportunity, affirmative action employer. Qualified women, minorities, veterans and individuals with disabilities are encouraged to apply.

Daniel Janies <[danjanie@yahoo.com](mailto:danjanie@yahoo.com)>

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## PennState ComparativeEvolutionaryGenomics

Postdoctoral position in comparative evolutionary genomics/human population genomics/statistical genomics at Penn State A postdoctoral position is available immediately in the laboratory of Kateryna Makova ([http://www.bx.psu.edu/makova\\_lab/](http://www.bx.psu.edu/makova_lab/)) at Penn State. The current focus of the lab is on deciphering molecular mechanisms of different mutations via whole-genome comparisons and on sex chromosome evolution.

As a successful candidate, you will come to our lab with relevant bioinformatics expertise, including some combination of programming experience, previous use of the R statistical package, and working knowledge of molecular evolution or population genetics. Once hired, you will analyze next-generation sequencing data sets and vertebrate genome alignments, and perform statistical and evolutionary modeling. You will work in close collaboration with statisticians to develop computational models, with wet-lab biologists to validate model predictions, and with the GALAXY team (<http://g2.bx.psu.edu>) to implement your computational tools. You will be joining a dynamic group with an established record ([http://www.bx.psu.edu/-makova\\_lab/Publications.php](http://www.bx.psu.edu/-makova_lab/Publications.php)), and active NIH and NSF funding. Penn State is a vibrant scientific community with particular strengths in computational genomics and molecular evolution.

The starting date is flexible, with an earlier date preferred. The initial contract is for 1 year, but can be extended for up to 3 years. Interested applicants should send pdfs with CV, a statement of research interests, and contact information of 3 references to [kmakova@bx.psu.edu](mailto:kmakova@bx.psu.edu), indicating \$B!H(Bpostdoctoral position\$B!I(B in the subject line.

Kateryna Makova, Ph.D. Associate Professor Department of Biology 305 Wartik Lab Penn State University University Park, PA 16802 Tel: 814-863-1619 Fax: 814-865-9131 E-mail: [kmakova@bx.psu.edu](mailto:kmakova@bx.psu.edu) Web: [http://www.bx.psu.edu/makova\\_lab/](http://www.bx.psu.edu/makova_lab/) Kateryna Makova <[kmakova@bx.psu.edu](mailto:kmakova@bx.psu.edu)>

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## SantaFeInst EvolutionaryBiol

The Omidyar Postdoctoral Fellowship at the Santa Fe Institute offers you:

- > unparalleled intellectual freedom
- > transdisciplinary collaboration with leading researchers worldwide
- > up to three years in residence in Santa Fe, NM
- > discretionary research and collaboration funds
- > individualized mentorship and preparation for your next leadership role
- > an intimate, creative work environment with an expansive sky

The Omidyar Fellowship at the Santa Fe Institute is unique among postdoctoral appointments. The Institute has no formal programs or departments. Research is collaborative and spans the physical, natural, and social sciences. Most research is theoretical and/or computational in nature, although it may include an empirical component. SFI typically has 15 Omidyar Fellows and postdoctoral researchers, 15 resident faculty, 95 external faculty, and 250 visitors per year. Descriptions of the research themes and interests of the faculty and current Fellows can be found at <http://www.santafe.edu/-research>. Requirements:

- > a Ph.D. in any discipline (or expect to receive one by September 2011)
- > computational and quantitative skills
- > an exemplary academic record
- > a proven ability to work independently and collaboratively
- > a demonstrated interest in multidisciplinary research
- > evidence of the ability to think outside traditional paradigms

Applications are welcome from:

- > candidates from any country
- > candidates from any discipline
- > women and minorities, as they are especially encouraged to apply.

The Santa Fe Institute is an Equal Opportunity Employer.

Deadline: 1 November 2010

To apply: [www.santafe.edu](http://www.santafe.edu) We accept online applications ONLY.

Inquiries: email to ofellowshipinfo at santafe dot edu

The Santa Fe Institute is a private, independent, multidisciplinary research and education center founded in 1984. Since its founding, SFI has devoted itself to creating a new kind of scientific research community, pursuing emerging synthesis in science. Operating as a visiting institution, SFI seeks to catalyze new collaborative, multidisciplinary research; to break down the barriers between the traditional disciplines; to spread its ideas and methodologies to other institutions; and to encourage the practical application of its results.

The Omidyar Fellowship at the Santa Fe Institute is made possible by a generous gift from Pam and Pierre Omidyar.

Barbara Kimbell Omidyar Fellowship Program Manager Santa Fe Institute 505-946-2724 [bkimbell@santafe.edu](mailto:bkimbell@santafe.edu)

Barbara Kimbell <[bkimbell@santafe.edu](mailto:bkimbell@santafe.edu)>

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## StanfordU EvolutionaryGenomics

Stanford University, Evolutionary genomics

A postdoctoral position is available in the lab of Hunter Fraser. The lab will combine experimental and computational approaches to studying the evolution of gene expression within and between species. Our long-term goals are to better understand 1) how new mutations affect gene expression; 2) what selective pressures act on these mutations; and 3) how changes in gene expression contribute to the evolution of other phenotypes. The project details are flexible, but may focus on analyzing genome-wide gene expression (RNA-seq) data from multiple species. Preference will be given to candidates with a strong background in computational biology, molecular evolution, and statistics. Familiarity with analysis of high-throughput sequencing (Solexa) data or quantitative/statistical genetics is a plus.

Stanford is an extremely stimulating environment, with many labs engaged in research on evolution and genomics. There is plenty of opportunity to interact with other labs, for example in the monthly evolutionary genomics joint lab meeting that includes labs from several departments. To apply, please email a CV,

brief description of research experience and interests, and contact information for at least two references to [hbfraser@stanford.edu](mailto:hbfraser@stanford.edu). The position can begin immediately. Salary and benefits are very competitive. For further information please see the lab's website, <http://www.stanford.edu/Ehbfraser/>. Hunter Fraser Assistant Professor Department of Biology Stanford University Stanford, CA [hbfraser@stanford.edu](mailto:hbfraser@stanford.edu)

Hunter Fraser <[hbfraser@stanford.edu](mailto:hbfraser@stanford.edu)>

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## StellenboschU 2 AbaloneGeneticDiversity

Postdoctoral positions available in the Department of Genetics, Stellenbosch University (1 September 2010)

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

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

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

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

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

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

These positions are available for 2 years with the possibility of extension. Commencement of duties: January 2011.

Interested researchers are requested to send their CV including details of at least 2 references to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za or Dr Aletta Bester-van der Merwe at aeb@sun.ac.za. Please indicate for which of the two positions you are applying.

Closing date: 26 September 2010.

roodt@sun.ac.za

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## StellenboschU Kob GeneticDiversity

Postdoctoral position available in the Department of Genetics, Stellenbosch University (1 September 2010)

A postdoctoral position is available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the focus on Genetic Diversity and Population Structure of farmed kob, *Argyrosomus japonicus* and

*Argyrosomus inodorus*, and the potential genetic impacts of farmed fish on associated wild fish populations. This project is a collaborative effort with Marine and Coastal Management (Dr Brett Macey) and the University of Pretoria (Prof Paulette Bloomer).

