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# E v o l D i r

March 1, 2009

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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### AMNH NewYork PathogenEvolution Apr2-3

EXPLORING THE DYNAMIC RELATIONSHIP BETWEEN HEALTH AND THE ENVIRONMENT CALL FOR POSTERS: SESSION ON PATHOGEN EVOLUTION AND THE ENVIRONMENT The Center for Biodiversity and Conservation Milstein Science Symposium American Museum of Natural History New York City, New York, USA 2 & 3 APRIL, 2009 <http://symposia.cbc.amnh.org/health> Health and the environment are deeply intertwined for populations, species, and ecosystems, as well as for human lives and livelihoods. Understanding these relationships is increasingly critical in the context of our changing world and the accelerating loss of biodiversity. This two-day

conference will present a diversity of viewpoints and experiences, spanning the natural, medical, and social sciences, as well as policy planning. Please visit <http://symposia.cbc.amnh.org/health> for the list of confirmed speakers and the program so far.

#### Call For Posters

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

Abstract Submission Deadline: 5 February 2009

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

To be considered for the Poster Session, please submit an abstract (see sample). <http://symposia.cbc.amnh.org/health>

symposia.cbc.amnh.org/archives/biocultural/pdf-docs/sample-abstract-submission.pdf Abstract Format Authors - List the contributing authors with the name of the presenting author in CAPITAL LETTERS. Order should be last name first for the first author, but first name first for all other authors. Write out full first names.

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

Title - Titles are limited to 150 characters or less.

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

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

Abstracts may be submitted by email to posters@amnh.org. The subject line of the email should read: (Poster Submission)

Poster Abstract Submission Deadline: 5 February 2009

Selection Committee Notification: 9 February 2009

If you require a decision before 5 February (e.g., for visa requirements to travel to New York), please state so in your email and we will do our best to accommodate your request.

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

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

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## Athens Georgia DiseaseEvolution May17-23

Ecology and Evolution of Infectious Diseases Notice of 7th Annual Workshop and Conference

Workshop and conference site: Athens, GA, USA (130 km NE of Atlanta airport)

Workshop dates: May 17-20, 2009 Conference dates: May 20-23, 2009 Website: [www.eeidconference.org](http://www.eeidconference.org)

Registration is now open for the 2009 Ecology and Evolution of Infectious Diseases Workshop and Conference in Athens, GA, USA: <http://www.eeidconference.org/-Registration/index.html> Workshop applications should be submitted by March 15. Graduate students and post-docs at universities and other institutions in the U.S. may apply at the same time for financial assistance for workshop fees, travel and housing.

Registration for the conference should be by April 15. Registration fees (\$60 for faculty and \$30 for graduate students and post-docs) can be paid online prior to the conference, with a link provided on the registration page.

Questions about this event can be directed to Sonia Altizer (saltizer@uga.edu), Pej Rohani (rohani@uga.edu) or Mike Antolin (michael.antolin@colostate.edu).

Sonia Altizer <saltizer@uga.edu>

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## Austria ImmunityParasiteCoEvolution May4-9 2

Please note: Application still open until Feb. 28th

ESF-FWF-LFUI Conference on 'The impact of the environment on innate immunity: the threat of diseases'

Dates: 4-9 May 2009

Location: University Centre Obergurgl (Ötz Valley, near Innsbruck), Austria

Scope: Innate immunity recently came into the focus of evolutionary biologists as an evolutionarily ancient, yet

astonishingly effective first-line defence against many parasites and pathogens that is shared by both vertebrates and invertebrates. This conference will focus on the question how environmental factors influence the co-evolution between innate defence mechanisms and parasite counter-defences.

Programme and applications: accessible online at [www.esf.org/conferences/09223](http://www.esf.org/conferences/09223)

Chair: Prof. Joachim Kurtz, University of Münster, DE  
Co-chairs: Dr. Sophie Armitage, University of Münster, DE - Prof. Paul Schmid-Hempel, ETH Zurich (CH)

Deadline for applications: extended to 28. February 2009

Grants: are available for young researchers to cover the conference fee and travel costs

Further information: [www.esf.org/conferences/09223](http://www.esf.org/conferences/09223) or Ms. Anne Blondeel Oman ([ablondeel@esf.org](mailto:ablondeel@esf.org))

Prof. Dr. Joachim Kurtz

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

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## Barcelona Sequencing2009 Oct1-3

NEXT GENERATION SEQUENCING: CHALLENGES AND OPPORTUNITIES

1-3 october 2009, Casa Convalescencia, Barcelona, Spain <http://ngs2009.uab.es> REGISTRATION IS LIMITED TO 150 PEOPLE

PROGRAM: This conference will focus on the computational and statistical challenges that pose NGS data. While wet lab prices are steadily decreasing, bioinformatic and statistical analyses have become a serious bottleneck. We have broadly organized the conference around two axes: technology and applications. The first part will embrace bioinformatic, statistical and computational problems. The second will raise some of the most emblematic areas where NGS has exerted a dramatic influence. The conference is designed to bring together keynote speakers, technological representatives and active researchers in the field

so that they can interact in a warm and stimulating atmosphere, and in a beautiful venue as is the early XIX century building known as Casa Convalescencia in Barcelona.

COMMUNICATIONS: Abstracts should be submitted before July 3, some will be selected for oral presentation.

REGISTRATION: The cost is 300 and includes admission, abstract book, meals (noon), coffee breaks and farewell cocktail on saturday. The meeting will be held in Casa Convalescencia (<http://www.uab-casaconvalescencia.org/>).

PLENARY SPEAKERS that have confirmed attendance so far, in alphabetical order: - Carlos Bustamante, Cornell University, NY, USA - Andrew Clark Cornell University, NY, USA - Frank Oliver Gloeckner, Max Planck Institute for Marine Microbiology, Germany - Philip Green, University of Washington, WA, USA - Martien Groenen, Wageningen Agricultural University, Holland - Roderic Guigó, Center for Genomic Regulation (CRG) Barcelona. Spain - Heinz Himmelbauer, Center for Genomic Regulation (CRG) Barcelona Spain - Michael Lynch, Indiana University IN, USA - Gabor Marth, Boston College, MA, USA - Gil McVean, Statistics Department, Oxford, UK - Douglas B. Rusch, Craig Venter Institute, MD, USA - Francisco M. De la Vega, Applied Biosystems, USA - Wang Jun, Beijing Genomics Institute at Shenzhen - Richard K. Wilson, Washington University MO, USA

INSTITUTIONAL SPONSORS Fundació Genoma Espanya: <http://www.gen-es.org/> Ministerio de Ciencia e Innovación: <http://www.micinn.org/> Universitat Autònoma de Barcelona: [www.uab.cat](http://www.uab.cat) PRIVATE SPONSORS Applied Biosystems: <http://solid.appliedbiosystems.com> Illumina: <http://www.illumina.com/> Roche: <http://www.roche-applied-science.com/> Keygene: <http://www.keygene.com> Miguel Perez-Enciso ICREA professor Dept. Ciencia Animal i dels Aliments Facultat de Veterinaria Universitat Autònoma de Barcelona 08193 Bellaterra, SPAIN Phone: +34 93 581 4225 Fax: +34 93 581 2106 [miguel.perez@uab.es](mailto:miguel.perez@uab.es) <http://www.icrea.cat/Web/ScientificForm.aspx?key=3D255> Come to the next generation meeting: <http://ngs2009.uab.es> [sebas@ramos.net](mailto:sebas@ramos.net)

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## Berlin FishEvolution Nov23-25

Dear colleagues,

We are happy to announce the International Conference: "Evolutionary Ecology of Fishes: Diversification, Adaptation and Speciation" to be held at the 23-25 November 2009 in Berlin (Germany).

Studies on fishes play a major role in the theoretical building of evolutionary ecology and the formation of species. To promote discussions and to bring together scientists and students active in the field of Evolutionary Ecology of Fishes is the aim of the forthcoming congress. Everybody who is interested is warmly welcome. See < <http://www.fishevolution.igb-berlin.de/> ><http://www.fishevolution.igb-berlin.de/> for details.

We would be happy to meet you in November in Berlin.

Dr. Jörg Freyhof Leibniz Institute of Freshwater Ecology and Inland Fisheries, Müggelseedamm 310, 12587 Berlin, Germany

Tel.: ++49/30/64181613

<http://www.igb-berlin.de/abt4/mitarbeiter/freyhof/-index.shtml> Joerg Freyhof <[freyhof@igb-berlin.de](mailto:freyhof@igb-berlin.de)>

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### BrownU Genomics Jun8-11

The American Genetic Association Annual Symposium will focus on the Genetics and Genomics of Environmental Change.

The conference will be held at Brown University in Providence, Rhode Island, 8-11 June 2009.

Registration will begin in mid-February. More information about the meeting can be found at the following website.

<http://www.brown.edu/Departments/EEB/-aga.symposium/> AGA.Symposium.Website.html

David Rand Professor of Biology Department of Ecology and Evolutionary Biology Box G-W, 80 Waterman Street Brown University Providence, RI 02912 Voice: (401) 863-2890 (Office - Walter Hall 202) (401) 863-1063 (Lab - BioMed Center 516-518) Fax: (401) 863-2166 email: [David.Rand@brown.edu](mailto:David.Rand@brown.edu) web page: <http://www.brown.edu/Departments/EEB/rand/index.htm> <http://research.brown.edu/research/profile.php?id=1100924991&r=1> [David.Rand@brown.edu](mailto:David.Rand@brown.edu)  
David.Rand@brown.edu

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### Cologne Genome Mar18-20

The Cologne Spring Meeting is an annual meeting on varying topics in the field of Genetics. It has a tradition going back to the early 1960's. The 2009 meeting – from March 18 to March 20 – will be on "The Variable Genome". The meeting features only invited talks, no parallel sessions, but ample opportunity for scientific discussions. The following speakers have confirmed their participation: Stephan Beck, Sebastian Bonhoeffer, Sydney Brenner, Brian Chadwick, Antony Dean, Manolis Dermitzakis, Anna Di Rienzo, Richard Durbin, Xavier Estivill, Adam Eyre-Walker, Timothy Frayling, Kelly Frazer, Laurence Hurst, Steve Jones, Andrew Leigh Brown, John Mattick, Rasmus Nielsen, Howard Ochman, Redmond O'Hanlon, Svante Pääbo, William Provine, Nikolaus Rajewsky, Stephan C. Schuster, Kári Stefánsson, Shamil Sunyaev, Amalio Telenti, Harmen van de Werken, Joris Veltman

For more information on the scientific programme, the venue, directions and accomodation, please see the website at <http://www.genetik.uni-koeln.de/-spring2009>. There is no registration fee.

[twiehe@uni-koeln.de](mailto:twiehe@uni-koeln.de) [twiehe@uni-koeln.de](mailto:twiehe@uni-koeln.de)

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### Crete Mediterranean Evolution Sep21-25

\*Irakleio, 23 Feb 2009\*

\*Dear colleague,\*

It is our pleasure to announce that the \*registration\* and the \*abstract submission\* of the \*/International Congress on the Zoogeography, Ecology and Evolution of Eastern Mediterranean/\* that will take place in Irakleio (Crete, Greece) between the 21<sup>st</sup> and the 25<sup>th</sup> of September (2009) are open. The deadline for receipt of abstracts and early registration will be May 31, 2009. This congress, which is the 11<sup>th</sup> of the "\*/International Congress on the Zoogeography and Ecology of Greece and Adjacent Regions/\*" series (11<sup>th</sup> ICZEGAR) includes \*all issues\*\* \*related to the animal systematic, phylogeny, phylogeography, and ecology in

the eastern Mediterranean region.

Visit our meeting website (<http://www.nhmc.uoc.gr/~iczegar11> < <http://smbe2009.org> >) for the most current information.

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

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

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

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

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

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

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

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

We would greatly appreciate your assistance in /disseminating/ this information among your colleagues and encourage them to participate. The attached file (poster.pdf) may serve as a small informative poster.

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

With Best regards

On behalf of the Organizing Committee Nikos Poulakakis

\* \*

– Nikos Poulakakis Postdoctoral Associate Department of Ecology and Evolutionary Biology YIBS-Molecular Systematics and Conservation Genetics Lab ESC 158 Yale University 21 Sachem St., New Haven, CT, 06520-8105 USA

Phone +12034323886 e-mail: niko-laos.poulakakis@yale.edu poulakakis@nhmc.uoc.gr

Nikos Poulakakis <poulakakis@nhmc.uoc.gr>

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## Ft Worden Washington Evolutionary Biol Apr23-25

The 4'th Evolutionary Biology in the Pacific Northwest meeting (EVO-WIBO) is now scheduled and will be held on April 23-25, 2010 at Ft. Worden St. Park on Washington's Olympic Peninsula. Mark your calendar! More information will become available on the meeting web site <http://www.zoology.ubc.ca/evo-wibo/> as the meeting date approaches.

Scott Nuismer Associate Professor Department of Biological Sciences University of Idaho Moscow, ID 83844 Phone: (208) 885 4096 FAX: (208) 885 7905 [http://www.webpages.uidaho.edu/~snuismer/Nuismer\\_Lab/snuismer@uidaho.edu](http://www.webpages.uidaho.edu/~snuismer/Nuismer_Lab/snuismer@uidaho.edu) [snuismer@uidaho.edu](mailto:snuismer@uidaho.edu)

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## HarvardU AnolisEvolution

Announcing a 2009 symposium on the biology of Anolis lizards.

We at the Museum of Comparative Zoology at Harvard University are pleased to announce a symposium focused on the biology of Anolis lizards to be held here at Harvard in Fall 2009. This weekend meeting follows a long but sporadic tradition of informal Anolis-themed gatherings dating back to the 1970s, and it is our honor to invite you to join us to discuss anoles during the first weekend of October.

All details, including registration, transportation, meeting schedule, and more may be found on the symposium website:

<http://webh01.ua.ac.be/funmorph/anthony/-anolis.symposium/> We hope to see you there!

Sincerely, Luke Mahler, Anthony Herrel, and Jonathan Losos

Luke Mahler <lmahler@oeb.harvard.edu>

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## Herzberg Switzerland EvolBiol Sep13-18

First announcement of the

Resurrection Ecology Symposium in Herzberg, Switzerland, September 13-18, 2009.