Exciting new industry initiatives are presently underway that are exploring the culture potential of indigenous marine finfish in South Africa. Two such species currently under investigation are the dusky kob *Argyrosomus japonicus* and silver kob *A. inodorus*. The proposed cage farming operations along the South African coastline have, however, raised concerns from both the public and conservation management authorities about the potential genetic impacts of farmed fish on wild populations. The current project is therefore aimed at the identification of populations or stocks along the southern African coast followed by the establishment of a broodstock management programme that can assist in the appropriate placement of farms and hatcheries as well as and minimize the potential negative genetic impact of farmed animals on wild fish populations.

The successful candidate will primarily be responsible for: 1) The development of molecular genetic markers that enable the detection of fine-scale patterns of genetic variation in populations with potentially shallow genetic sub-structure. 2) The identification of populations/stocks of *A. japonicus* and *A. inodorus* along the southern African coast based on species-specific microsatellites. 3) Assisting with the formulation of recommendations for kob farming along the South African coast.

Minimum requirements: PhD with specialization in Population and/or Evolutionary Genetics or any closely related discipline. Candidates should have proficiency in the relevant population analysis software packages and experience with microsatellite data will be an added advantage. The ideal candidate should also have proven project management experience and ability to set deadlines and meet milestones.

This position is available for 3 years and commencement of duties is set for January 2011.

Interested researchers are requested to send their CV including details of at least 2 references to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za.

Closing date: 26 September 2010

roodt@sun.ac.za

pawilson@trentu.ca

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## TrentU Evolution

Post-Doctoral Fellowship - Trent University

We are seeking a post-doctoral fellow with research interests in the broad areas of landscape genetics, evolutionary and population ecology, and/or habitat modeling, to undertake an analysis of large-scale genetic structuring and evolutionary relationships among carnivore and ungulate populations in North America. We are integrating this work with landscape ecology to determine ecological factors affecting genetic diversity, and with corticosteroid assays to assess population health across the range in species such as Canada lynx. Using several mammal species as models we are also interested in documenting patterns of evolutionary divergence due to natural or anthropogenic barriers to dispersal. The post-doctoral fellow may pursue one or more of the above research projects, and also will be given the opportunity to develop an independent research program within the framework of existing funding.

### Application Procedures

Applicants should hold a PhD in Landscape/Population Ecology, Genetics, or a related area. Priority will be given to candidates with demonstrated expertise in population genetics, landscape ecology, population ecology and/or spatial modeling. All candidates should submit a letter of application, curriculum vita, and names and contact information for three referees to Dr. Paul Wilson and Dr. Dennis Murray, Department of Biology, Trent University, 1600 West Bank Drive, Peterborough, ON Canada K9J 7B8 (email: [dennismurray@trentu.ca](mailto:dennismurray@trentu.ca), web page: [www.people.trentu.ca/~dennismurray](http://www.people.trentu.ca/~dennismurray); [pawilson@trentu.ca](mailto:pawilson@trentu.ca), web page: [web.me.com/pauljwilson/Wilson\\_CRC/Home.html](http://web.me.com/pauljwilson/Wilson_CRC/Home.html)).

The position will close as soon as a suitable candidate is found. The one-year term may start immediately, but no later than January 1, 2010, and a second year may be available pending satisfactory progress and funding.

The Ontario Post-Doctoral Fellowship Program was developed to recruit and retain outstanding young scientists to spend two years as post-doctoral fellows in an Ontario research institution. The successful Fellow will receive \$50,000 annually + benefits.

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## UArizona PlantPhylogenomics

Postdoc – Plant Phylogenomics – University of Arizona

A two-year postdoctoral position is available in my lab to work on a large collaborative project on genome evolution in *Oryza* (rice and its wild relatives). The project's PI is Rod Wing at the University of Arizona, and collaborators include myself (Mike Sander-son), Manyuan Long (University of Chicago), Carlos Machado (University of Maryland), Scott Jackson (Purdue University), Doreen Ware (Cold Spring Harbor), and Detlef Weigel (Max Planck Institute, Tübingen). The project's goals focus on leveraging new genomic data sets at several scales to study diverse aspects of genome evolution, ranging from the origin of new genes, diversification of gene families, population genomic analyses, and reconstructing gene and species trees (phylogenomics). The postdoc's responsibilities will be to spearhead the phylogenomic analyses in my lab. These promise to be a rich analytical challenge given the rampant discordance in gene trees already discovered in *Oryza* and the complications of gene flow, domestication, and frequent polyploidization. The candidate should have extensive experience in phylogenetic analysis of molecular sequence data, and one or more of the following interests or experience: population genetics/coalescent theory; algorithms/bioinformatics experience; experience in plant systematics, especially in taxa with closely related species. Opportunities for close collaboration with other co-PIs in the project are extensive and will be encouraged.

The position is in the Department of Ecology and Evolutionary Biology at the University of Arizona, with a starting salary of \$45,000/yr, including full benefits. It is potentially renewable for up to 3 years. Computational resources in my lab include a high performance computing cluster, web servers, database storage server, a viz wall for scientific visualization, and dedicated system administration support. The Department has a strong program in evolutionary genomics, including an ongoing NSF IGERT training program, and a number of faculty working in that area: Jeremiah Hackett, Matt Sullivan, Michael Nachman, Noah Whiteman, Mike Worobey and Mike Barker (joining January 2011).

The position is open until filled and is available immediately. Please send a CV and a brief statement of

research interests and experience to me at the address below, and arrange to have two letters of reference sent (e-mail is fine). A formal application will also be required through the university's HR website (<http://www.hr.arizona.edu>). For further information, please contact

Mike Sanderson, Professor Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721 sanderm@email.arizona.edu

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Michael J. Sanderson

Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

Office: BSW 412 Phone:520-626-6848

lab web site: <http://loco.biosci.arizona.edu> PhyLoTA Browser: <http://phylota.net> r8s software: <http://loco.biosci.arizona.edu/r8s> UA Biodiversity Informatics Initiative: <http://loco.biosci.arizona.edu/bdii> sanderm@email.arizona.edu

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## UCaliforniaSantaBarbara CommunityPhylogenetics

\*Postdoctoral Position UCSB Community Phylogenetics\*

We seek a highly motivated and productive postdoctoral researcher to work on a newly NSF-funded, collaborative research on the Dimensions of Biodiversity. Stage 1 of the project is to work at the University of California-Santa Barbara in the laboratory of Todd Oakley. The postdoc will collect high-throughput sequencing data to elucidate the phylogenetic relationships of North American freshwater green algae. The postdoc will use the resulting phylogeny, along with publicly available distribution data, to test the hypothesis that algae co-occurring in lakes are phylogenetically non-random assemblages. The phylogeny estimated in stage 1 will form the foundation for collaborative research led by Bradley Cardinale at the University of Michigan and Charles Delwiche at the University of Maryland who will run experiments designed to identify the evolutionary and genetic basis of species niches, and then determine how niche differences influence co-existence and the productivity of algal communities.

The position requires an individual with a PhD and experience in community ecology, phylogenetics, phycol-

ogy or related fields. Outstanding molecular, computational and/or quantitative skills are particularly advantageous.