[www.resurrection-ecology.net](http://www.resurrection-ecology.net) This symposium aims to gather together active researchers in ecology, evolutionary biology, paleolimnology, and paleoecological disciplines to 1) present results of investigations, 2) to further define the emerging field of "resurrection ecology", and 3) share techniques (as talks or posters).

Our invited speakers are:

John Colbourne Indiana University, USA Luc De Meester Katholieke Universiteit, Belgium Nelson Hairston Jr. Cornell University, USA Charles Kerfoot Michigan Technological University, USA Peter R. Leavitt University of Regina, Canada Mathew Leibold University of Texas at Austin, USA Larry J. Weider University of Oklahoma, USA

Testing modern populations for evolutionary and ecological properties has always involved a paradox. How can one test responses that presumably occurred over several past generations? Here we advocate an alternative, experimental approach, one that combines modern ecology with paleoecology. The practice of retrieving viable propagule stages for assays opens up a new field and simultaneous experimental testing can: 1) allow experimental evaluation of alternative evolutionary and ecological theories, 2) test paleoecological conjectures, and 3) provide an "in situ" historical bioassay for gauging the importance of ecosystem perturbations.

The Herzberg Conference site will provide a relaxing venue, crafted to encourage an atmosphere for creative ferment, synthesis, and lively debate.

Spread the word - pre-registration is open!

We look forward to meeting you, Nora Brede and Piet Spaak, Eawag Dübendorf, Switzerland

[info@resurrection-ecology.net](mailto:info@resurrection-ecology.net)

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## Innsbruck EvolutionInnateImmunity May4-9

Final call for applications

ESF-FWF-LFUI Conference on 'The impact of the environment on innate immunity: the threat of diseases'

Dates: 4-9 May 2009

Location: University Centre Obergurgl (Ötz Valley, near Innsbruck), Austria

Scope: Innate immunity recently came into the focus of evolutionary biologists as an evolutionarily ancient, yet astonishingly effective first-line defence against many parasites and pathogens that is shared by both vertebrates and invertebrates. This conference will focus on the question how environmental factors influence the co-evolution between innate defence mechanisms and parasite counter-defences.

Programme and applications: accessible online at [www.esf.org/conferences/09223](http://www.esf.org/conferences/09223)

Chair: Prof. Joachim Kurtz, University of Muenster, DE Co-chairs: Dr. Sophie Armitage, University of Muenster, DE - Prof. Paul Schmid-Hempel, ETH Zurich (CH)

Deadline for applications: 8 February 2009

Grants: are available for young researchers to cover the conference fee and travel costs

Further information: [www.esf.org/conferences/09223](http://www.esf.org/conferences/09223) or Ms. Anne Blondeel Oman ([ablondeel@esf.org](mailto:ablondeel@esf.org))

Prof. Dr. Joachim Kurtz

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## KansasCity Genomics Jun11-14 Registration

## Frontiers in Arthropod Genomics

## 3rd ANNUAL ARTHROPOD GENOMICS SYMPOSIUM

June 11-14, 2009, in Kansas City, USA

[www.k-state.edu/agc/symp2009](http://www.k-state.edu/agc/symp2009)

Early registration deadline: Friday, March 20.  
Brochure available at: [www.k-state.edu/agc/symp2009](http://www.k-state.edu/agc/symp2009)

## KEYNOTE SPEAKERS:

\*Fotis C. Kafatos, Imperial College London, Evolutionary, functional and population genomics of mosquitoes: The perspective of a malariologist.

\*William M. Gelbart, Harvard University, Opportunities & Challenges for Arthropod Genomics and Informatics in the NextGen World.

## FEATURED SPEAKERS:

\* Volker Brendel, Iowa State University, Opportunities and challenges for automated genome annotation and modeling in a time of unlimited access to sequence data

\* Susan J. Brown, Kansas State University, Profiling genome transcription during *Tribolium* development: From egg to eternity

\* Jay D. Evans, USDA-ARS Bee Research Lab, Maryland, Chasing your honey: Genomic studies of honey bees and their pathogens

\* Marian R. Goldsmith, University of Rhode Island, The new silk road: From *Bombyx* to butterflies

\* David G. Heckel, Max Planck-Institute for Chemical Ecology, Jena, Germany, Insect defenses in chemical co-evolution: Transcriptional responses of the generalist herbivore *Helicoverpa armigera* to plant defense compounds, phytohormones, and insecticides

\* Kristin Michel, Kansas State University, Mosquito salivary gland interactions with malaria parasites

\* Terence Murphy, National Center for Biotechnology Information/NIH, Arthropod genome support at NCBI and the challenges of annotating genomes in the 21st century

\* Marcelo Ortigao, Kansas State University, Sand fly functional genomics and beyond

\* Yoonseong Park, Kansas State University, Evolutionary processes of the partnership between neuropeptides and their receptors

\* José Ribeiro, Laboratory of Malaria and Vector Research, NIH/NIAID, An insight into the spitome of the blood sucking Nematocera

\* Denis Tagu, French Natl Inst. for Agricultural Research, Rennes, France, The pea aphid genome to study phenotypic plasticity

\* Doreen Ware, Cold Spring Harbor Laboratory, Annotation and comparative analysis of plant genomes

\* Stephen K. Wikel, University of Texas Medical Branch, Galveston, Tick-host-pathogen research in the post-genomic era

POSTER SESSIONS: There will be two poster sessions. A few platform presentations will be chosen from submitted poster abstracts. Deadline: May 15, 2009.

SYMPOSIUM PROGRAM: The symposium sessions will begin Thursday evening, June 11, and continue on Friday and Saturday, with additional events on Saturday evening and Sunday morning. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Workshops will be held Thursday prior to the Symposium and Friday evening. Activities will conclude by noon on Sunday, June 14.

ROUNDTABLE DISCUSSION: Sunday morning will highlight a roundtable discussion led by members of the ArthropodBase Consortium regarding the generation of integrated arthropod genome databases and tools for genome projects. Symposium attendees are invited to join the fun as we share our progress by providing feedback on these projects and proposing new possibilities.

REGISTRATION: The early registration fee is \$295 (\$150 for graduate and undergraduate students) on or before March 20, and will include a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and breakfast on Sunday.

VENUE: The symposium will take place at the historic Marriott Hotel in downtown Kansas City. Participants are invited to stay Saturday night for an optional evening of jazz and KC barbeque.

INFORMATION: Visit our website, [www.k-state.edu/agc/symp2009](http://www.k-state.edu/agc/symp2009), for complete details and brochure. Add your name to the Symposium mailing list, by sending your contact information to [dmerrill@k-state.edu](mailto:dmerrill@k-state.edu).

## QUESTIONS:

Contact us at (785) 532-3482 or [dmerrill@ksu.edu](mailto:dmerrill@ksu.edu).

Please share this announcement with colleagues and students!

SPONSOR: Center for Genomic Studies on Arthropods Affecting Human, Animal and Plant Health, Kansas State University

Susan J. Brown, Professor



Director, Center for Genomic Studies on  
Arthropods Affecting Human, Animal and Plant  
Health

and

Robin E. Denell, Distinguished Professor  
Chair, AGC Symposium Organizing Committee

by

Doris Merrill, Program Coordinator  
K-State Arthropod Genomics Center  
Division of Biology, Kansas State University  
116 Ackert Hall, Manhattan, KS 66506-4901  
(785) 532-3482, dmerrill@k-state.edu

[www.k-state.edu/agc](http://www.k-state.edu/agc)

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## Leiden EvolutionPlantPollinator Mar15

It has been confirmed that the \*Evolution of plant-pollinator interactionssymposium proposed \*in the framework of systematics 2009 in Leiden (Netherlands: <http://www.biosyst.eu/>) \*was accepted\*.

Several of you have already manifested their interest (i) in taking part in that symposium, (ii) in presenting a communication. This was very helpful as a support of the proposal. It is now time to define the definitive list of speakers and to give a backbone to the symposium. I would be delighted if the interested speakers could firmly confirm their participation in the symposium \*before March 15th\* and if they could prepare \*an abstract\* of their contribution to the symposium (~1,000 characters organized as a summary). The abstracts would be welcome before \*end of March\*.

I think it is worth to underline, that I am now applying to make the proceedings of this symposium published in a book in the Cambridge University Press.

Finally, I wish to underline three last point: (i) the present mail (basically the 3rd on the topic) is the last general mailing, in the future only people having manifested their interest will be further contacted; (ii) I wish to tune broadly the symposium theme [i.e. 'Evolution of plant-pollinator interactions'], communications \*about all zoological/botanical groups\* are welcome; (iii) my list of contacts is of course limited, \*feel free

to pass this message to potentially interested colleagues (incl. students,...)\*!

Yours, Seb

–

The pollinators are increasingly focusing the attention of the scientific community. The pragmatic rationale of that interest is inherent to the economical value of pollination, estimated to 150+ billions /year. That interest for pollination and pollinators is amplified by the multiple observations of population regressions and diversity erosion, in many different regions and habitats around the World. The model for evolutionary biology that represents the pollinator-host-plant relationships, also contributes to catch the energy of many scientists.

In that context of increasing need for understanding how pollinators interact with and within their ecological web, insight in pollinators evolution are highly valuable.

In the last years, the setting up of large information systems (ecological databases, taxonomic websites, survey programs,) the rise of the computational capacities (allowing to bring together large amount of varied kinds of information), even of individual computers and the easy access to always larger parts of the species genomes, provided bases for more comprehensive studies of the pollination service and its evolutionary dimension.

The group-wide character mapping of the floral choices patterns has provided strong insights concerning the evolutionary relationships of pollinators and host plants. Likewise, the opportunity of accurately dating the phylogenetic topologies has offered an opportunity of understanding why some rapid specialisation events occurred, while some other groups remained indefinitely generalist. In the micro-evolutionary scale, textbook examples have been depicted in the molecular co-evolution of Orchids and pollinators. Finally, several studies, thanks to genome sequencing initiatives or using alternative techniques, have characterized the transcriptomes of pollinators and wide opened a door on the ways in which pollinators perceive their environment.

In that context of need for improved information concerning the pollinators and their relationships to environments and of highly active scientific sphere producing very large amount of data, it sounds us useful to set up a specific symposium, which will act as a forum facilitating quality exchanges between authorities. –

Dr Sébastien Patiny (Entomologist) 1070 Brussels BELGIUM url : <http://sites.google.com/site/patinys/>  
Sébastien Patiny <patiny.s@gmail.com>

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## London e-Biosphere Jun1-3 Registration

Registration is now open for the e-Biosphere 09 International Conference on Biodiversity Informatics at [www.e-biosphere09.org](http://www.e-biosphere09.org) < <http://www.e-biosphere09.org/> > . A discounted early registration fee will be available through 1 April 2009. Computer demonstration booths and exhibit areas are also available and information and application forms are posted on the Conference website.

Important dates:

\* 1 March 2009: Deadline for submission of poster abstracts < <http://www.e-biosphere09.org/webforms/abstract> > and applications for travel bursaries < <http://www.e-biosphere09.org/webforms/travel> > . \* 1 April 2009: Deadline for applications for exhibit space and database/software demonstrations \* 1 April 2009: Announcement of accepted poster abstracts and awards for travel bursaries \* 1 April 2009: End of reduced early registration fees \* 15 April 2009: Deadline for proposals for discussion group topics and side-events \* 1 May 2009: Registration deadline \* 1 May 2009: Release of abstract volume \* 1 May 2009: Realease of Final Conference Announcement and program \* 1-3 June 2009: e-Biosphere 09 Conference

The conference organizers have also created a series of electronic discussion forums under the umbrella of the "Online Conference Community < <http://forum.e-biosphere09.org/> > " (OCC; <http://forum.e-biosphere09.org/>). The OCC offers researchers and users of Biodiversity Informatics the opportunity to interact and prepare for the conference which will take place in London on 1-3 June 2009.

The OCC has been divided into 14 subcommunities for more focused discussions. These correspond to major research topics related to Biodiversity Informatics and its use by different groups. One session of the conference will be devoted to break-out discussion groups which will correspond with these online subcommunities, giving the participants the opportunity to meet in person to continue their interactions.

The conference organizers offer two challenges to researchers and users of Biodiversity Informatics. Subcommunities will have the opportunity to submit manuscripts that respond to these challenges for possi-

ble publication in the Conference Proceedings Volume. The challenges are:

1. Prepare a real-time demonstration for the three days of the e-Biosphere 09 conference that shows how information on new discoveries enters, propagates, and becomes interconnected with the rest of Biodiversity Informatics. For example, can a newly discovered species be described, published, and documented worldwide through a cascade of information through interconnected databases, all in three days?
2. Prepare a Position Paper that describes the information resources, database interoperability, and data analysis capabilities that each subcommunity will need five to ten years from now. For example, what new information resources and informatics capabilities will agricultural researchers need? What interoperability will they need concerning plant biology, agricultural pests, pathogens, invasive species, environmental factors, to name a few?

Questions concerning the e-Biosphere 09 Conference can be sent to [inquiries.e-biosphere09@si.edu](mailto:inquiries.e-biosphere09@si.edu).