Funding is available for a 12-month position, for a minimum of 1 year, and will be extended provided satisfactory progress on research. The successful candidate will be expected to interface with multiple collaborators and to become an integral member of an interactive and collaborative lab group, as well as to supervise and/or mentor students. There will be opportunities for the candidate to pursue his or her own research program within the broader context of the grant proposal, and in collaboration with the PI, lab, and outside collaborators.

UCSB provides a rich academic and living environment, especially for biologists interested in the interface of ecology and evolution. UCSB ranked first in the nation in research impact in the area of Ecology/Environment for the period 2001-2005 by the Institute for Scientific Information (Science Watch, November 2006). UCSB is home to the National Center for Ecological Analysis and Synthesis ([www.nceas.ucsb.edu](http://www.nceas.ucsb.edu)). Santa Barbara has a Mediterranean climate that facilitates year-round outdoor activities, including surfing, kayaking, biking and hiking.

The starting date is flexible and will remain open until filled. For primary consideration, applicants should apply by October 31, 2010. Informal inquiries are encouraged, prior to formal application. To formally apply, please send the following:

1. A curriculum vitae
2. Names of 3 referees willing to provide a letter of recommendation upon request
3. A brief statement of how your research goals fit with research at the interface of community ecology and evolutionary biology

E-mail applications are preferred: oakley@lifesci.ucsb.edu

<<mailto:oakley@lifesci.ucsb.edu>>

Mailed applications are also acceptable to:

Todd Oakley

Ecology Evolution Marine Biology

University of California- Santa Barbara

Santa Barbara, CA 93106

The University of California is an Equal Opportunity / Affirmative

Action Employer.



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 Todd H. Oakley Professor Ecology Evolution and Marine Biology University of California-Santa Barbara Santa Barbara, CA 93106 (805) 893-4715 <http://www.lifesci.ucsb.edu/eemb/labs/oakley/> todd.oakley@lifesci.ucsb.edu

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### UCopenhagen PhytophthoraGenomics

Postdoctoral Fellowship in ancient *Phytophthora infestans* genomics

A two-year postdoctoral fellowship (with possibility of extension) is available at the Centre for GeoGenetics, Natural History Museums of Denmark, University of Copenhagen. Funded by Lundbeckfonden (The Lundbeck Foundation), the position will be available to commence following January 1st, 2011.

Project area: The oomycete *Phytophthora infestans* is one of the most destructive commercial crop pathogens. As the causative agent of potato late blight, the most important disease of the world's fourth largest food crop, conservative estimates suggest it carries an annual economic cost of 6.7 billion USD. First observed in the US in 1843, it rapidly spread to Europe, and within 2 years had gained notoriety for causing the Irish potato famine of 1845, which played a significant effect on western history, due to the mass famine and population displacement caused - an estimated 1.5 million Irish died from starvation, and a further 1.5 million were forced to emigrate. *Phytophthora infestans* exhibits a remarkable speed of adaptation to control strategies such as genetically resistant cultivars, and the recent appearance of strains resistant to the phenylamide fungicide metalaxyl, and the continual arrival of increasingly virulent genotypes has led it to reach epidemic proportions globally.

Placed jointly within the Bioinformatics group headed by Professor Anders Krogh (Institute of Biology), and the Pathogen Paleogenomics group headed by Assoc. Professor Tom Gilbert (Natural History Museum), the role of the successful applicant will be twofold. Firstly, the applicant will be expected to develop computational tools with which to assemble and analyse ancient genomic sequences. Secondly, the applicant will be expected to apply these (and other tools) to genome level sequence analysis of historic *Phytophthora infestans*

samples in order to reconstruct 150 years of its genomic evolution.

Qualifications: For consideration, applicants must have the following key skills: a) PhD in bioinformatics or a related field b) Demonstrated experience in the analysis of Next Generation DNA Sequencing data (in particular Illumina platform) or genome assembly c) Ability to program in PERL or Python, or similar d) Having published in high-quality international peer-reviewed journals Skills of additional, although not requisite, interest include: a) Understanding of molecular biology, evolutionary biology, ancient DNA b) Ability to work with LINUX and program in other languages (e.g. C, C++) c) Genome sequencing centre experience d) Experience with target-capture sequence data

As the members and collaborators of the Centre are international, the working language of the Centre is English, thus excellent English speaking, reading and writing skills are required.

Application: The application must contain: Curriculum vitae (incl. the applicants email address) List of publications Motivation for applying (0.5 A4-page) Transcript of university examinations (in English) Contact details of 2 persons for references (note references are welcome, but not explicitly needed, at time of submission)

For further information please contact Associate Professor Tom Gilbert ([tgilbert@snm.ku.dk](mailto:tgilbert@snm.ku.dk))

Applications should be e-mailed as one pdf-file marked "Postdoctoral Fellowship" to Tom Gilbert ([tgilbert@snm.ku.dk](mailto:tgilbert@snm.ku.dk)).

Deadline for applications is 1st November 2010 at 12:00 noon. Applications received after the deadline may not be considered.

Tom Gilbert <[mtpgilbert@gmail.com](mailto:mtpgilbert@gmail.com)>

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### UGeorgia EvolutionaryGeneticsAging

The Promislow lab at the University of Georgia is seeking an enthusiastic, independent postdoctoral researcher to study the genetic architecture of aging in *Drosophila*. Current projects include studies on aging in molecular networks, and on natural genetic variation for somatic mutation rate. The goal of these projects is to better understand the causes and consequences of

aging in natural populations. The successful candidate will apply genetic and genomic approaches to the study of aging in flies. Specific experiments will include large-scale analyses of genomic and metabolomic networks, in vivo measures of somatic mutation rate, and genome wide association studies to map variation in network structure and mutation rate. Preference will be given to candidates with experience in population genetics, genomics, and/or systems biology & network analysis.

The position is initially available for two years, and may be extended. The postdoc will be among a dynamic, interactive group of evolutionary geneticists at the University of Georgia in Athens, GA.

Applications should be sent by Sept. 17, 2010 by email to Daniel Promislow (promislow@uga.edu). Applicants are requested to send a single PDF file that includes a cover letter, a CV and one or two representative publications. Applicants should also arrange for three letters of recommendation to be sent by email.

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

Daniel Promislow <promislow@uga.edu>

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### UGeorgia InfectiousDiseaseEvolution

A Postdoctoral Associate is sought to join a theory-based research lab at the University of Georgia (PI: Dr. Andrew Park) to apply computational and/or mathematical approaches to understanding pathogen evolution. Applicants are encouraged to submit a short (one-page) research proposal. The lab, which is located in the University of Georgia Odum School of Ecology has broad interest in infectious disease evolution including immune escape, virulence evolution, the emergence of trade-offs, cross-species transmission and responses to intervention. The starting salary will be \$41,715 plus benefits. Start date is negotiable. Inquiries may be communicated by email. Along with the short research proposal, applicants are requested to send a letter of introduction and CV and to arrange for three letters of recommendation to be sent to awpark@uga.edu.

Review of applications will continue until the position is filled.

Dr Andrew Park Assistant Professor University of Georgia Odum School of Ecology & Dept. Infectious Diseases, College of Veterinary Medicine Athens, GA,

30602-2202, USA

Ph 706 610 0784 || Fx 706 542 4819 || Skype awp222 ||  
Web geospiza.ecology.uga.edu/parklab

Andrew Park <awpark@uga.edu>

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### UKonstanz MolEvolution

POSTDOC POSITION - in molecular evolution, genomics, bioinformatics

An opening for a postdoc position is available immediately in the GeCKo - the Genomics Center of the University of Konstanz - <http://cms.uni-konstanz.de/en/genomics-center/> .