David E. Schindel, Executive Secretary

Consortium for the Barcode of Life 202/633-0812; fax 202/633-2938; portable 202/557-1149 Email: [SchindelD@si.edu](mailto:SchindelD@si.edu) CBOL WEBSITE: <http://www.barcoding.si.edu> < <http://www.barcoding.si.edu/> >

Office and overnight delivery address:

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

Postal mailing address:

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

"Schindel, David" <[schindeld@si.edu](mailto:schindeld@si.edu)>

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## London MolluscEvolution Apr2

Molluscs in Ancient Lakes - An Ecological Perspective Symposium - Thursday April 2nd, 2009 The Linnean Society, London Sponsored by the Malacological Society

Ancient lakes are well known as aquatic island systems with high alpha and beta species diversity. Molluscs, especially gastropods, have formed a number of diverse

endemic radiations in these systems. Ecological context is critical in both mechanisms of divergence and co-existence. This symposium will bring together specialists who have approached the ecology and evolution of molluscan species flocks in several ancient lake systems and using a range of methods. The speakers will cover many of the big topics in ecology for these systems: food, babies, parasites, deep time, communities and conservation. This symposium will be relevant to all with an interest in mechanisms of diversification in species-rich groups in island systems or in benthic ecology in aquatic systems. (10:45 Arrivals) 11:00 ' Georges Dussart (President Malac Soc & Canterbury Univ.) - Opening and welcoming remarks 11:10 ' Ellinor Michel (Natural History Museum, London) - Introduction to Ancient Lakes as Model Systems 11:20 ' Thomas von Rintelen (Museum fuer Naturkunde & Humboldt Univ., Berlin, DE) - Show me thy teeth: Trophic morphology in the gastropod species radiations of the ancient lakes of Sulawesi 12:00 ' Peter McIntyre (Univ. Michigan, USA) - Life history and trophic ecology in a Lake Tanganyika (E. Africa) gastropod radiation: an experimental isotopic approach 12:40 ' Lunch (including MalacSoc AGM meeting) 1:40 ' Martin Genner (Univ. Bristol & MBA, UK) - Invasives vs. endemics in Lake Malawi (E. Africa): Competitive advantage, parasite release and massive multiplication of *Melanoides* 2:20 ' Frank Wesselingh (Naturalis, Natural History Museum, Leiden, NL) - The changing ecological context for molluscs in long-lived lakes through deep time. 3:00 ' tea and coffee and posters 3:40 ' Thomas Wilke (Univ. Giessen, DE) - Does ecology drive the evolution of endemic gastropod species in ancient Lake Ohrid (Macedonia)? 4:20 ' Christian Albrecht (Univ. Giessen) ' Lost and found: Conservation of ancient lake molluscs 5:00 ' Depart punctually for further discussion in local hostelry

Poster contributions on freshwater molluscs are welcome. Advance registration is requested (to allow us to provide appropriate refreshments in the poster session/coffee break) by writing to [e.michel@nhm.ac.uk](mailto:e.michel@nhm.ac.uk) A nominal contribution of 5 GBP is requested on arrival. Further updates and abstracts will be available on the MalacSoc website [www.malacsoc.org.uk](http://www.malacsoc.org.uk) < <http://www.malacsoc.org.uk> > . Directions to the LinnSoc are available on <http://www.linnean.org/index.php?id=215> < <http://www.linnean.org/index.php?id=215> > .

Weblinks for speakers:

Dr Ellinor Michel <http://www.sorayavillalba.com/ellinor/index.php> Dr Thomas von Rintelen <http://www.museum.hu-berlin.de/mitarbeiter/-mitarbeiter.asp?lang=1&name=thomas.rintelen> Dr Peter McIntyre <http://www.snre.umich.edu/profile/pbmcintyre> Dr Martin Genner <http://www.bio.bris.ac.uk/people/staff.cfm?key=1295>

[www.naturalis.nl/wesselingh](http://www.naturalis.nl/wesselingh) < <http://www.naturalis.nl/wesselingh> > Prof. Thomas Wilke <http://www.uni-giessen.de/cms/faculties/f08/departement-of-biology/tsz-en/wilke/staff/wilke> <<http://www.uni-giessen.de/cms/faculties/f08/-departement-of-biology/tsz-en/wilke/staff/wilke>> Dr Christian Albrecht <http://www.uni-giessen.de/cms/faculties/f08/departement-of-biology/tsz-en/wilke/staff/albrecht>

Ellinor Michel <[e.michel@nhm.ac.uk](mailto:e.michel@nhm.ac.uk)>

## Lyon Evolution Behaviour Apr6-10 2

There are still some places available to attend the 5th Meeting "Ecology & Behaviour" !

Postgraduate student or postdoctoral researcher in Behavioural Ecology ? This is the opportunity to present your results in a friendly atmosphere in front of an international audience of young researchers...

Dead-line for registration is on March 2nd.

All informations are available at : <http://serl2009.univ-lyon1.fr/spip.php?lang=en> Looking forward to meet you in April, All the best,

SERL team.

[oudenhove@biomserv.univ-lyon1.fr](mailto:oudenhove@biomserv.univ-lyon1.fr)

## Schoorl Netherlands PhD Students Aug14-19

15th European Meeting for PhD Students in Evolutionary Biology (EMSPEB) 14 - 19 August 2009. Schoorl, the Netherlands.

The EMPSEB is an annual meeting for PhD students working in various fields of evolutionary biology to share their research among each other and with a selected group of established scientists that give plenary lectures. This year's EMPSEB will take place in the dunes of the Netherlands. All attendants are giving the opportunity to present their work and the meeting is explicitly designed to create an opportunity for

graduate students to expand personal networks and discuss scientific work in a relaxed environment. The list of invited speakers include: Kevin Forster, Michael Hochberg, Claus Wedekind, Franjo Weissing, Patricia Beldade, David Hughes, Eva Kisdi, Joachim Kurtz and Virpi Lummaa.

Registration opens on 15 February and closes on 1 April 2009.

For more information please visit our website: [www.empseb2009.nl](http://www.empseb2009.nl) < <http://www.empseb2009.nl/> >

We hope to see at EMPSEB 2009

“Kurvers, Ralf” <Ralf.Kurvers@wur.nl>

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## StAndrews Darwin200 Feb9-12

Darwin 200 in St Andrews

February 2009 marks the bicentennial of Charles Darwin and 150 years of 'On the Origin of Species', one of the most influential books of the XIX century.

This very special occasion will be celebrated all over the world, and St Andrews (Fife, Scotland) is no exception.

We have put together a series of events that will take place from the 9th-12th of February. Most of these are free of charge and open to the public.

On February 12th, speakers from the University of St Andrews' Schools of Biology, Psychology, Philosophy, Divinity and History will be talking about the impact of Darwin's ideas on their research areas. Topics range from the Origin of Life to the Evolution of Culture and Language, and from the Teaching of Evolution to the links between Evolution and Human Nature. The final talk of the day will be from historian Dr Robert Prescott, 'On the track of the Beagle', relaying his exciting rediscovery of Darwin's famous ship.

For more information, please consult our webpage:

<http://darwin.st-andrews.ac.uk> Enquiries are welcome, and may be sent to: [darwin@st-andrews.ac.uk](mailto:darwin@st-andrews.ac.uk)

Best regards,

Daniel

– Daniel Barker <http://bio.st-andrews.ac.uk/staff/db60.htm> The University of St Andrews is a charity registered in Scotland : No SC013532

[db60@st-andrews.ac.uk](mailto:db60@st-andrews.ac.uk) [db60@st-andrews.ac.uk](mailto:db60@st-andrews.ac.uk)

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## StMalo France Biodiversity May17-20 CallAbstracts

Dear colleagues,

We encourage submissions of abstracts (deadline 28 february 2009) for the:

International Conference on Polyploidy, Hybridization and Biodiversity ICPHB2009 that will take place at the Palais du Grand Large, Saint-Malo (France) on 17-20 may 2009.

The recent years have seen significant advances in understanding the consequences of reticulate evolution and genome duplication that appear a major feature of eukaryotic lineages. The meeting aims at promoting knowledge exchanges and discussions on the latest developments concerning these major drivers of genome shaping and speciation. A wide range of topics will be covered such as the consequences of polyploidy on biodiversity, hybrid and polyploid speciation, meiosis and fertility in polyploid species, genome evolution and structure, transposable elements and DNA methylation, epigenetics and gene regulation, heterosis, phenotypic variation ... Registration is now open at <http://www.icphb2009.univ-rennes1.fr/> , oral and / or poster contributions are welcome.

Saint-Malo is a beautiful and well-known medieval city on the NW coast of France (Brittany region). It is visited by thousands of tourists every year due to its historical centre, attractive coasts and magnificent landscapes. We are looking forward to seeing you in Saint-Malo, France in May 2009!

Scientific Committee: Ainouche M. (France), Alix K. (France), Chalhoub B. (France), Chen J. (USA), Chèvre A-M. (France), Colot V. (France), Comai L. (USA), Doyle J. (USA), DHont A. (France), Grandbastien M-A. (France), Jahier J. (France), Jenzewski E. (France), Kovarick A. (CZ), Leitch A. (UK), Mittelsten Scheid O. (Austria), Pires C. (USA), Quixin S. (China) Rieseberg L. (Canada), Soltis P. (USA), Thiellement H.(France), Van de Peer Y. (Belgium), Veitia R. (France) , Wendel J. (USA)

M. L. AINOUCHE Evolution des Genomes et Speciation, Equipe MOB (Mecanismes à l'Origine de la Biodiversite) UMR CNRS 6553 Ecobio, Universite de Rennes 1 - CAREN Campus Scientifique de Beaulieu, Bat. 14A 35 042 Rennes Cedex France Ph. 33 (0)2 23 23 51 11

Fax 33 (0)2 23 23 50 47

Malika Ainouche <Malika.Ainouche@univ-rennes1.fr>

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**Trondheim**  
**PopGeneticsConservation May23-26**  
**2**

Conservation Genetics: Integrating Population Genetics and Conservation Biology

The networking programme ConGen within the European Science Foundation (ESF) announces a conservation genetics conference to take place in Trondheim, Norway, 23-26 May 2009. The conference integrates theoretical, experimental and applied approaches to conservation genetics, and will present up-to-date knowledge in population genetics, conservation and evolutionary biology, and genomics, by leading researchers in these fields.

Local organisers are the Norwegian Institute for Nature Research (NINA), Trondheim, Norway, and the Norwegian University of Science and Technology (NTNU), Trondheim, Norway. The conference's scientific committee is Kuke Bijlsma, University of Groningen, Volker Loeschcke, University of Aarhus, Juha Merilä, University of Helsinki, Isabelle Olivieri, Université Montpellier II, and Ettore Randi, Istituto Nazionale per la Fauna Selvatica.

Key speakers include John Avise, University of California at Irvine, Fred Allendorf, University of Montana, and Michael Soulé, Colorado. We also invite contributions as short oral presentations or posters.

The conference will be held at Rica Nidelven Hotel, Trondheim (Norway).

Information about the conference, with online registration, is available at <http://www.nina.no/?io=1001707> < <http://www.nina.no/?io=1001707> >

Deadline for registration is 1 March 2009.

Best wishes,

Kjetil Hindar, Øystein Flagstad and Laila Saksgård, NINA

Hans Stenøien, Gunilla Rosenqvist and Henrik Jensen, NTNU

“Hindar, Kjetil” <Kjetil.Hindar@nina.no>

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**Turin ESEB HostParasiteEvolution**  
**Aug24-29**

ESEB 2009 Symposium no. 26 'Post-genomic approaches to host-parasite evolution' 24 - 29 August Turin

As the deadline for abstracts approaches (the 15th), we'd like to invite you to submit abstracts to the above symposium. Invited speakers are Bregje Wertheim, University of Groningen and Frank Jiggins, University of Cambridge.

This session I hope will be both interesting and informative. More importantly, I personally warrant that I will buy all contributors a drink in Turin.

All relevant instructions at: <http://www.eseb2009.it/uk/> Organisers Steve Paterson (s.paterson@liverpool.ac.uk) Stuart Piertney (s.piertney@aberdeen.ac.uk)

– Dr Steve Paterson School of Biological Sciences University of Liverpool Liverpool, UK, L69 7ZB Tel. (+44) 151 795 4521 Fax. (+44) 151 795 4408 E-mail s.paterson@liv.ac.uk Web page: <http://pcwww.liv.ac.uk/~stevep11/PatHome.html> S.Paterson@liverpool.ac.uk S.Paterson@liverpool.ac.uk

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**Turin ESEB ParasiteEvolution**  
**Aug24-29**

We are inviting abstract submissions for oral and poster presentations in the symposium “Integrating ecology with parasite evolution” to be held on August 28 2009 at the European Society for Evolutionary Biology (ESEB) meeting in Turin, Italy (August 24-29 2009).

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

DESCRIPTION OF SYMPOSIUM: The enormous abundance of parasites and their effects on wild populations, agriculture and human health have given rise to a rapidly growing field centered on using evolution-

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

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

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

jderood@emory.edu jderood@emory.edu

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## Turin ESEB Polyploidy Aug24-29

### REMINDER

We'd like to remind you of the approaching deadline (15 February 2009) for submitting an abstract to ESEB and thus to our symposium

“Ecological consequences of polyploidy in plants and animals”.

Please note that the symposium has previously been advertised under its unabridged title “Polyploidy at the population level: ecological and population genetic consequences in plants and animals”. We apologise if this may have caused any confusion. Do not hesitate to contact us with any queries regarding this.

The symposium (nr 23) will take place at the next ESEB conference (24-29 august, Turin, Italy). We will

have space for five contributions besides the two invited contributions.

### ORGANISERS:

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

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

### INVITED SPEAKERS

Brian Husband (plants), University of Guelph <http://www.uoguelph.ca/ib/people/faculty/husband.shtml> France Dufresne (Daphnia), University of Québec à Rimouski [http://www.uqar.quebec.ca/biologie/-departement/dufresne\\_france.asp](http://www.uqar.quebec.ca/biologie/-departement/dufresne_france.asp) SUBMISSION

To submit your abstract (deadline 15 February 2009) and information about the congress, please go to <http://www.eseb2009.it/uk> Ecological consequences of polyploidy in plants and animals

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

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

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

Marc Stift

Barbara Mable

Division of Ecology & Evolutionary Biology Graham Kerr Building University of Glasgow Glasgow G12 8QQ, SCOTLAND Office: +44 (0)141 330 6637 m.stift@bio.gla.ac.uk b.mable@bio.gla.ac.uk

m.stift@bio.gla.ac.uk m.stift@bio.gla.ac.uk

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## Turin ESEB Speciation Aug24-29 Abstracts

REMINDER: SPECIATION symposium ESEB 2009 Abstract submission: 3 days left (deadline: 15 February 2009)

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

This symposium is supported by the European Networking Programme on Frontiers in Speciation Research (FroSpects) coordinated by the European Science Foundation (ESF).

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

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

given to studies addressing the genomics of behavioural divergence, the role of non-genetic mechanisms in promoting the evolution of premating isolation (cultural transmission, imprinting, epigenetics etc.) and the neurophysiological basis of behavioural divergence.

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

We expect to have 5 contributed talks. There is no limit on the number of poster presentations.