Through funding of the “excellence initiative” of the German Science Foundation we recently established a genomics center - including both Roche 454 FLX and Illumina GAIIx next generation sequencing as well as ABI Sanger sequencing platforms. We are particularly interested in someone with expertise in molecular evolution, genomics and bioinformatics. Recently, this area of research at the University of Konstanz was strengthened further by the appointment of a “junior professorship” in bioinformatics.

Candidates should have a strong background in bioinformatics and/or molecular evolutionary biology and should be experienced in molecular biology techniques and/or computational biology. The person we are looking for should be willing to coordinate the daily operations of the GeCKo together with Prof. Axel Meyer, the director of the GeCKo.

The postdoc position is also affiliated with the new graduate school in chemical biology (for more information visit <http://www.chembiol.uni-konstanz.de/>) and the new International Max-Planck Research School in Organismal Biology (<http://cms.uni-konstanz.de/organismal-biology/>).

Appointments will be commensurate with experience at a TV-L salary scale that includes extensive health and retirement benefits. The initial contract period would be for two years with the potential for additional years of funding.

The University of Konstanz is an equal opportunity employer and one of the nine excellence± universities in Germany. It offers a stimulating research environment and is located in a lovely geographic setting in one of the most beautiful areas of Germany.

Applications should be send as one pdf file to axel.meyer@uni-konstanz.de and include a CV, statement of research interests and email addresses of two references. Review of applications will commence on October 15st 2010. Starting date is flexible.

Prof. Axel Meyer, Ph.D. Lehrstuhl f<sup>l</sup>r Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 (0)7531 88 3069

[www.evolutionsbiologie.uni-konstanz.de](http://www.evolutionsbiologie.uni-konstanz.de) Axel Meyer  
<axel.meyer@uni-konstanz.de>

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### UManchester Dictyostelium Social Evolution

Postdoctoral position in The Genetics of Social Evolution in Dictyostelium discoideum at the University of Manchester

We are seeking an enthusiastic postdoctoral researcher to join a team led by Dr. Chris Thompson, Dr Jason Wolf and Dr. Danny Rozen. This joint project will use a multidisciplinary approach to understand the genetics of social evolution, using the social amoeba Dictyostelium discoideum as a model system. This is based on our recent discovery of complex partner specific social interactions in this system (Buttery N.J., Rozen D.E., Wolf J.B., Thompson C.R.L., Current Biology, 2009 vol 19 p. 1373-7). This project is multidisciplinary, utilising a combination of quantitative genetics, experimental evolution, molecular genetics and mathematical modelling to understand the multivariate elements of social evolution. You should currently hold or be about to obtain a PhD in a relevant field.

The post funded by the NERC and is available for up to 3 years.

Informal enquiries may be addressed to: Dr Chris Thompson. Tel: 0161 275 1588 or email: christopher.thompson@manchester.ac.uk

Application forms and further particulars can be obtained at <http://www.manchester.ac.uk/aboutus/-jobs/> or from

The Directorate of Human Resources Tel: +44 (0) 161

275 8836 Email: Lifesciences-hr@manchester.ac.uk

The closing date for applications is 29 September 2010. Please quote reference LS/10832

Daniel Rozen Faculty of Life Sciences Michael Smith Building Oxford Road, Manchester M13 9PT UK

phone: +44 (0)161 275 5094 fax: +44 (0)161 275 5082

daniel.rozen@manchester.ac.uk

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### UMass WeedyRiceEvolutionaryGenomics

A postdoctoral position is available in the lab of Ana Caicedo in the Biology Department at the University of Massachusetts Amherst, to work on the evolutionary genomics of weedy rice. The successful candidate will work closely with collaborators at Washington University (Olsen lab), the National Rice Research Center (Jia and Gealy labs), and the University of Arkansas (Burgos lab). Major responsibilities will include identifying genes underlying weed-adaptive traits via comparative genome scans, and use of SNP information to determine the evolutionary origin of weedy alleles. The position will involve generation, management, and analyses of whole genome sequence data. Opportunities will also exist for the development of independent research projects. A Ph.D. in population genetics, bioinformatics, or a related field is required, as well as excellent written and oral communication skills. Experience with molecular evolutionary analyses and programming is desirable, as is interest in working with next-generation sequencing data. The position is available for one year with possible extension for up to three years. While this is a non-benefited position, health insurance will be provided for the individual. Information about the lab can be found at: <http://www.bio.umass.edu/biology/caicedo/>. To apply, please send a brief cover letter with your research interests, a CV, and three letters of recommendation to: Search #R39911, c/o Lisa Barry (lisab@bio.umass.edu) Biology Department, Morrill Science Center, University of Massachusetts, Amherst, MA 01003-5810. Consideration of applications will begin October 20, 2010 and continue until the position is filled.

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

Ana L. Caicedo, Ph.D. Assistant Professor 221 Morrill Science Center phone: (413) 545-0975 Biology Department fax: (413) 545-3243 University of Massachusetts email: caicedo@bio.umass.edu Amherst, MA 01003 <http://www.bio.umass.edu/biology/caicedo> caicedo@bio.umass.edu

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## UParisSud11 PathogenComparativeGenomics

Proposal for a Post Doctoral position

Supervisor: Cécile Fairhead

UMR 8621 CNRS/ Université Paris-Sud 11

Institut de Génétique et Microbiologie

Team “Structure and Evolution of Fungal Chromosomes”

Orsay, France

<http://www.igmors.u-psud.fr/-spip.php?article666&lang=en>

Comparative genomics to study the emergence of eucaryotic pathogens

Opportunistic fungal infections, and in particular candidiasis, have become major nosocomial infections since the 1980's. *C. glabrata* now ranks as the second cause of candidiasis after *C. albicans*. It belongs to a group which includes 3 species isolated in the environment (ie non-pathogenic), and 3 pathogenic species. Thus this group constitutes an excellent model for the study of the evolution of pathogenicity in phylogenetically related species. The genome of *C. glabrata* was sequenced in 2004 and we have now obtained the sequence of the five other species' genomes.

The aim of this post-doctoral project is thus to compare the characteristics of the yeasts' genomes in relation to their way of life and their capacity for adaptation. Orthology tables will be constructed. Absent and amplified genes, and genes subjected to positive selection pressure will be searched for. Gene maps (synteny maps) will be constructed in order to test the hypothesis of massive chromosome rearrangements in pathogenic yeast species.

The candidate should have a strong background in bioinformatics and genomics. He/she will work in close partnership with O. Lespinet (IGM), and, with regards to the positively selected genes, with G. Aguileta (CRG,

Barcelona, Spain) and T. Giraud (ESE, Orsay).

The Postdoctoral position is funded for 18 months by the Région Ile-de-France (DIM Malinf). Net salary will be around 2000EUR per month. The applicant should have defended his/her PhD thesis no more than 5 years before the beginning of this position, and not have already had a post-doc of 18 months or more, funded by the Région. Potential candidates should send a C.V., the names of three references and a letter of motivation by email to [cecile.fairhead@u-psud.fr](mailto:cecile.fairhead@u-psud.fr). The deadline for application is November 1, 2010.

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Tatiana

Tatiana Giraud

Departement Genetique et Ecologie Evolutives Laboratoire Ecologie, Systématique et Evolution UMR 8079 CNRS-UPS-AgroParisTech Bâtiment 360 Université de Paris-Sud 91405 Orsay cedex France

phone: +33 1 69 15 56 69 + 33 6 34 64 45 14 fax: +33 1 69 15 46 97

English: [http://www.ese.u-psud.fr/pages\\_perso/-spip.php?article21](http://www.ese.u-psud.fr/pages_perso/-spip.php?article21) Francais: [http://www.ese.u-psud.fr/pages\\_perso/spip.php?article41](http://www.ese.u-psud.fr/pages_perso/spip.php?article41)

<http://www.ese.u-psud.fr/> Tatiana Giraud  
<tatiana.giraud@u-psud.fr>

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## UPierreMarieCurie Bioinformatics

Post-doctoral position in yeast genomics, at the Université Pierre et Marie Curie (UPMC) 'CNRS, 75006 Paris, FRANCE

A CNRS-funded position in bioinformatics is available for two years, to be filled before December 2010. The post-doctoral fellow will join an interdisciplinary laboratory gathering biologists, mathematicians, physicists and computer scientists around the unifying theme of microorganism genomics.

This position is part of a large collaborative project funded by the ANR, which relies on a unique combination of comparative, functional and population genomics to comprehensively describe, both at the inter- and intra-specific levels, an entire eukaryotic clade. The objective is to unravel the molecular mechanisms driving the evolution of major cellular processes such as replication, recombination, phenotypic diversification and genome dynamics, through the study of a poorly

explored monophyletic group of yeasts. This clade offers an outstanding compromise between a broad evolutionary range, a good conservation of genome organization and major heterogeneities in GC-content. This unique combination associated with a remarkable experimental flexibility will provide the opportunity to decipher the molecular bases of major evolutionary changes, both at the structural and at the functional levels.

The post-doctoral fellow's main project will be to explore the mechanisms of genome evolution through the combined analysis of large data sets issued from whole genome sequencing and resequencing data, ancestral genome reconstruction and genome-wide replication/recombination patterns. This work will permit to answer long-standing questions about the interplay between replication/recombination and the dynamics of chromosome structure, gene birth, mutation rate and GC-content in eukaryotic genomes.

The post-doctoral fellow should be qualified in data analysis, programming and statistics. A good experience in genomics is required. We are looking for highly motivated candidates who have an interest for fundamental biological questions related to genome evolution.

Contact: gilles.fischer\_at\_upmc.fr

Further information about the host laboratory can be found at:

[http://www.upmc.fr/fr/recherche/pole\\_4/-pole\\_vie\\_et\\_sante/genomique\\_des\\_microorganismes\\_fre.3214.html](http://www.upmc.fr/fr/recherche/pole_4/-pole_vie_et_sante/genomique_des_microorganismes_fre.3214.html)

Few Publications of the team:

Payen C., Fischer G., Marck C., Proux C., Sherman D.J., Coppée J.-Y., Johnston M., Dujon B., Neuvéglise C. Unusual composition of a yeast chromosome arm is associated with its delayed replication. (2009) *Genome Research* 19(10):1710-1721 The Genolevures consortium. Comparative genomics of protoploid Saccharomycetaceae. (2009) *Genome Research* 19(10):1696-709. Payen C, Koszul R, Dujon B and G Fischer, Segmental duplications arise from Pol32-dependent repair of broken forks through two alternative replication-based mechanisms (2008) *PLoS Genetics* Sep 5;4(9):e1000175 Fischer G, Rocha EP, Brunet F, Vergassola M and B Dujon. Highly variable rates of genome rearrangements between Hemiascomycetous yeast lineages. (2006) *PloS Genetics*, 2(3):e32, 253-61 Koszul, R, Dujon B and G Fischer. Stability of large segmental duplication in the yeast genome. (2006) *Genetics*, 172(4):2211-22 Koszul R., Caburet S., Dujon B. and G. Fischer. Eucaryotic genome evolution through

the spontaneous duplication of large chromosomal segments. (2004) *The EMBO Journal*, 23, 234-43 Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich JM., Beyne E., Bleykasten C., Boisramé A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud JM., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard GF., Straub ML., Suleau A., Swennene D., Tekaiia F., Wésolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P. & Jean-Luc Souciet. Genome evolution in yeasts. (2004) *Nature*, 430, 35-44.

Gilles Fischer

FRE3214 CNRS <sup>3</sup>Génomique des Microorganismes<sup>2</sup> Université Pierre et Marie Curie Equipe Biologie des Génomes Les Cordeliers 15 rue de l'Ecole de médecine 75006 PARIS

[http://www.upmc.fr/fr/recherche/pole\\_4/-pole\\_vie\\_et\\_sante/genomique\\_des\\_microorganismes\\_fre.3214.html](http://www.upmc.fr/fr/recherche/pole_4/-pole_vie_et_sante/genomique_des_microorganismes_fre.3214.html)

tel: +33 (0)1 44 27 81 39

Gilles Fischer <gilles.fischer@upmc.fr>

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## UProvence Speciation

2 years Post doc position speciation at post genomic era the candidate should have a robust bioinformatics background. the position can start the 10/01/2010 contact Pierre Pontarotti Pierre.pontarotti@univ-provence.fr

Pierre Antoine Pontarotti

Directeur de Recherche CNRS

UMR 6632 Université de Aix Marseille/CNRS . Equipe Evolution biologique et Modélisation <http://sites.univ-provence.fr/evol/> Pierre PONTAROTTI <Pierre.Pontarotti@univ-provence.fr>

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## URochester PopulationGenomics

Postdoctoral position, University of Rochester

A postdoctoral position is currently available in the laboratory of Daniel Garrigan in the Biology Department at the University of Rochester. The Garrigan laboratory focuses on using population genomics data to address questions about speciation in natural populations. The candidate for this position will be involved in one (or more) of several projects involving genome assembly and alignment, and the statistical analysis of population structure, gene flow and natural selection using data from a variety of model taxa, including primates and *Drosophila*.

The successful candidate should have a strong background in population genetics and bioinformatics. Knowledge of programming languages and proficiency in unix-based computational environments is desirable. The group interacts and collaborates with other laboratories in the department, including those of Daven Presgraves, Allen Orr, and John Jaenike.

Please direct inquiries and electronic applications (please attach a pdf of a CV, copies of relevant publications and two letters of recommendation) to Daniel Garrigan at dgarriga@bio.rochester.edu. The starting date is negotiable and the compensation level will depend upon experience.

Daniel Garrigan Department of Biology University of Rochester Rochester, NY dgarriga@bio.rochester.edu  
daniel.garrigan@rochester.edu

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## USheffield 2 EvolutionInsectImmunity

Two postdoctoral positions opening soon.

This is an ideal opportunity for ambitious postdoctoral research fellows to work at the interface between evolution of insect immunity, bacterial resistance evolution and evolutionary applications. This project explores a novel approach to understanding why microbial resistance evolution against insect immune systems is rare

and how this can inform antibiotic therapies.

Two postdoctoral positions are available in Jens Rolffs group at the University of Sheffield, UK.