Organisers: Carole Smadja, University of Sheffield, United Kingdom ([c.smadja@sheffield.ac.uk](mailto:c.smadja@sheffield.ac.uk)) Anneli Hoikkala, University of Jyväskylä, Finland ([anneli.hoikkala@jyu.fi](mailto:anneli.hoikkala@jyu.fi)) Axel Meyer, University of Konstanz, Germany ([axel.meyer@uni-konstanz.de](mailto:axel.meyer@uni-konstanz.de)) Roger Butlin, University of Sheffield, United Kingdom ([r.k.butlin@sheffield.ac.uk](mailto:r.k.butlin@sheffield.ac.uk))

Carole Smadja, PhD Website: <http://www.carole-smadja.staff.shef.ac.uk> Department of Animal and Plant Sciences The University of Sheffield (S102TN)

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

[C.Smadja@sheffield.ac.uk](mailto:C.Smadja@sheffield.ac.uk)

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## Turin ESEB Symbiosis Aug24-29

Subject: ESEB meeting 2009: Symbiosis Symposium

We would like to invite abstract submissions for oral and poster presentations in the symposium Diversity of host-microbe symbioses to be held at the European Society for Evolutionary Biology (ESEB) meeting in Turin, Italy (August 24-29, 2009).

Description: This symposium evaluates the role of symbiotic microorganisms on the evolution of their multicellular hosts with a specific focus on the microbes' taxonomic diversity as well as their function in determining host fitness and speciation rates. Our symposium will promote cross-disciplinary exchange by bringing together biologists from different fields, including medical researchers.

Invited speakers:

Claudio Bandi, Università degli Studi di Milano, Italy

Thomas Bosch, Kiel University, Germany

To submit your abstract (deadline 15 February 2009) and obtain further

information about the congress, please go to <http://www.eseb2009.it/uk> Organisers:

Maurizio Casiraghi, Università degli Studi di Milano Bicocca, Italy

([maurizio.casiraghi@unimib.it](mailto:maurizio.casiraghi@unimib.it))

Hinrich Schulenburg, University of Kiel, Germany

([hschulenburg@zoologie.uni-kiel.de](mailto:hschulenburg@zoologie.uni-kiel.de))

Telmo Pievani, Università degli Studi di Milano Bicocca, Italy

([telmo.pievani@unimib.it](mailto:telmo.pievani@unimib.it))

Christian Braendle, Institute of Developmental Biology and Cancer, Nice, France

([braendle@unice.fr](mailto:braendle@unice.fr))

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## Turin ESEB SystemsBiol Aug24-29

\*\*\* Deadline Sunday, 15 Feb 2009 \*\*\*

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

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

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

tems to whole organisms.

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

We are looking forward to seeing you in Turin.

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

About evolutionary systems biology

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

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

In this symposium we aim to bring together researchers with an interest in the adaptive landscape at any level and researchers who want to contribute towards a synthesis of evolutionary genetics with mechanistic models of life. We believe that the new excitement in systems biology is an excellent opportunity for progress in



many fundamental evolutionary questions, if the new models that are being constructed can be extended to include fitness correlates that turn them into powerful tools for investigating the adaptive landscape. We also expect systems biology to benefit from including the rich quantitative approaches that have been developed within evolutionary genetics.

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

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## UFloridaGainesville SEEC Mar27-29 Abstracts

\*If you have already submitted an abstract, thank you. The most important updates to this request: the new deadline is February 10, 2009 and our site is now fully functional: \*<http://snre.ufl.edu/seec> Abstracts for papers and posters are now being accepted for the Southeastern Ecology and Evolution Conference (SEEC), to be held March 27-29, 2009 at the Paramount Plaza Hotel & Suites in Gainesville. Graduate students, undergraduate students, and postdoctoral researchers are invited to submit an abstract for SEEC. Presenters should be affiliated with a college or university in the southeastern United States, or with a school from outside the region but doing their research in the southeast. Abstracts related to ecology and evolution are welcomed. Examples of topics from previous conferences are: behavior, biodiversity, conservation, functional morphology, population ecology, and systematics.

Abstracts should be no more than 250 words, and may be sent to [seec2009@gmail.com](mailto:seec2009@gmail.com).

Along with your abstract please submit the following:

Name

Institutional affiliation

Status (undergraduate, graduate, or postdoc)

Whether the abstract is for a paper or poster presentation

If you would like to volunteer to moderate paper presentations

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

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

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

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## UIdaho SSE Mentoring Jun12-17

Childcare and Mentoring Programs at Evolution 2009, 12-17 June 2009, Moscow ID, USA With a recent grant from the Elsevier New Scholars Program <http://www.elsevierfoundation.org/scholar.html>, we are launching childcare services to parents who will be attending the Evolution conference and a new mentoring program available to all members of SSB, SSE and ASN. We have received funding to support these new programs for the Evolution conferences from 2009 to 2011, and both will be available options on the Evolution 2009 online registration site. We encourage all members to take advantage of these opportunities, which are detailed below. If you have any questions about either of these two programs, please contact Leah Larkin ([llarkin@pacific.edu](mailto:llarkin@pacific.edu)) or Heidi Meudt ([heidim@tepapa.govt.nz](mailto:heidim@tepapa.govt.nz)). Childcare. Professional childcare services will be available on-site at the conference. Attendees who wish to use the childcare services should sign up on the online meeting registration form indicating the number of children and their ages. Childcare will be available from 8-5 pm on each day of the conference; options will also be available for evening events. Please indicate your interest in the online registration form, and we will contact you regarding prices and details. A subsidy is available to help offset the cost of childcare services at the conference for a limited number of graduate students, postdocs and early-career parents. Please indicate your interest in applying for the subsidy, which will be allocated on a first-come, first-served basis. Evolution Mentoring Program. We are launching a FREE tri-society mentoring program through MentorNet. MentorNet is an award-winning mentoring organization that matches mentors with compatible protégés for an eight-month pairing, which includes weekly or biweekly e-mail discussion prompts to foster supportive mentoring relationships. When you create a profile in MentorNet's system and specify that you are a member of the Evolution Mentoring Program, their proprietary software will recommend suitable matches between established scientist mentors and early-career protégés (including

graduate students, post-doctoral researchers, and assistant professors) from SSB, ASN, and SSE. Paired mentors and protégés will have the opportunity to meet one another (and other participants) at a tri-society symposium luncheon at the conference as they begin their eight-month pairing. If you are a member of SSB, ASN or SSE and are interested in participating in this FREE tri-society mentoring program as either a mentor or a protégé, you can establish a profile from a Mentor-Net link on the Evolution meeting website indicating your experience and academic interests. To ensure that matches are made within the three societies, be sure to specify "Evolution Mentoring" as a requirement in your preferences. Interested mentors may sign up here ([www.MentorNet.net/mentor](http://www.MentorNet.net/mentor)), and interested protégés may sign up here ([www.MentorNet.net/protege](http://www.MentorNet.net/protege)).

Monet and the Impressionists The richest and largest collection of Impressionist paintings to come to New Zealand - only at Te Papa. Exhibition on now! Visit [www.tepapa.govt.nz/monet](http://www.tepapa.govt.nz/monet) for more details

Heidi Meudt <HeidiM@tepapa.govt.nz>

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### Idaho SSE rafting opportunity

At the end of the upcoming 2009 Evolution meetings at University of Idaho, there will be several fieldtrips. In addition to the ones posted on the meeting website, a professional rafting company is launching a 2-day rafting trip right after the meetings. The setup is described below; note that you will need to register directly with the rafting company.

The Salmon River offers some of the best rafting in the world. Travelling the canyon of this river, also known as the River of No Return, you will not only experience the tempers of glorious whitewater, but experience the second deepest canyon in North America. The timing of the trip will permit some spectacular birding opportunities (golden eagles, Lewis' woodpeckers, etc.), and there may be a chinook salmon fishery open. This is a 2-day trip, with early departure from Moscow on June 17, and return in the evening of June 18. You will spend the night camping on one of the many sandy beaches along the river.

The trip is tailored for meeting participants by Wapiti River Guides, and raft capacity is limited to twelve people, so register early. The cost is \$299, and it is paid directly to Wapiti. To reserve your spot, contact them at 1-800-488-9872 and let them know that you will at-

tend the Evolution meetings. You will be asked to pay 25% down when you register. We will arrange transportation from Moscow to the river in Riggins; the cost is unknown at this time.

Dr. Olle Pellmyr Program chair, Evolution 2009  
pellmyr@uidaho.edu pellmyr@uidaho.edu

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### Idaho SSE Registration

The registration site for Evolution 2009, the joint meetings of the Society for the Study of Evolution, American Society of Naturalists, and the Society of Systematic Biologists, at the University of Idaho is now live. The meeting website can be found at <http://evolution-meetings09.org>. It provides information on all logistic aspects of the meeting.

We look forward to welcoming you to Moscow in June.

For the Evolution 2009 organizing committee,

Olle Pellmyr

pellmyr@uidaho.edu pellmyr@uidaho.edu

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### Idaho SSE UndergradDiversity

Undergraduate Diversity at SSE/SSB 2009

For the seventh consecutive year, the Undergraduate Diversity at SSE/SSB program, funded by the Undergraduate Research and Mentoring in the Biological Sciences (URM) program at NSF, will take place at the 2009 meeting of the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB) in Moscow, ID. This year we have teamed up with staff at the National Evolutionary Synthesis Center (NES-Cent) to send up to 25 undergraduates to the meetings to present posters and receive mentoring from graduate students, postdocs and faculty in evolutionary biology. For full information and links to the application portal see

<http://www.oeb.harvard.edu/faculty/edwards/-community/application.html> The deadline for applications this year is April 1, 2009. However, proposals will be reviewed and accepted on a rolling basis, SO IT IS ADVANTAGEOUS TO APPLY

EARLY. Applications can be made online through a special portal at the National Evolutionary Synthesis Center (NESCent) [http://www.nescent.org/eog/-signup\\_evolution09diversity.php](http://www.nescent.org/eog/-signup_evolution09diversity.php). Applications consist of a title, author line and abstract of the poster to be presented by the undergraduate; a one-page statement of academic interests and career goals; and a letter of recommendation. The personal statement should address how attending the Evolution meetings will help meet these goals, and should indicate whether or not the student plans to attend graduate school, if this is known. The letter of recommendation, ideally from the undergraduate's research advisor, should indicate how inclusion of the student will increase diversity of the group participants. All materials required for application can be found at the NESCent application portal. Details on selection criteria are available at the program headquarters at

<http://www.oeb.harvard.edu/faculty/edwards/-community/application.html> We can only accept applications from students who are US citizens or permanent residents. Applications will be accepted only from students registered or very recently graduated from U.S. institutions, including Puerto Rico (i.e., no later than having finished classes during the winter or spring semesters before the meeting) and traveling to the meeting from within the US. Students demonstrating a need for funds to attend SSE/SSB will be given preference, and will be selected so that as a group, they will maximize cultural diversity among undergraduates at the meetings.

You can also contact one of the program organizers for more information:

Scott V. Edwards ([sedwards@fas.harvard.edu](mailto:sedwards@fas.harvard.edu)) Richard Kliman ([rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu))

at NESCent: Jory Weintraub ([jory@nescent.org](mailto:jory@nescent.org))  
[sedwards@fas.harvard.edu](mailto:sedwards@fas.harvard.edu) [sedwards@fas.harvard.edu](mailto:sedwards@fas.harvard.edu)

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## UIowa SMBE Jun3-7 OriginOfSpecies

Hi everybody,

First of all, Happy Darwin Anniversary! Secondly, this is an invitation to participate in a symposium on the origin of species at SMBE 2009 (Iowa City June 3-7): "Genomics of Speciation & Recent Divergences"

Symposium description: With the recent availability of full genome sequences in several pairs of closely related species, we are now at a stage where a genome-wide picture of species divergence is within reach. These new data are complemented by theory on the role of recombination in the divergence process and by statistical methods assessing gene flow during divergence. Recent studies have clearly shown that speciation history may be complex and that the genomes of incipient species diverge at strikingly heterogeneous rates. Although much of this heterogeneity may be accounted for by stochasticity of the genetic drift process, the role of natural selection in promoting or preventing genomic divergence between nascent species remains highly debated. For example, can genomic regions experiencing reduced introgression act as <sup>3</sup>genomic islands of speciation<sup>2</sup>, impeding gene flow of linked regions and thereby increase intergenomic divergence and drive reproductive isolation? In particular, while genomic co-adaptations developing independently in each species are believed to select against the transfer of genetic material from one species into the genomic background of the other, other forces such as balancing selection may actually favor introgression. This symposium will present the depth of scholarship and the variety of evolutionary processes involved in genomic divergence by conveying top researchers actively involved in studies on a wide range of organisms. We anticipate that it will be a nice opportunity to bring together genomicists for a fine-scale description of the heterogeneity of divergence across the genome with population geneticists for more precise, hypothesis-driven studies on candidate genes.

Invited speakers list is not yet finalized. There will be six 15 min slots available for contributed talks. The deadline for abstract submission for contributed talks is April 1st. Poster presentations are also welcome!

Visit the meeting website (<http://smbe2009.org>) for further information about the conference.

See you in Iowa!

/Johan Lindell, Niclas Backström, Vincent Castric, and Jody Hey

Contact info: Johan Lindell <[johan.lindell@ebc.uu.se](mailto:johan.lindell@ebc.uu.se)> Department of Evolutionary Biology, Uppsala University, Sweden

Niclas Backström <[niclas.backstrom@ebc.uu.se](mailto:niclas.backstrom@ebc.uu.se)> Department of Evolutionary Biology, Uppsala University, Sweden

Vincent Castric <[Vincent.Castric@univ-lille1.fr](mailto:Vincent.Castric@univ-lille1.fr)> CNRS, Université de Lille, France

Jody Hey <[Hey@Biology.Rutgers.Edu](mailto:Hey@Biology.Rutgers.Edu)> Department of

Genetics, Rutgers University, United States

– Johan Lindell, Ph.D. FORMAS Postdoctoral Fellow

Department of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

Phone: +46 18 4716444 Fax: +46 18 4716310 E-mail: Johan.Lindell@ebc.uu.se <http://www.egs.uu.se/-evbiol/Persons/Johan.html> <http://www.anst.uu.se/-johli118/Home.html> johan.lindell@ebc.uu.se johan.lindell@ebc.uu.se

## UIowa SMBE Jun3-7 Registration

\*\*SMBE 2009, Iowa City\*\*

“Darwin to the Next Generation ”

The 17th annual meeting of the Society for Molecular Biology and Evolution-SMBE 2009-will be held in Iowa City June 3-7, 2009, on the campus of The University of Iowa.