Essential requirements: A PhD or equivalent experience in microbiology (post 1) or insect immunology/molecular biology (post 2). A track record of publishing 1st author papers in leading specialist or multidisciplinary journals. A strong interest in interdisciplinary research and interactions.

The positions are funded by the European Research Council (ERC) for five years and will start in November or soon thereafter. The job details and application forms will be posted on the Sheffield University homepage (<http://www.shef.ac.uk/jobs/>) soon. For further information, please contact Jens Rolff (jor@sheffield.ac.uk) (<http://e3.group.shef.ac.uk/people/jens-rolff/>).

Jens Rolff <jor@sheffield.ac.uk>

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## UStellenbosch CytogenomicsAfricanAntelope

UStellenbosch.CytogenomicsAfricanAntelope

University of Stellenbosch: Evolutionary Genomics Group

A two-year postdoctoral fellowship is available immediately in the Robinson lab to study molecular cytogenetic relationships of bovids, and African antelope in particular. The Bovidae are noteworthy for the dominance of Robertsonian (Rb) chromosomal fusions in shaping the genomes of many species. Our recent work on this group shows the use of these rearrangements in determining evolutionary relationships is problematic, and that homoplasy predominates in the chromosomal dataset. In sharp contrast, variation in the morphology of the X chromosome appears to hold considerable promise for resolving some of the persistent problems associated with the classification of this group of mammals.

We propose to: (i) Identify intrachromosomal rearrangements of the X chromosome using high density BAC mapping and analysis by microdissected painting probes and FISH. (ii) Develop high-resolution comparative maps that define the borders and orientation of rearranged segments in a species-rich taxonomic sample, and test these data for defining evolutionary rela-

tionships among species of the subfamilies and tribes of Bovidae. (iii) Shed light on the molecular mechanisms underlying the transposition and inversion of reshuffled segments.

A background in molecular biology, a proven track record in the use of chromosome painting or gene mapping by fluorescence in situ hybridization (FISH), and experience in using bioinformatic tools and methods of genome analysis is required. A strong interest phylogenetics would be an advantage.

Applicants should provide a CV, statement of research experience and names of three academic referees to:

Professor Terry Robinson (E-mail: [tjr@sun.ac.za](mailto:tjr@sun.ac.za)) Department of Botany & Zoology Stellenbosch University Private Bax X1 Matieland 7602 South Africa <http://www.sun.ac.za/botzoo>

Tel: +27 21 808 39 55 Fax: +27 21 808 24 05

<[tjr@sun.ac.za](mailto:tjr@sun.ac.za)>

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## Valencia Dublin GenomeDuplication

Position available: Post-doctoral position Duration: one year with possible extension to one year more Starting Date: 1st of November Group and Place: Group of Integrative and Systems Biology, Department of Abiotic stress, Instituto de Biología Molecular y Celular de Plantas (CSIC-Universidad Politécnica de Valencia), Valencia (Spain), and Evolutionary Genetics and Bioinformatics Laboratory, University of Dublin, Trinity College Dublin (Ireland). Group Leader: Mario A. Fares Project title: The Impact of Genome Duplication in the Evolutionary innovation of functional traits Brief Project Description: It is widely accepted that genome duplication has played a major role in the emergence of biological diversity. This is particularly noticeable in plants (for example in Angiosperms) where both the emergence and persistence of genome duplication are heavily correlated with the evolution of novel ecological capabilities. Gene duplication is an important generator of genetic variability, which is the source of phenotypic variation. How important a mechanism is genome duplication in the emergence of functional novelties? What genome-wide changes are accompanying the emergence of these novelties? How gene/genome duplication synergizes with other mechanisms to facilitate functional innovation? In this project we will address all these questions and other related ones follow-

ing theoretical (computational) and experimental approaches. The computational approaches will be based on the analysis of genome-wide functional divergence after gene duplication using full genomes from organisms that have undergone one or more genome duplication events during their evolution. The second computational approach will consist on simulation studies of models of gene duplication in digital organisms. The experimental approaches will simulate in vivo duplication processes in model bacterial and yeast cells, which will be followed by the experimental evolution of these cells. Candidates should hold a PhD in a discipline of life sciences (Biology, Biochemistry, Microbiology, etc.). No previous experience in computer programming is required, although it is preferred. Our group is young, enthusiastic and is experienced in several areas such as experimental evolution, bioinformatics and evolutionary ecology. The candidate is also expected to have a strong interaction with members of the group based in Ireland (TCD). Interested candidates please contact me for further information at: Dr. Mario A. Fares Email: [mfares@ibmcp.upv.es](mailto:mfares@ibmcp.upv.es) or [faresm@tcd.ie](mailto:faresm@tcd.ie)

“Mario A. Fares” <[mfares@ibmcp.upv.es](mailto:mfares@ibmcp.upv.es)>

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## Vienna NGS data analysis

A postdoctoral position is available to work on Illumina sequencing data analysis

We are seeking for a highly motivated researcher, who is interested to join a team of postdocs and PhD students collaborating on the analysis population re-sequencing and RNA-Seq data. The successful candidate will have strong bioinformatic skills, a solid background in biology, and a good communication aptitude. We particularly encourage scientists to apply, who have also interest to pursue their own research project(s).

The post is based at the Institute of Population Genetics at the Vetmeduni Vienna. The institute hosts a dynamic group of researchers covering a diverse range of topics, such as functional *Drosophila* genetics, population genetics and bioinformatics (<http://i122server.vu-wien.ac.at/pop>). The Vienna research area is one of the centers of population genetics and evolutionary biology in Europe (<http://www.evolvienna.at>), with a particular strength in quantitative biology.

The position is immediately available and the search continues until the position is filled.

Applications should be sent to C. Schlötterer (christian.schloetterer@vetmeduni.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 Bau-  
mann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390  
<http://i122server.vu-wien.ac.at/pop> Vienna Graduate  
School of Population Genetics [http://www.popgen-  
vienna.at](http://www.popgen-<br/>vienna.at) VetCore Illumina Sequencing Service [http://-  
/i122server.vu-wien.ac.at/pop/seq/VetCore2.htm](http://-<br/>/i122server.vu-wien.ac.at/pop/seq/VetCore2.htm)  
schlotc@gmail.com

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## WashU

### WeedyRiceEvolutionaryGenomics

A postdoctoral position is available in Kenneth Olsen's lab at Washington University in St. Louis, for work on a recently funded NSF project examining the evolutionary genomics of weedy rice. This project seeks to understand the mechanisms underlying the evolution of weedy strains of rice, which have become a major agricultural weed worldwide. The position will involve close collaboration with researchers at the University

of Massachusetts-Amherst (Caicedo lab), the National Rice Research Center (Gealy and Jia labs), and the University of Arkansas (Burgos lab).

The successful candidate will be responsible for coordinating a SNP genotyping project and conducting a QTL mapping study of weed-adaptive traits. Opportunities will also exist for collaboration on population genetic analyses of neutral and candidate gene sequences, as well as the development of independent research projects. A PhD in population genetics, bioinformatics, or plant genetics is required, as are excellent written and oral communication skills. Prior experience with next generation sequence data, SNP genotyping, or other large genetic datasets is desirable. Information on the Olsen lab can be found at: <http://biology4.wustl.edu/olsen/>. The position is available for one year, with the possibility of extension for up to three years of support. Starting date is negotiable. Applications should include a brief cover letter (including contact information for three references) and a CV, which should be submitted electronically to: [kolsen@wustl.edu](mailto:kolsen@wustl.edu). Review of applications will begin October 20 and continue until the position is filled.

Kenneth M. Olsen, PhD Assistant Professor Biology Department, Box 1137 Washington University St. Louis, MO 63130-4899

Ph. (314) 935-7013 Fax (314) 935-4432

email: [kolsen@wustl.edu](mailto:kolsen@wustl.edu)

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## WorkshopsCourses

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**Cambridge CompMolEvolution  
Apr11-20**



## Computational Molecular Evolution

11-20 April 2011 Hinxton, Cambridge, UK <http://tinyurl.com/2vllzx4> Deadline for applications: 26 November 2010

Course summary This Wellcome Trust Advanced Course aims to provide researchers with the theoretical knowledge and practical skills required to carry out molecular evolutionary analysis on their own data, as well as on data drawn from sequence databases. The course will combine basic assumptions and ideas fundamental to the field with discussion of cutting-edge methodologies, and is therefore relevant to researchers with a range of different experience levels.

This course is essentially the same as that which was run successfully in Hinxton in 2009 and in Crete in 2010 (see <http://abacus.gene.ucl.ac.uk/CoME>).

Programme \* interpretation of molecular phylogenetic trees and sequence alignments \* genomics resources, sequence searching and and sequence alignments \* phylogeny reconstruction and models \* hypothesis testing in phylogenetics \* coalescent model and inference from population data

Course organisers \* Nick Goldman (European Bioinformatics Institute, Hinxton, UK) \* Ziheng Yang (University College London) \* Aidan Budd (European Molecular Biology Laboratory, Heidelberg) \* Alexandros Stamatakis (Technical University of Munich)

Guest instructors \* Martin Embley (University of Newcastle, UK) \* Adrian Friday (University of Cambridge, UK) \* Olivier Gascuel (LIRMM-CNRS, Montpellier, France) \* Javier Herrero (European Bioinformatics Institute, Hinxton, UK) \* John Huelsenbeck (University of California, Berkeley, USA) \* Carolin Kosiol (University of Veterinary Medicine, Vienna, Austria) \* Adam Leache (University of Washington, USA) \* Aoife McLysaght (Trinity College Dublin, Ireland) \* Bill Pearson (University of Virginia, USA) \* Bruce Rannala (University of California, Davis, USA) \* Antonis Rokas (Vanderbilt University, USA) \* Jeff Thorne (North Carolina State University, USA) \* Maria Anisimova (ETH Zurich, Switzerland) \* Aglaia Antoniou (Institute of Marine Biology and Genetics, HCMR, Greece) \* Natalie Cusimano (LMU Munich, Germany) \* Clemens Lakner (Florida State University, USA) \* Tim Massingham (European Bioinformatics Institute, Hinxton, UK)

For full details, see <http://tinyurl.com/2vllzx4> Nick Goldman <goldman@ebi.ac.uk>

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## CzechRepublic ComparativeGenomics Jan9-21

Workshop on Comparative Genomics, Europe 2011

Cesky Krumlov, Czech Republic

9 - 21 January 2011

Application Deadline: 15 October is the preferred application deadline, after which time people will be admitted to the course following review of applications by the admissions committee. However, later applications will certainly be accepted.

<http://www.molecularevolution.org/workshops/WCG>  
Scott A. Handley, Michael Cummings and Dag Ahrens, Co-Directors Naiara Rodriguez-Ezpeleta, Associate Directors

The Workshop on Comparative Genomics consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of comparative genomics focusing on next-generation sequencing data. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in comparative genomics. Included among the faculty are developers and other experts in the use of computer programs and packages such as AUGUSTUS, Ensembl, GMOD/GBrowse, MEGAN, MIRA, and Scripture who provide demonstrations and consultations. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of short-read sequence data, analytical methods, comparative structure of genomes, SNP detection and analysis, genome visualization tools and related areas are encouraged to apply for admission. Lectures and computer laboratories total ~90 hours of scheduled instruction. Admission is limited and highly competitive, with admissions decisions determined by an international committee. No programming experience is required.

Topics to be covered include:

- Sequencing technologies: short-read sequencing technologies of various types
- Assembly and alignment: basic analyses in de novo and re-sequencing studies
- Gene finding and annotation: functional description of genomic data
- Genome characterization: gene content; genome structure; synteny; SNPs
- Assigning sequences to taxonomic groups in metagenomic studies
- Evolu-

tionary genomics - Population genomics

2010 Fee: 1800 USD. Fee includes opening reception and mid-course dinner, but does not include other meals or housing. Special discounted pricing has been arranged for hotels, pensions and hostels.

Offered in partnership with the Graduate Research School in Genomic Ecology (GENECO) <http://www.geneco.se/> For more information and online application see the Workshop web site -

<http://www.molecularevolution.org/workshops/WCG>

The Workshop on Molecular Evolution is also being offered immediately after the Workshop on Comparative Genomics.

<http://www.molecularevolution.org/workshops/WME>  
mike@umiacs.umd.edu

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### CzechRepublic MolEvol Jan23-Feb11

Workshop on Molecular Evolution, Europe 2011

Cesky Krumlov, Czech Republic

23 January - 4 February 2011, individual research session 4 - 11 February 2011

Application Deadline: 1 October 2009

<http://www.molecularevolution.org/workshops/WME>  
Michael P. Cummings, Scott A. Handley and Naiara Rodriguez-Ezpeleta Co-Directors

The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in molecular evolution. Included among the faculty are developers and other experts in the use of computer programs and packages such as BLAST, BEAST, Clustal W and Clustal X, FASTA, FigTree, Genealogical Sorting Index, GARLI, LAMARC, MAFFT, Migrate-N, MrBayes, PAML, PAUP\*, and SeaView who provide demonstrations and consultations.

The course is designed for established investigators, postdoctoral scholars, and advanced graduate students with prior experience in molecular evolution and related fields. Scientists with strong interests in molecular evolution, phylogenetics, population genetics, and related fields are encouraged to apply for admission.

Scheduled lectures and computer laboratories total ~90 hours of 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.

Topics to be covered include:

- Protein evolution and 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 and Bayesian theory and practice in phylogenetics and population genetics: coalescent theory; estimation of population genetic parameters - Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conservation; population genetics - Detecting positive selection: theory and practice; codon models - Dating phylogenies: theory and practice
- Molecular evolution of recently diverged species

2011 Fee: 1800 USD, plus an additional 750 USD for the highly recommended, but optional, third week of all-computer laboratory for work on your own data with guidance and consultation of some faculty and teaching assistants. Fees include opening reception and mid-course dinner, but do not include other meals or housing. Special discounted pricing has been arranged for hotels, pensions and hostels.