Visit our meeting website (<http://smbe2009.org>) for the most current information.

The SMBE 2009 scientific program will include 4 plenary talks and 23 symposia. Half of the symposia were developed by members of the Organizing Committee and the other half were selected by the Scientific Program Committee from among many proposals submitted from the SMBE community. In sum, the program will feature ~215 talks; more than half will be contributed talks selected on a competitive basis from submitted abstracts. We anticipate that 300-400 poster contributions will be highlighted in two evening poster sessions.

SYMPOSIA:

\* Biological networks from genes to populations \* Epigenetics, environment & evolution \* Evolution of networks \* Genome evolution after polyploidy \* Genomics of speciation & recent divergences \* Historical roots of molecular evolution \* Impacts of next generation sequencing on evolution \* Insect evolutionary genomics \* Molecular arms races \* Molecular basis of speciation \* Molecular evolution of biological complexity \* Molecular evolution of noncoding genes \* Molecular evolution of plant:other interactions \* Mutation accumulation in eukaryotic genomes \* Origin & evolution of animal genomes \* Population genomics: selection, demography & mutation \* Population genomics: the-

ory, computation & adaptation \* Primate functional & comparative genomics \* Reproductive protein function & evolution \* Sex-specific demography using the X \* Teaching molecular evolution \* Types of molecular evolution \* Vanishing genomes

UPDATES: Abstract deadline for award consideration: March 16th Early registration closes: April 1st Abstract deadline for consideration as contributed talk: April 1st (all abstracts received after April 1st will be posters) Abstract deadline for inclusion in the program book: May 15th

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

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

email <[john-logsdon@uiowa.edu](mailto:john-logsdon@uiowa.edu)> web <<http://-cgg.biology.uiowa.edu>><<http://cgg.biology.uiowa.edu>> <<http://euplotes.biology.uiowa.edu>><<http://-euplotes.biology.uiowa.edu>>

[john-logsdon@uiowa.edu](mailto:john-logsdon@uiowa.edu) [john-logsdon@uiowa.edu](mailto:john-logsdon@uiowa.edu)

## UIowa SMBE Mentoring Awards Jun3-7

SMBE UNDERGRADUATE DIVERSITY MENTORING PROGRAM AWARDS

2009 Annual meeting of the society for molecular biology and evolution

JUNE 3-7, Iowa City, IA

CONFERENCE WEBSITE

<http://cgg.biology.uiowa.edu/smbe/index.php>

DEADLINE FOR RECEIPT OF APPLICATIONS/NOMINATIONS: March 16th, 2009

Program outline

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students from underrepresented groups to participate in a Diversity Mentoring Program. The goals of this program are: (1) to promote diversity at the SMBE annual meeting, (2) to provide students with

the opportunity to experience the excitement of attending and presenting at an international scientific conference, and (3) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field.

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

Specific mentoring activities will include:

- \* Attending conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the 'goings-on' at a multi-day scientific conference.
- \* Interacting with the student during some mealtimes, coffee breaks and other social gatherings.
- \* Introducing the student to other undergraduates, graduate students, postdoctoral fellows and faculty members as a way of facilitating connections with potential future graduate supervisors and colleagues.
- \* Attending the poster session and SBME Undergraduate Diversity Program Award reception with the student in order to minimize/ overcome the anxiety often felt by first-time conference attendees.
- \* Serving as a contact point for the student to help resolve any issues surrounding conference registration, travel and accommodation.

#### Eligibility

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

#### Meeting Participation

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

#### Award

10 awards will be given. Award recipients will receive a travel award to cover the cost of airfare, accommodation, and registration expenses. The travel award amount will not exceed \$1,000 for within- USA contestants and \$1,500 for all other contestants. Each participant will also receive online student access to the Society journal, *Molecular Biology and Evolution*.

#### Application

1. Faculty members may nominate undergraduates

by sending a brief letter/email of recommendation to John Archibald (john.archibald[at]dal.ca). The letter should outline the student's eligibility for the award and confirm their current academic status. Also, indicate if your student would be able to present a poster. -OR- 2. Students may apply for the award themselves by providing information to John Archibald (john.archibald[at]dal.ca) on their background, academic status and an email address for their current supervisor. Students should also indicate whether they are able to present a poster.

#### Deadline

The deadline for receipt of nominations/applications is March 16th.

John M. Archibald, Ph.D. Associate Professor and Associate Graduate Coordinator Associate Director, CIFAR Program in Integrated Microbial Biodiversity Department of Biochemistry & Molecular Biology Dalhousie University Sir Charles Tupper Medical Building 5850 College Street, Halifax, Nova Scotia B3H 1X5, Canada

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

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## UIowa SMBE ReproductiveProtEvolution Jun3-7

REPRODUCTIVE PROTEIN FUNCTION AND EVOLUTION at SMBE Congress Iowa City, June 3-7, 2009

Dear colleagues,

We would like to invite interested people to submit abstracts for oral and poster presentations for the symposium "REPRODUCTIVE PROTEIN FUNCTION AND EVOLUTION", which will take place at the next Congress of the Society for Molecular Biology and Evolution in Iowa city, IA, United States (3-7 June 2009).

Abstract Submission Deadline: April 1st

Description: Reproductive proteins are responsible for traits influencing reproductive success and contributing to reproductive isolation of animal and plant species by regulating essential processes that fundamentally influence fitness. Specific genes acting at several stages of reproduction have been recently identified in different organisms, including genes involved in the regula-

tion of the interaction among male and female gametes as well as genes encoding sperm nuclear basic proteins (SNBPs) involved in DNA packaging in the sperm nucleus. Research on reproductive proteins has also benefited from advances in genomics and proteomics, which have allowed the identification and evolutionary analysis of entire suites of these proteins in both model and non-model systems. The understanding of the structure, role, tempo and mode of evolution of reproductive proteins has been a major issue in evolutionary biology and molecular evolution during the last five years, leading to the discovery that reproductive proteins evolve more rapidly than other genes, frequently as the result of adaptive evolution. The large amount of work published in recent years on this topic constitutes a perfect venue for the comprehensive review of different points of view, experimental approaches, and theoretical studies on the evolutionary biology of these proteins. We think this topic would represent a very interesting update in the evolution of a group of proteins that bears critical interest not only to people involved in reproduction research, but to a broad audience who should be able to enjoy the presentation of the recent state-of-the-art research in this field.

#### CONFIRMED SPEAKERS:

Alberto Civetta, University of Winnipeg (Canada)  
Richard G. Harrison, Cornell University (USA)  
Therese A. Markow, University of California at San Diego (USA)  
Michael F. Palopoli, Bowdoin College (USA)

Visit the meeting website (<http://smbe2009.org>) for further information about the conference, see you guys in Iowa City!

[Juan Ausi3, Chema Eirin-Lopez, Geoff Findlay]

Contact info:

Juan Ausio, University of Victoria, Victoria, Canada, [jausio@uvic.ca](mailto:jausio@uvic.ca)  
Jose M. Eirin-Lopez, University of A Coruna, A Coruna, Spain, [jeirin@udc.es](mailto:jeirin@udc.es)  
Geoff Findlay, University of Washington, Seattle, United States, [gfindlay@u.washington.edu](mailto:gfindlay@u.washington.edu)

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Jose Maria EIRIN-LOPEZ, B. Sc., Ph. D. Marie Curie OIF Post Doctoral Fellow Department of Biochemistry & Microbiology University of Victoria Petch Building, Room 258 Victoria (BC) - V8W 3P6 CANADA

Voice: +1 250 721 7069 Fax: +1 250 721 8855 email: [che@uvic.ca](mailto:che@uvic.ca) [jeirin@udc.es](mailto:jeirin@udc.es)

XENOMAR Group CHROMATIN STRUCTURE & EVOLUTION: <http://www.udc.es/grupos/xenomar/-chromevol> Jose Maria Eirin-Lopez <[che@uvic.ca](mailto:che@uvic.ca)>

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## UIowa SMBE UndergradMentors Jun3-7

### CALL FOR MENTORS SMBE UNDERGRADUATE DIVERSITY MENTORING PROGRAM AWARDS

2009 Annual meeting of the society for molecular biology and evolution

JUNE 3-7, Iowa City, IA

#### CONFERENCE WEBSITE

<http://csg.biology.uiowa.edu/smbe/index.php> Program outline

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

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

#### WE ARE SEEKING INDIVIDUALS INTERESTED IN BEING A MENTOR. Specific activities will include:

- \* Attending conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the 'goings-on' at a multi-day scientific conference.
- \* Interacting with the student during some mealtimes, coffee breaks and other social gatherings.
- \* Introducing the student to other undergraduates, graduate students, postdoctoral fellows and faculty members as a way of facilitating connections with potential future graduate supervisors and colleagues.
- \* Attending the poster session and SBME Undergraduate Diversity Program Award reception with the student in order to minimize/overcome the anxiety often felt by first-time conference attendees.
- \* Serving as a contact point for the student to help resolve any issues surrounding conference registration, travel and accommodation.

### Conference participation

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

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

If you are interested in mentoring an undergraduate at this years SMBE meeting please email John Archibald (john.archibald[at]dal.ca).

John M. Archibald, Ph.D. Associate Professor and Associate Graduate Coordinator Associate Director, CIFAR Program in Integrated Microbial Biodiversity Department of Biochemistry & Molecular Biology Dalhousie University Sir Charles Tupper Medical Building 5850 College Street, Halifax, Nova Scotia B3H 1X5, Canada

Phone: (902) 494-2536 Fax: (902) 494-1355 Webpage: <http://myweb.dal.ca/jmarchib/> Nirenberg's second reading in Moscow electrified the audience, Crick later wrote. (Whereupon, in the interest of historical accuracy, Seymour Benzer, who had been in Moscow too, mailed Crick a photograph taken of that audience, in which several people appeared to be asleep.)

Horace Freeland Judson, *The Eighth Day of Creation*

John Archibald <jmarchib@dal.ca>

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## ULondon SAGE2009 Sep14-17

**ABSTRACT SUBMISSION CLOSING 31 MARCH 2009!!**

SAGE2009 Conference - "Southeast Asian Gateway Evolution"

14-17 September 2009: Royal Holloway University of London

<http://sage2009.rhul.ac.uk> The Southeast Asian Gateway is the site of the Indonesian Throughflow between the Pacific and Indian Oceans. It is the only low latitude link between the worlds oceans, and is increasingly regarded as an important influence on global climate. The throughflow passes through the present zone of collision between Australia and SE Asia. The collision began about 25 million years ago, but SE Asia has a long

history of growth by the addition of continental fragments rifted from Gondwana dating back to the Palaeozoic. The fauna and flora display a similar complexity which is partly linked to the geology.

There is a centre of maximum diversity in the marine and terrestrial ecosystems in the Indo-Australian archipelago, and the gateway contains numerous biogeographic boundaries. The centre of the region, known to biologists as Wallacea after Alfred Russel Wallace of Wallaces Line, is an unusual region of high faunal and floral endemism. Plate tectonic reconstructions suggest that geology has played a major role in shaping the distributions of biota and the tectonic development of the region is one key to understanding the links between oceanic circulation, climate and life. However, these links are not well documented and connections between different processes are uncertain. Understanding the geological and biological history of the region, and the evolution of biodiversity, is of considerable importance in managing current and future change.

This will be a three-day multidisciplinary meeting to discuss this important region with an emphasis on reporting new ideas and exchanging views between a wide range of Earth and Life Scientists. It will promote interaction between Earth and Life Scientists working in the region. The programme will include plenary sessions, overview presentations, and breakouts for specialist groups. We seek contributions on all geological and biological aspects of the Southeast Asian Gateway, the region including Indonesia, Malaysia, the Philippines, Indochina, New Guinea and the NW Shelf of Australia.

Details of keynote speakers, accommodation, registration, pre and post conference field trips, abstract submission and important dates are available at: <http://sage2009.rhul.ac.uk/> Abstracts of not more than 400 words should be submitted by 31st March 2009.

\*\*\*\*NOTE\*\*\*\* A limited amount of funding (up to £500) will be made available to one individual from each of the following categories to allow them to attend the meeting and present either a poster or talk:

one student based in SE Asia and working on molluscs  
one researcher based in SEA Asia early career or student researchers

After submitting an abstract, please apply for funding via email to [sage2009@nhm.ac.uk](mailto:sage2009@nhm.ac.uk) . Letters of application should be no longer than 1 side A4 and include a brief biological sketch and summary of current research projects. Students should include a letter of recommendation from a supervisor.

We look forward to your participation in this meeting.

SAGE2009 Organising Committee

Ken Johnson, David Gower, Brian Rosen, Lukas Ruber,  
Suzanne Williams

Dr Lukas Ruber Department of Zoology The Natural  
History Museum Cromwell Road London SW7 5BD UK

Tel: +44 (0)20 7942 6208 Fax: +44 (0)20 7942 5054  
e-mail: l.ruber@nhm.ac.uk

[www.lukasruber.com](http://www.lukasruber.com) [www.nhm.ac.uk/zoology](http://www.nhm.ac.uk/zoology) Forth-  
coming meeting: Southeast Asian Gateway Evolution  
(14-17 September 2009) <http://sage2009.rhul.ac.uk/>  
Lukas Ruber <l.ruber@nhm.ac.uk>

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### UNebraskaLincoln MEEC Mar27-29 LastCallForAbstracts

Dear Colleagues,

This year's Midwest Ecology and Evolution Conference (MEEC) is fast approaching. As we would hate for anyone to miss the conference and since all MEEC attendees must register, please take note of the registration and submission deadlines listed below.

\*MEEC\* is a conference for graduate and undergraduate students to present research via oral and poster presentations. This year's conference will be hosted at the University of Nebraska-Lincoln from March 27-29, 2009. Keynote speakers will include David Quammen, David Hillis, and Svata Louda, with a special lunch discussion with the 2008 evolution educator of the year Randy Moore. For more information about MEEC 2009, please visit [midwesteec.org](http://midwesteec.org).

While faculty and post-docs are asked not to present at MEEC 2009, they are strongly encouraged to attend the conference to support and network with top students from throughout the Midwest. .

Abstract submission and meeting registration should be completed online at [midwesteec.org](http://midwesteec.org).

- Abstract Submission Deadline: \*February 15, 2009\* -  
Conference Registration Deadline\*: February 15, 2009\*  
- Hotel Special Rate Deadline\*: February 15, 2009\*

Sincerely,

MEEC 2009 Steering Committee

TJ Bliss, Chair Matthew Giovanni Travis Hinkelman

Travis Hinkelman <[travis.hinkelman@gmail.com](mailto:travis.hinkelman@gmail.com)>

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### UNorthCarolina Wilmington Darwin Mar19-21

NEW ABSTRACT SUBMISSION DEADLINE FRIDAY FEB 6TH REGISTRATION FOR STUDENTS IS NOW FREE (the Friday P.M. banquet will still be \$25) OUTSTANDING PLENARY SPEAKERS

Darwin's Legacy: Evolution's Impact on Science and Culture

March 19-21, 2009

UNCW's Evolution Learning Community will be hosting "Darwin's Legacy: Evolution's Impact on Science and Culture," a multidisciplinary student conference on March 19-21, 2009.

The conference will be a unique opportunity for undergraduate and graduate students in the natural sciences, social sciences, humanities and arts who are conducting research or creative endeavors related to evolution to present their research, investigate graduate study opportunities, network, enhance their resumes, and enrich the body of knowledge surrounding evolution.

With the exception of the four keynote speakers, all presentations will be made by students.

Keynote Speakers: David Buss, University of Texas, (<http://homepage.psy.utexas.edu/homepage/-Group/BussLAB/>), Peter Carruthers, University of Maryland (<http://www.philosophy.umd.edu/Faculty/-pcarruthers/>), David Mindell, California Academy of Sciences (<http://www.ummz.umich.edu/molsys/-mindell.html>), Kevin Padian, University of California, Berkeley (<http://www.ucmp.berkeley.edu/-people/padian/home.php>)

Michael A. McCartney Associate Professor Dept. of Biology and Marine Biology Center for Marine Science UNC Wilmington 5600 Marvin Moss Lane Wilmington, NC 28409 Phone 910-962-2391 Fax 910-962-2410

"McCartney, Michael" <[mccartneym@uncw.edu](mailto:mccartneym@uncw.edu)>

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### UWisconsinMadison StatGenetics May4-6



Symposium: Statistical Genetics of Livestock in the Post-Genomics Era May 4-6, 2009 University of Wisconsin - Madison

The web site of the symposium "Statistical Genetics of Livestock in the Post-Genomic Era" is finally up and running. Please check out the following link:

<http://www.wisc.edu/dysci/sglpge/> We have a great list of invited speakers, plus there will be a poster session for contributed papers, so please join us if you're available in early May.

Sincerely,

Dr. Kent Weigel and Dr. Guilherme Rosa Symposium co-chairs

The Symposium organization acknowledges funding support from the USDA-NRI 43.0 Animal Genome Program.

–

Guilherme J. M. Rosa Assistant Professor Department of Dairy Science University of Wisconsin - Madison

444 Animal Science Building 1675 Observatory Dr. Madison, WI 53706 USA

Phone: +1 (608) 265-8617 Fax: +1 (608) 263-9412 E-mail: [grosa@wisc.edu](mailto:grosa@wisc.edu) <https://mywebspace.wisc.edu/~grosa/web/>

"Guilherme J. M. Rosa" <[grosa@wisc.edu](mailto:grosa@wisc.edu)>

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## UWisconsin StatisticalGenomics May4-6

Symposium: Statistical Genetics of Livestock in the Post-Genomics Era

May 4-6, 2009

University of Wisconsin - Madison

The symposium "Statistical Genetics of Livestock for the Post-Genomic Era" will be held at the University of Wisconsin - Madison on May 4-6, 2009. This meeting will provide an important opportunity to share and discuss state-of-the-art bioinformatics and statistical genetics methodologies as applied to livestock and companion animals. The symposium will be structured around four themes (Animal Functional Genomics, Systems Biology, Whole Genome Enabled Animal Selection, and Whole Genome Association Analysis), each with top-notch invited speakers covering contemporary

topics in statistical genetics, data mining, and bioinformatics approaches applied to animal genomics. Additionally, there will be a poster session for delegates to present their latest research results. Please mark your calendars!

Registration fee\*:

If received by March 31: \$250 per person (\$125 for graduate students)

After March 31: \$300 per person (\$150 for graduate students)

\* Registration fee includes coffee breaks, cheese and wine poster session, and lunch and dinner on Tuesday.

For those who wish to present a poster, abstracts will also be due by March 31.

Detailed information about registration, housing, and abstracts will be soon available at the conference web site, so please watch for the announcement.

Three housing options will be offered, including the Best Western InnTowner (\$92 single or double), The Lowell Center (\$89 single, \$99 double), and the Farm & Industry Short Course Dorms (\$35 single, \$48 double, \$54 triple, plus \$8 parking). All are within walking distance of the Ebling Symposium Center.

Again, details regarding housing, registration, and abstracts will be available via the conference web site. If you have any questions, please do not hesitate to contact Kent Weigel ([kweigel@wisc.edu](mailto:kweigel@wisc.edu)) or Guilherme Rosa ([grosa@wisc.edu](mailto:grosa@wisc.edu))

Tentative Program:

Monday, May 4 (Afternoon) - Whole Genome Association Analysis

1:00 - 1:30 Opening Ceremony 1:30 - 2:10 Keynote Speaker: Dr. Jim Crow, University of Wisconsin 2:10 - 2:50 Dr. Moshe Soller, Hebrew University of Jerusalem, Israel 2:50 - 3:30 Dr. Agustin Blasco, Polytechnic University of Valencia, Spain 4:00 - 4:40 Dr. David Allison, University of Alabama - Birmingham 4:40 - 5:20 Dr. Bill Hill, University of Edinburgh, United Kingdom 5:30 - 7:30 Poster Session (with Cheese and Wine)

Tuesday, May 5 (Morning) - Animal Functional Genomics

8:30 - 9:10 Dr. Max Rothschild, Iowa State University 9:10 - 9:50 Dr. Sunduz Keles, University of Wisconsin 9:50 - 10:30 Dr. Miguel Perez-Enciso, Universitat Autònoma de Barcelona, Spain 11:00 - 11:40 Dr. Rob Tempelman, Michigan State University 11:40 - 12:20 Dr. Alicia Carriquiry, Iowa State University 12:30 - 1:30 Lunch

Tuesday, May 5 (Afternoon) - Systems Biology

1:30 - 2:10 Dr. Miguel Toro, INIA, Spain 2:10 - 2:50 Dr. Daniel Sorensen, University of Aarhus, Denmark 2:50 - 3:30 Dr. Dan Nettleton, Iowa State University 4:00 - 4:40 Dr. Henner Simianer, Univ. Goettingen, Germany 4:40 - 5:20 Dr. Jean-Louis Foulley, INRA, France 5:30 - 8:30 Drinks & Dinner

Wednesday, May 6 (Morning) - Whole Genome Enabled Animal Selection

8:30 - 9:10 Dr. Ben Hayes, Dept Primary Industries Research Victoria, Australia 9:10 - 9:50 Dr. Bjorg Heringstad, University of Life Sciences, Norway 9:50 - 10:30 Dr. Rohan Fernando, Iowa State University 11:00 - 11:40 Dr. Ignacy Misztal, University of Georgia 11:40 - 12:40 Panel Discussion:

Dr. Bill Muir, Purdue University

Dr. Paul VanRaden, AIPL, USDA

Dr. Brian Kinghorn, University of New England, Australia

Please mark in your calendars! Additional information will be sent out soon.

Sincerely,

Dr. Kent Weigel and Dr. Guilherme Rosa Symposium co-chairs

The Symposium organization acknowledges funding support from the USDA-NRI 43.0 Animal Genome Program.

Guilherme J. M. Rosa Assistant Professor Department of Dairy Science University of Wisconsin - Madison

444 Animal Science Building 1675 Observatory Dr. Madison, WI 53706 USA

Phone: + 1 (608) 265-8617 Fax: + 1 (608) 263-9412 E-mail: [grosa@wisc.edu](mailto:grosa@wisc.edu) <https://mywebspaces.wisc.edu/~grosa/web/> [grosa@wisc.edu](mailto:grosa@wisc.edu)

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## AmericanU EvoDevo

Lab opening for M.S. students in Biology at American University

The Angelini Lab is currently seeking qualified and interested applicants for the AU Biology Masters program. This is a competitive program offering funding opportunities during the academic year, summers, and travel. Successful applicants will complete a course of study and conduct independent research.

The lab is broadly interested in the developmental and molecular genetic aspects of morphological evolution (e.g. "evo-devo"). Using a combination of developmental genetic and phylogenetic methods, we seek to understand the interactions and functions of genes and their networks in terms of the evolutionary histories that have led to animal diversity. Insects and other arthropods have been our study organisms.

American University is located in Washington, DC, and affords students unparalleled access to world-class research institutions, prestigious internship opportunities, and memorable learning experiences outside of the classroom.

Applicants should have completed a bachelor's degree in the biological sciences, and have an interest in genetics and evolution. Applications to the Biology Department for 2009 will be considered on a rolling basis. GRE scores are required, and the Biology or Biochemistry, Cell and Molecular Biology subject test are encouraged but not required.

For more details, please visit our website: (<http://www.american.edu/cas/bio/people/faculty/angelini/>) or e-mail Dr. Angelini ([angelini@american.edu](mailto:angelini@american.edu)).

David R. Angelini, Ph.D. American University Department of Biology, Hurst Hall 101 4400 Massachusetts Ave NW Washington, DC 20016-8012 phone: 202-885-2028 e-mail: [angelini@american.edu](mailto:angelini@american.edu) website: <http://www.american.edu/cas/bio/people/faculty/angelini/> [angelini@american.edu](mailto:angelini@american.edu)

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## CentralMichU InsularLakeBiogeography

MS Graduate Research Assistantship – Insular lake biogeography using unionids and fish. Biology Department, Central Michigan University, Mount Pleasant, MI

Responsibilities: The successful applicant will conduct a two-year research project on the landscape genetics of freshwater mussels and their host fish on insular lakes of Lake Michigan Islands.

QUALIFICATIONS: The successful applicant should be highly motivated and have a B.S. in fisheries, ecology, biology, zoology or closely related field and should be able to work independently in the field and lab. I also will give special consideration to students with previous lab experience with microsatellite DNA, PCR, genotyping. Field experience, such as experience with boats, lake sampling, identification of unionid mussels, fisheries, aquatic invertebrates also is desirable. Minimum academic qualifications include 3.0 GPA (on a 4.0 system), GRE scores must be sent to CMU graduate school for approval. Additional graduate program information can be found at: [http://www.bio.cmich.edu/grad\\_app.admiss.htm](http://www.bio.cmich.edu/grad_app.admiss.htm) (deadline for Teaching Assistantship applications is Feb 15 2009, but exceptions can be made)

Note: This position is dependant on final funding approval.

Salary: \$15,000 per year plus tuition waiver.

Closing Date: Until filled. Selection will be made by May 2009.

Contact: SEND a cover letter explaining your interest and qualifications, resume (CV), copies of transcripts (unofficial ok), and the names and phone numbers of three references to:

Dr. Dave Zanatta Assistant Professor Biology Department Central Michigan University 186 Brooks Hall Mount Pleasant, MI 48859

email: [zanat1d@cmich.edu](mailto:zanat1d@cmich.edu) office: 989-774-7829 fax: 989-774-3462 Homepage: <http://www.cst.cmich.edu/users/zanat1d/> [zanat1d@cmich.edu](mailto:zanat1d@cmich.edu) [zanat1d@cmich.edu](mailto:zanat1d@cmich.edu)

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## ETHZurich SpecificParasites

ETH Zürich, Institute of Integrative Biology (IBZ)

The Experimental Ecology Group (Prof. Paul Schmid-Hempel) is seeking to fill a Ph.D. Position

(Genetics and specificity of host-parasite interactions) to work on questions of specificity in host-parasite interactions using *Bombus* spp. and their parasites (protozoa) as the study system. The framework for this study is given by the extreme level of specificity in the interaction of *Crithidia* and *Bombus* in experimental and natural populations of various *Bombus* species. The questions are the possible involvement of specific vs. general immune defences, transmission pathways, strong selection by the host, and how genotypic variation in parasite population is maintained. The project will involve field sampling, genetic typing with molecular tools, and will integrate this advance with existing genomic resources to establish relationships and test ideas about the ecology and evolution of populations and species differentiation in the field.

The ideal candidate likes to work and is fascinated by these questions and the bumblebee system, has interests and sees the possibilities at the crossroads of ecology, genetics and evolution. Any of the relevant fields such as evolutionary ecology, population genetics or evolutionary biology are favourable backgrounds.

Salary and other conditions in accordance with local regulations. The normal duration of a PhD at ETH is 3 years. Special conditions for acceptance into the PhD program of ETH may apply; a degree equivalent to a M.Sc. is normally required. Preferred starting date is spring 2009 or soon thereafter. Please send applications, with CV, names of referees, and short statement of your interests in this position to Prof. Paul Schmid-Hempel, preferably by email (psh@env.ethz.ch). Screening of applications will start 15 March 2009 and until post is filled. For more information, you may check our web page ([www.eco.ethz.ch](http://www.eco.ethz.ch)) or email.

Prof. Paul Schmid-Hempel ETH Zurich Institute of Integrative Biology (IBZ) Experimental Ecology ETH-Zentrum CHN K11 CH-8091 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) paul.schmid-hempel@env.ethz.ch paul.schmid-hempel@env.ethz.ch

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## Exeter SexualSelection

A PhD position at the University of Exeter. Dr David Hosken & Dr John Hunt are seeking a motivated student to work on sexual selection.

Project details: Female mate-choice is responsible for the evolution of some of the most spectacular male characters. One leading explanation for why mate choice evolves is that females preferentially mate with male possessing good genes to gain genetic benefits for their offspring. However, because females cannot directly assess male genes, they must rely on phenotypic traits that signal a male's genetic quality: that is, phenotype must reliably map onto genotype. The problem is that the genotype-phenotype relationship is environment-dependent, so that whenever the environment fluctuates and genotype-by-environment interactions exist, females may no longer be able to gain reliable information about male quality. This project will examine the consequences of a fluctuating environment on the evolution of female mate choice and the male sexual trait(s) it targets.