For more information and online application see the Workshop web site -

<http://www.molecularevolution.org/workshops/WME>

The Workshop on Comparative Genomics is also being offered immediately before the Workshop on Molecular Evolution, see <http://www.molecularevolution.org/workshops/WCG> Michael P. Cummings, PhD Center for Bioinformatics and Computational Biology Biomolecular Sciences Building University of Maryland College Park, MD 20742 USA mike@umiacs.umd.edu phone: +1.301.405.9903 fax: +1.301.314.1341 <http://serine.umiacs.umd.edu> <http://serine.umiacs.umd.edu>

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### Edinburgh ComplexDiseaseGWAS Oct15

The successes, challenges and prospects for next generation GWAS analyses for complex diseases 15.Oct.2010 Edinburgh <http://www.allpower.de/-pages/ICSB2010.html> The hopes for personalized medicine reached new heights with increasingly detailed SNP-arrays and affordable large scale sequencing, however these hopes were tempered by the relatively low predictive power for the observed disease heritability by the resulting genome wide association studies (GWAS). With this special topics workshop titled The successes, challenges and prospects for next generation GWAS analyses for complex diseases, we are aiming to identify new statistical and computational methods to overcome the current roadblocks in medical genomics.

The workshop takes place in Edinburgh as part of this years International Conference on Systems Biology (ICSB2010) on the 15. October and features a fantastic list of high profile researchers from a wide range of disciplines and institutes around the world. The workshop will create a productive environment, where new collaborations are formed and new experimental setups discussed. Please visit the workshops web page for more details of the program and information how to register.

Cheers Denis

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“Denis C. Bauer” <d.bauer@uq.edu.au>

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## Phyloseminar MSalemi Sept20

Please come to a free online seminar this coming Monday:

Marco Salemi speaks Monday, September 20th at 15h PDT (3:00pm) on “Phylogenetic challenges in the retroviridae branch of the tree of life”

The representation of all virus families within a single phylogenetic tree may be a misleading description of their evolutionary history. First, it is unlikely that all viruses originated from a unique common ancestor. Second, viruses (retroviruses in particular) can integrate into the host genome and be transmitted vertically as well horizontally. Third, different viral genera can evolve according to dramatically different molecular

clocks. Three paradigmatic examples from the retroviridae family will be considered here: the simian foamy viruses (SFVs); the primate T-lymphotropic viruses (PTLVs), which include HTLV and STLV, and the primate lentiviruses (PLVs), which include SIV, HIV-1 and HIV-2. SFV is an example of an ancient virus that has been co-evolving with its primate hosts over the last 30 million years. PTLVs emerged around 300 thousand years ago and are characterized by frequent interspecies transmissions and multiple introductions into human populations since prehistoric times. PLVs have a much more recent origin and only within the last 200 years have been able to spread successfully within the human population. The complex relationship between population dynamics and evolutionary time-scale of these retroviruses, as well as the challenge of their integration within the tree of life will be discussed.

For more information on how to attend this and other seminars, visit [phyloseminar.org](http://phyloseminar.org).

[ematsen@gmail.com](mailto:ematsen@gmail.com)

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## Phyloseminar PLemey Sept9

Note that we ended up having a technical difficulty last presentation, and this is an announcement for the rescheduled talk.

Philippe Lemey speaks Thursday September 9 at 9am PDT on “Phylogenetic diffusion models and their applications in viral epidemiology”

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

for phylogeographic hypothesis testing.

For more information on how to attend this and other seminars, visit [phyloseminar.org](http://phyloseminar.org).

[phyloseminar.org](http://phyloseminar.org)

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## RiodeJaneiro Biodiversity Dec5-17

\*\*\*\*\*VERSION EN CASTELLANO ABAJO\*\*\*\*\*

ACCEPTING APPLICATIONS for the seventh intensive course of the Red de Genética de la Conservación (ReGeneC): “Genetics and the Conservation of Biodiversity,” December 5-17, 2010.

Application deadline: October 15, 2010. See “Preinscripción,” <http://regenec.ula.ve/taller/dec2010/preinscripcion.html> for application process details.

This 12-day intensive graduate course, directed primarily at Latin American postgraduate students and young professionals, will be offered in Spanish at the Laboratório Nacional de Computação Científica (Petrópolis, Rio de Janeiro, Brazil). Participating faculty confirmed to date represent five Latin American countries (Argentina, Brazil, Chile, Uruguay, and Venezuela), and a wide array of scientific perspectives within this maturing field.

The course combines discussion sessions, hands-on data analysis, and in-depth review and presentation of ongoing research by participating students, with formal lectures in project design, marker choice, statistical analysis, phylogenetics, phylogeography, and population genetics. Throughout the course, we emphasize practical applications to the real-world process of conservation.

Organized by Universidade Federal do Rio de Janeiro in collaboration with ReGeneC members, this year's course is supported by the Conselho Nacional de Pesquisas (CNPq), American Genetics Association (AGA), Instituto de Ecología y Biodiversidad (IEB), Banco do Brasil, and the Red de Datos de la Universidad de Los Andes (RedULA).

For more information, please visit our website <http://->

[regenec.ula.ve/taller/dec2010/](http://regenec.ula.ve/taller/dec2010/) or send an email to [regenec@gmail.com](mailto:regenec@gmail.com) or [regenec@ula.ve](mailto:regenec@ula.ve).

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PREINSCRIPCIÓN ABIERTA para el séptimo curso intensivo de la Red de Genética de la Conservación (ReGeneC): “La Genética y la Conservación de la Biodiversidad,” 5-17 de diciembre de 2010.

Fecha límite: 15 de octubre de 2010. Ver “Preinscripción,” <http://regenec.ula.ve/taller/dec2010/preinscripcion.html> para detalles del proceso de preinscripción.

Este curso intensivo de 12 días, dirigido principalmente a estudiantes de posgrado y jóvenes profesionales latinoamericanos, se ofrecerá en Castellano en el Laboratório Nacional de Computação Científica (Petrópolis, Rio de Janeiro, Brazil). Participan, en el curso, investigadores de cinco países latinoamericanos (Argentina, Brasil, Chile, Uruguay y Venezuela), con una amplia gama de enfoques dentro de este campo emergente.

El curso combinará sesiones de discusión, clases prácticas de análisis de datos y revisión profunda y presentaciones de investigación activa por los estudiantes, con ponencias formales en diseño de proyectos, selección de marcadores, análisis estadísticos, filogenia, filogeografía y genética de poblaciones. A través del curso, se enfatizarán aplicaciones prácticas al proceso de conservación en el mundo real.

Organizado por la Universidad Federal de Rio de Janeiro, en colaboración con los otros miembros de la ReGeneC, esta versión del curso recibe apoyo financiero del Conselho Nacional de Pesquisas (CNPq), American Genetics Association (AGA), Instituto de Ecología y Biodiversidad (IEB), Banco do Brasil, y la Red de Datos de la Universidad de Los Andes (RedULA).

Para más información, visite nuestro sitio web <http://regenec.ula.ve/taller/dec2010/> o contáctenos por correo electrónico en las siguientes direcciones: [regenec@gmail.com](mailto:regenec@gmail.com) o [regenec@ula.ve](mailto:regenec@ula.ve).

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Maria A. Oliveira-Miranda Executive Coordinator ReGeneC [regenec@gmail.com](mailto:regenec@gmail.com)

[kmrodriguezclark@gmail.com](mailto:kmrodriguezclark@gmail.com)

Instructions: To be added to the EvoDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvoDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvoDir direct them to the email [evolDir@evol.biology.McMaster.CA](mailto:evolDir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA) and processed later. In either case, please do not expect an instant response.

## Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.