Closing date for applications is the 12th of March 2009, with start date October 2009 (at the latest). For more information contact Dr Hosken (D.J.Hosken@exeter.ac.uk)

Dr DJ Hosken Associate Professor in Evolution Centre for Ecology & Conservation School of Biosciences University of Exeter, Cornwall Campus Tremough, Penryn, Cornwall TR10 9EZ UK D.J.Hosken@exeter.ac.uk <http://www.biosciences.ex.ac.uk/staff/profiles/-external.php?id=David.hosken>

DJ Hosken <D.J.Hosken@exeter.ac.uk>

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## ExeterU CricketSpeciation

PhD Studentship available October 2009. Exeter University.

Behavioural and genomic studies of sexual selection and reproductive isolation in wild field crickets.

To address the question of what drives speciation we need to identify the factors causing divergence between natural populations. Our recent work provides the opportunity to develop field crickets as a model system for such a study, utilizing next-generation sequencing and behavioural studies to identify the genetic basis of divergence. This project will involve field collections of crickets, molecular genetic work to establish phylogeographic relationships of populations and behavioural experiments to establish patterns of phenotypic divergence and premating and postmating isolation between populations of the field cricket *Gryllus campestris*. This

will allow the student to test predictions from existing hypotheses for the evolution of reproductive isolation, and to examine the genetic basis of behaviour in wild insects.

During the last ice-age field crickets (and other animals and plants) were confined to refugia in the South of Europe, but the ancestry of current populations is unknown. The student will use molecular genetics to reconstruct the post-glacial history of this species and the relationships between extant populations. Wild populations will be collected from mainland Europe, reared in field enclosures in Spain and used in mate choice and offspring viability experiments to measure the degree of pre-mating and post-mating reproductive isolation between populations. Combined with measures of phenotypic divergence, this will allow the student to test competing hypothesis for the origin of reproductive isolation; e.g. are populations that are simply more genetically divergent most reproductively isolated, or is environmental adaptation more important? What are the contributions of pre-mating vs post-mating mechanisms of reproductive isolation?

For more information about the project contact Dr Tom Tregenza (T.Tregenza@exeter.ac.uk) To apply please send a cover letter, C.V., and contact information for two academic referees to T.Tregenza@exeter.ac.uk

T.A.Richards@exeter.ac.uk  
T.A.Richards@exeter.ac.uk

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## Frankfurt SpongeEvolution

Frankfurt am Main, Germany: Research Associate (PhD) position in taxonomy, phylogeography and evolution of Antarctic sponges.

We invite applications for a research associate (PhD) position in a project funded by the German Research Foundation (DFG) âPhylogeny of selected key taxa of Antarctic deep-sea Porifera (Sponges) and the history of their radiation.â in the DFG Priority Program SPP1158: "Antarctic Research in comparison with Arctic Ice regions". The project is located in the department Marine Zoology of Senckenberg Forschungsinstitut und Naturmuseum.

Sponges play an important ecological role as active filter feeders and contribute significantly to the flow of nutrients and pelago-benthic coupling, particularly notable for the extraordinary rich sponge populations of

the Antarctic shelf. However, an unexpectedly high diversity and abundance of Porifera was found in the Antarctic deep-sea, partly exceeding those of the shelf, but nothing is known yet about the colonization history, evolution or phylogenetic relationships of Southern Ocean sponge communities. In this project, we aim to resolve the systematic and phylogenetic relationships of selected Antarctic sponge taxa and reconstruct their phylogeographic history in comparison with the sponge faunas of other World oceans, mainly the Arctic. We use an integrative approach that combines molecular techniques with morphological and palaeontological data to achieve an understanding of the colonisation and the history of diversification of Antarctic Porifera, pivotal to assess the potential of these fragile communities for their resilience to global change. This project is carried out in close collaboration with Prof. Dr. Gert Wörheide, GeoBioCenterLMU of the Ludwig-Maximilians-Universität (LMU) München.

We are seeking a highly motivated applicant with interest and experience in taxonomy, phylogeny and zoogeography of marine animals demonstrated by an above-average MSc (or equivalent, e.g. German diploma) degree in zoology or a related field. Applicants from abroad are encouraged to apply. The successful candidate will join a well established working group with access to valuable invertebrate collections, well-equipped lab and library. Our Focus is biodiversity of marine animals, and our research includes morphologically based taxonomy and phylogeny in comparison with results from molecular investigations. Also food web analysis by means of stable isotopes will be part of this project. Participation in marine expeditions may be required. More information about our department and current research projects can be found at [www.senckenberg.de](http://www.senckenberg.de) (Research: Departments: Marine Zoology: Marine Vertebrates I). Requirements: Degree in Biology (MA, MSc, or equivalent degree) or related field; very good and demonstrated knowledge in methodology of morphological-taxonomic investigations and in phylogeny and zoogeography of marine animals, including computer programs for such analyses; excellent English language skills.

The position is initially available for 24 months (starting by the 1.04.2009, or as soon as possible), with possible extension depending upon performance and availability of funding. It will be paid according to the German TV salary scheme BAT 2a/2 (TV-L E13/2).

Application: Send application including letter of intent, CV, PDFs of master (or diploma) thesis, publications (if available), and details of 2 referees as PDF (only) by email to Dr. Dorte Janussen ([dorte.janussen@senckenberg.de](mailto:dorte.janussen@senckenberg.de)). E-mails containing

applications should state the keyword “ANTARCPOR” in beginning of the subject line.

Senckenberg Forschungsinstitute und Naturmuseum is a multidisciplinary research institution, including more than 10 research institutes with different scientific focus distributed all over Germany. Since July 2008 a new centre of excellence exists in Frankfurt am Main with the title “Biodiversity and Climate” (Bio+C), founded by Senckenberg in cooperation with Johann Wolfgang Goethe-University and other partners. This interdisciplinary institute investigates the coupling of processes linked with biodiversity and climate change in space and in time, including short-term, intermediate and long-term processes (“evolution and climate change”) in terrestrial and marine ecosystems. It is financed with 18.2 Mio. by the LOEWE initiative of the federal state Hessen (Hessische Landes-Offensive zur Entwicklung Wissenschaftlich-ökonomischer Exzellenz).

The Senckenberg Institution is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled. Senckenberg is committed to at equal opportunity of the genders, and women are encouraged to apply.

PD Dr. Dorte Janussen Sektion Marine Evertebraten I Forschungsinstitut und Naturmuseum Senckenberg Senckenberganlage 25 D-61350 Frankfurt am Main

Tel.: +49 (0)69 7542 1306

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## Iceland 2 Stickleback Evolution

\*Opportunity for a M.Sc. study in Evolutionary Ecology of Sticklebacks in Iceland \*

Holar University College ([www.holar.is](http://www.holar.is) < <http://www.holar.is/> > ) (Assoc. Prof. Bjarni K. Kristjánsson and Prof. Skuli Skulasson), seeks a M.Sc. student to study microevolutionary change over space and time in threespine stickleback, *Gasterosteus aculeatus*. The work is done in collaboration with Dr. Katja Räsänen, Dept. of Aquatic Ecology, EAWAG (the Swiss Federal Institute of Aquatic Science and Technology, which is a Swiss-based and internationally operating aquatic re-

search institute within the ETH domain, [www.eawag.ch](http://www.eawag.ch) < <http://www.eawag.ch/> >).

The ongoing global biodiversity crisis emphasizes the need to understand the processes that create, maintain and change biological diversity. Of particular importance is to understand the role of evolutionary processes and their interplay with ecology. We will study microevolutionary processes on a spatial and temporal scale in threespine stickleback populations from Lake Mývatn area (Iceland), which has been the target of intense ecological studies during the past decades. Two main questions will be addressed: how does i) variation in ecological complexity and ii) temporal variation in selection affect phenotypic and genetic divergence in stickleback over space and time? The study is aimed to promote understanding on the ecological and evolutionary feedback mechanisms within ecological communities and to aid in decisions on how to protect and use our natural resources.

The M.Sc. project will focus on spatial variation in phenotypic and genetic divergence of stickleback on a small geographic scale. A B.Sc. (or equivalent) degree in biology or related area is mandatory. The ideal candidate has a strong interest in evolutionary ecology, is independent and works well in a team, and is willing to work both in the field and lab. Some experience in molecular genetics is desirable. The position is funded through the Icelandic Science foundation (RANNIS) for two years and will be filled as soon as a good candidate is found (target date 1. May 2009).

The student will be located and registered at Dept. of Aquaculture and Fish Biology, Hólar University College. Parts of the work will take place at the Dept. of Aquatic Ecology, EAWAG in Switzerland. The Dept. of Aquaculture and Fish Biology, Hólar University College ([www.holar.is](http://www.holar.is)), situated in Skagafjörður, North of Iceland, and is an international centre for research, instruction, and continuing education in aquatic biology, aquaculture, and fish biology. The working language is English.

Applicants should send an application letter with a statement of research interests and relevant experience, curriculum vitae with a list of publications (if any), copies of academic qualifications, and the names and e-mail addresses of three referees as a single pdf file to Bjarni K. Kristjánsson ([bjakk@holar.is](mailto:bjakk@holar.is)) by March 15.

For questions contact Bjarni K. Kristjánsson or Katja Räsänen ([Katja.Rasanen@eawag.ch](mailto:Katja.Rasanen@eawag.ch) < <mailto:Katja.Rasanen@eawag.ch> >; <http://www.eawag.ch/kuerze/personen/homepages/rasaka/> )

Dr. Bjarni K. Kristjánsson, Associate Professor  
Holar University College,

Háeyri 1, 550 Sauárkrókur, Iceland;

<http://www.holar.is/bjakk.html>. \*Opportunity for a Ph.D. study in Evolutionary Ecology of stickleback in Iceland \*

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## ImperialCollegeLondon Bird MigrationDisease

PHD SCHOLARSHIP AT IMPERIAL COLLEGE LONDON

Project: European birds as a model system for predicting epidemiology of epizootic disease

Supervisor: Prof Ian Owens, Department of Life Sciences

Project

The Grantham Institute for Climate Change at Imperial College London is funding a series of PhD studentships in climate-related research ranging from understanding the likelihood of sudden, catastrophic climate events to the impact on disease within ecosystems. One of these studentships is to test the effect that changes in migration routes may have on the spread of disease, using European birds as a model system. The student will make extensive use of GIS databases and analyses and will be mainly based in the Ecology and Evolution Group at Imperial College's Silwood Park Campus, which is approximately 20 miles South West of London, but would also have strong links to other research groups interested in climate change and disease. Silwood Park has a very strong reputation for research in ecology and evolution and is home to a large group of researchers, including approximately 200 postgraduate students.

The specific aims of the project will be to:

1. Digitally map the migratory routes of European birds.
2. Construct environmental models of migratory distributions.
3. Use climate models to predict changes in migratory routes.
4. Predict the effect of climate change on bird-borne disease.

The project would suit either a biologist interested in the effects of climate change or a physical scientist wishing to move into the climate impacts research area. Links to the relevant climate expertise are available through the Grantham Institute.

Applications and further information

Applications for PhDs at Imperial College must be completed online (see link below). Once you have submitted your application, please email the Grantham Institute directly ([granthamphd@imperial.ac.uk](mailto:granthamphd@imperial.ac.uk)) so that we can process your application. For further information please see the following websites or contact the Campus Administrator at Silwood Park, Mrs Diana Anderson ([d.anderson@imperial.ac.uk](mailto:d.anderson@imperial.ac.uk)).

Imperial College application process:  
<http://www3.imperial.ac.uk/pgprospectus/howtoapply/applicationforms>

Grantham Institute: <http://www3.imperial.ac.uk/climatechange> Ecology and Evolution Group at Silwood Park: <http://www3.imperial.ac.uk/biology/research/ecologyandevolution>

– Prof. Ian P.F. Owens Division of Biology & NERC

Centre for Population Biology Department of Life Sciences Imperial College London Silwood Park Ascot, Berkshire SL5 7PY, UK

<http://www.imperial.ac.uk/lifesciences> <http://www.imperial.ac.uk/biology>  
<http://www.imperial.ac.uk/cpb> <http://www.imperial.ac.uk/people/i.owens> Ian Owens <i.owens@imperial.ac.uk>

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## InstZool London FrogPopulations

Are humans spreading a virulent wildlife disease between British frog populations?

The common frog, *Rana temporaria*, has been experiencing mass die-offs in the UK due to an invasion into country of ranavirus FV35. Our partner, FrogLife and the CASE partner, the Institute of Zoology (IoZ) have been tracking the pattern of these unusual frog mortalities since 1992. The virus appears to have spread from the first infections in the southeast of England into the southwest, North and Wales.

The student will examine this data for disease sparks that are due to human activity, such as moving frogspawn or ornamental fish. The student will then map the distribution of viral genotypes, to challenge these preliminary interpretations.

The IoZ will provide training in the first year in the isolation and characterisation of the virus. The student will conduct fieldwork in the summers of the first two years, and obtain samples in the key locations throughout the disease range. There will be regular (monthly) visits to FrogLifes base in Peterborough, and with the local partner at Imperial in London.

A background in genetics, epidemiology or mathematical biology would be an advantage, but enthusiasm for the project is the essential requirement. A driving license will be a great advantage. Diplomacy and skill in dealing with pond owners will be essential.

Further details:

See: <http://webspace.qmul.ac.uk/ranichols/-Project%20summary.pdf> Or email Richard Nichols, r.a.nichols@qmul.ac.uk

Deadline for applications: Feb 28th 2009

Prospective students should submit a 1 page CV and a maximum of 1 page of additional information, which should indicate why you are interested in this project

and what skills you can bring to it.

This is an NERC funded CASE studentship, so it comes with a stipend for those qualifying as UK students. It is also open to students from other EU countries, but you would have to fund your own living expenses.

Richard Nichols Professor of Genetics <http://webspace.qmul.ac.uk/ranichols/research.htm> Richard Nichols <r.a.nichols@qmul.ac.uk>

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## LundU PlantSystematics

Lund University announces the following vacancy:

PhD studentship in Evolution within the discipline of Plant Evolution and Systematics

With placement at the Department of Ecology, Section for Plant Ecology and Systematics, Faculty of Science, Lund University.

Reference Number: N 2009/119 Starting Date: As soon as possible Information: Prof. Honor C. Prentice +46 46 2228971 (+46 73 5968334) Honor.C.Prentice@ekol.lu.se Prof. Anders Tunlid +46 46 2223757 (+46 70 3140067. Anders.Tunlid@mbioekol.lu.se Worker's unions at Lund University: OFR, SACO och SEKO

Project title: Allelic variation and protein function in a plant community context

Project description: This interdisciplinary project represents a collaboration between the Section of Plant Ecology and Systematics, and the Section of Microbial Ecology within the Department of Ecology, Lund University.

The project will focus on genomic ecology and community genomics and will develop a novel system for the study of gene variation and function in the context of natural plant communities. Molecular differentiation will be investigated at a pair of loci coding for a key metabolic enzyme, phosphoglucose isomerase (PGI), in the wild plant *Festuca ovina*, and the distribution and function of individual PGI alleles will be explored in natural populations within grassland plant communities on the Baltic island of Uland. The project will involve characterization of sequence differentiation between the multiple alleles at the two loci and the development of allele-specific primers. Relationships between individual alleles and fine-scale niche-variation within natural grassland communities will be investi-



gated and the functional consequences of the allelic variation will be inferred through analyses of predicted protein structures.

The PhD project will be linked to the Research School in Genomic Ecology within the Centre for Genomic Ecology (CGE). Genomic ecology represents a new interdisciplinary field on the interface between ecology, evolutionary and molecular biology, and genomics. The long-term goal of CGE is to achieve an integrated understanding of the molecular, evolutionary and ecological mechanisms and processes that are involved in the generation of the immense diversity of form and function that characterizes living organisms. The Research School in Genomic Ecology will provide the PhD student with access to advanced courses and opportunities for placements in other laboratories as well as a stimulating social network. Further information about CGE and the research school can be found at <http://www.ekol.lu.se/research/genomic-ecology>. Qualifications: Applicants should have a Master's degree (or equivalent) in biology, with specialization in botany, plant ecology, plant genetics, molecular ecology, molecular genetics, or a similar subject area. Experience with molecular techniques is a central requirement for the position. Competence with univariate and multivariate statistics, bioinformatics and plant cultivation is also a desirable merit. A very good knowledge of written and spoken English is required. A valid driving licence is also a desirable merit.

Additional information: A Swedish PhD represents four years of full-time study. Of these four years, three years are devoted to research activities and one year is devoted to advanced course work, in which course points are obtained via attendance at research-level courses given in Lund or elsewhere in Europe.

Regulations concerning appointment as a full PhD student can be found in HF 5 Chap 1-7 and SFS 1998:80. Also consult the admission regulations found at: <http://www.science.lu.se/o.o.i.s/4964> An educational stipend is awarded for the first 18 months of full-time study, following which time the student is appointed as a full doctoral student. Regulations concerning educational stipends for doctoral students can be found in SFS 1995:938 and 1998:81. Regulations concerning appointment as a full PhD student can be found in HF 5 Chap 1-7 and SFS 1998:80. Those who hold an educational stipend or a doctoral student appointment must first be accepted for postgraduate study. To be accepted, a student must be judged to have the competence necessary to complete a course of postgraduate study. In addition to pursuing postgraduate studies, the doctoral student may also perform other duties - including teaching and administration - according to the specific regulations.

The university strives for a more even gender representation within postgraduate education.

Applications are made on a specific application form found on the web site: <http://www.science.lu.se/o.o.i.s/13456> The application must reach the Registrar, Kansli N, Lund University, Box 118, SE-221 00 Lund, Sweden, not later than Wednesday 8 April 2009. All

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## NaturalHistoryMuseum London CichlidSpeciation

Natural History Museum PhD Studentship

Of large and small fish: testing ecological speciation in Lake Tanganyika cichlids

We seek a highly motivated and productive PhD student to work on a research project on ecological speciation in Lake Tanganyika cichlids. The importance of natural selection is increasingly emphasized in studies of speciation. The cichlids of the East African Great Lakes are among the most spectacular examples of rapid speciation and adaptive radiation. Surprisingly, the role of ecological speciation in the evolution of these fish faunas remains largely untested.

The aim of the PhD project is to test for ecological speciation within a candidate model system of ecological speciation from Lake Tanganyika using population genetic data (AFLPs), and by measuring ecological and mating preferences under aquarium conditions.

The successful candidate for this project will have to compete with two other candidates from different projects for a full-time NHM PhD studentship.

Applicants should have a Masters or equivalent research experience in molecular ecology, behavioural ecology or related fields as well as broad interest in systematics and evolution. They should be able to work on complex and demanding projects and enthusiastic about participating in extensive fieldwork in Africa.

The successful candidate will be supervised by Dr Lukas R<sup>1</sup>ber (The Natural History Museum; [l.ruber@nhm.ac.uk](mailto:l.ruber@nhm.ac.uk)) and Dr Martin J. Genner (Univer-

sity of Bristol; M.Genner@bristol.ac.uk). For further information please contact LR (with Cc: to MJG).

Closing date for applications is Friday 13 March.

Dr Lukas Ruber Department of Zoology The Natural History Museum Cromwell Road London SW7 5BD UK

Tel: +44 (0)20 7942 6208 Fax: +44 (0)20 7942 5054 e-mail: l.ruber@nhm.ac.uk

[www.lukasruber.com](http://www.lukasruber.com) [www.nhm.ac.uk/zoology](http://www.nhm.ac.uk/zoology) Forthcoming meeting: Southeast Asian Gateway Evolution (14-17 September 2009) <http://sage2009.rhul.ac.uk/> Lukas Ruber <l.ruber@nhm.ac.uk>

## NHN-Leiden PlantSystematics

Faculty of Mathematics and Natural Sciences

Vacancy number 8-251

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

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

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

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

Who fits the shoe?

You must have a degree (drs./MSc) in Biology and a strong interest and experience in plant taxonomy preferably including molecular and/or SEM/TEM techniques. To obtain the available position you have to write a research proposal of max 2 pages, preferably based on the collections available and the research performed at the NHN and/or botanical garden. Other research projects are also welcomed if the main focus is on

morphology, anatomy and phylogenetics. As a person you are a driven and self-confident scientist with excellent technical, analytical and communicational skills.

The position

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

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

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

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

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

Leiden University / Faculty of Mathematics and Natural Sciences

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

Human Resource department

P.O. Box 9504

2300 RA Leiden

The Netherlands

Or by mail to [m.vanschoonhoven@science.leidenuniv.nl](mailto:m.vanschoonhoven@science.leidenuniv.nl)  
<<mailto:m.vanschoonhoven@science.leidenuniv.nl>>

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

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

“Mols, J.B. (Johan)” <[Mols@nhn.leidenuniv.nl](mailto:Mols@nhn.leidenuniv.nl)>

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## NorthCarolinaStateU InsectBiodiversity

North Carolina State University Department of Entomology Insect Museum

Two graduate assistantships are available (PhD-level preferred) for exceptional students broadly interested in biodiversity, phyloinformatics, evolution, and systematics. Selected candidates will work with a large team of engaging, approachable, and highly motivated researchers that have diverse interests and skill sets. Assistantships pay for tuition and fees and provide \$19,000 stipend per annum.

â Project 1 will address biodiversity questions involving ensign wasps (Hymenoptera: Evaniidae) in Costa Rica. The student will focus on digital approaches to species revision/description, including opportunities to explore novel methods for integrating systematics with the Web (e.g., Tree of Life and/or Encyclopedia of Life), phylogenetics (estimating relationships), and species hypothesis testing using molecular (DNA barcoding) and morphological data.

â Project 2 broadly addresses questions of Hymenoptera evolution and/ or functional morphology, with a student directly involving him or herself in the development of informatics resources (anatomical ontology development/testing, Web programming, database design), while pursuing a related project of his or her own

conception. This student will have the opportunity to describe species, address biodiversity questions, work with molecular data, and learn phylogenetic methods.

Desirable qualities for applicants: excellent oral and written communication skills, a willingness to engage both the public and research communities, a penchant for foreign travel, familiarity with insect taxonomy and natural history.

Students will have the opportunity to learn and develop fundamental biodiversity tools as part of their graduate training, including Web application development, databases in evolutionary biology, data mining, ontology design/implementation, PCR, primer design, phylogenetic methods, advanced microscopy. Prior exposure is beneficial but not required, and we will consider applicants with degrees in computer science, anatomy, bioinformatics, information visualization, or other related fields.

How to apply: North Carolina State University hosts a top-rated Entomology program, and as a vertex of North Carolinaâs Research Triangle, we benefit from close proximity to a large community of evolutionary biologists and our affiliation with the National Evolutionary Synthesis Center (NESCent; <http://www.nescent.org/>). Interested students should send a CV, names of two references, and a one-page statement of purpose to Dr. Andrew Deans via email: [andy\\_deans@ncsu.edu](mailto:andy_deans@ncsu.edu).

Review of applications commences March 25, 2009 continues until candidates have been selected. Interested students should also apply to the NCSU Department of Entomology: <http://www.cals.ncsu.edu/entomology/students/how-do-i-apply> More details and contact information available here: <http://deanslab.org/> <http://insectmuseum.org/> /AA/EOE. ADA Accommodations: Dr. Andrew R. Deans [andy\\_deans@ncsu.edu](mailto:andy_deans@ncsu.edu) 919-515-2833.// NC State welcomes all persons without regard to sexual orientation./

Andrew R. Deans Department of Entomology North Carolina State University Campus Box 7613 2301 Gardner Hall Raleigh, NC USA 27695-7613

phone: +1 (919) 515-2833 fax: +1 (919) 515-7746  
skype: ardeans <http://www4.ncsu.edu/~ardeans/>  
Andy Deans <[andy\\_deans@ncsu.edu](mailto:andy_deans@ncsu.edu)>

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## TrentU CommonReed PopulationGenetics

### Invasive plant evolution

We seek a highly motivated and productive graduate student to work on a research project on the population genetics and evolutionary dynamics of the common reed, *Phragmites australis*. This species comprises both invasive and native lineages that each exhibit very different patterns of genetic variation and ecological amplitudes. Preliminary work on this species in our labs has revealed unexpected and intriguing relationships between invasiveness, genetic diversity, and adaptation. Further work will be based on assessments of quantitative traits and adaptive evolution. Laboratory and greenhouse work will be conducted at Trent University, Ontario, Canada, with field work in northeastern North America and Western Europe.

Applicants should have research experience in molecular ecology, population genetics or related fields as well as broad interest in evolutionary processes. They should be able to work on complex and demanding projects and be enthusiastic about both field and lab work.

Applicants should send a letter with a statement of research interests and relevant experience, curriculum vitae with a list of publications (if any), copies of academic qualifications, and the names and e-mail addresses of three referees as a single pdf file to Joanna Freeland (joannafreeland@trentu.ca; <http://people.trentu.ca/joannafreeland>) or Marcel Dorken (marceldorken@trentu.ca; <http://people.trentu.ca/marceldorken>) by March 15.

Joanna Freeland <joannafreeland@trentu.ca>

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## TulaneU EvolutionFrogMorphology

\*Tropical biology/amphibian lab at Tulane University accepting graduate student\*

I will soon be joining the faculty of Tulane University's Department of Ecology and Evolutionary Biology

and have an opening for a graduate student (Masters or Ph.D.) to start in my lab in Fall 2009. My two ongoing research projects are investigating (1) the evolution of morphological variation among poison dart frogs and (2) the roles of environmental and behavioral heterogeneity in shaping amphibian host-pathogen interactions. However, my research interests are broad and I welcome students interested in a variety of research questions involving tropical biology and/or amphibians.

For more information, please see my website (URL below) or email me directly at cori@tulane.edu.

<http://coririchards.googlepages.com/home> –

Corinne L. Richards-Zawacki, Ph.D.  
email:cori@tulane.edu <email%3Acori@tulane.edu>

Assistant Professor (fall 2009) Tulane University, Department of Ecology and Evolutionary Biology

Cori Richards <coririchards@gmail.com>

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## UAuckland BayesianPhylogeography

Two PhD scholarships are available in the Computational Evolution Group (<http://comepevol.auckland.ac.nz/>) under the supervision of Dr Alexei Drummond, co-founder of the BEAST software package for Bayesian evolutionary analysis.

The successful candidates will be involved in developing a Bayesian unification of geographical population dynamics and phylogenetics with a focus on human pathogenic viruses. Current phylogenetic models provide inferences about genetic variation, however this research will focus on the roles of landscape, geography, dispersal and migration, in shaping (viral) genetic histories. The successful candidates would work on two novel classes of tractable phylogenetic models that explicitly include the spatial distribution of samples and the geographic features of surrounding habitats. While the primary focus of the research will be on viral pathogens, the proposed work will have the potential to establish a new foundation for phylogeographic modeling in general. Besides developing methodology, the successful candidates will be involved in developing a new version of the BEAST software to include both phylogeographical modeling and visualization.

The research will be conducted in collaboration with Dr Marc Suchard's research group in UCLA and the successful candidates will have the opportunity to spend

one month a year in Los Angeles.

The successful candidates will have a background in applied mathematics, statistics, computer science or evolutionary biology.

Students will be affiliated with either the Bioinformatics Institute or the Department of Computer Science depending on their background and preference.

Applications should be sent to Assoc. Prof. Alexei Drummond ([alexei@cs.auckland.ac.nz](mailto:alexei@cs.auckland.ac.nz)) by 20th March 2009, and include a CV, and the names of two references.

[alexei@cs.auckland.ac.nz](mailto:alexei@cs.auckland.ac.nz) [alexei@cs.auckland.ac.nz](mailto:alexei@cs.auckland.ac.nz)

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## UAuckland BayesianViralPhylogeography

PhD scholarships in Bayesian computer modeling and visualization of virus phylogeography

Two PhD scholarships are available in the Computational Evolution Group (<http://compevol.auckland.ac.nz>) at the University of Auckland under the supervision of Dr Alexei Drummond, co-founder of the BEAST software package for Bayesian evolutionary analysis.

The successful candidates will be involved in developing a Bayesian unification of geographical population dynamics and phylogenetics with a focus on human pathogenic viruses. Current phylogenetic models provide inferences about genetic variation, however this research will focus on the roles of landscape, geography, dispersal and migration, in shaping (viral) genetic histories. The successful candidates will work on two novel classes of tractable phylogenetic models that explicitly include the spatial distribution of samples and the geographic features of surrounding habitats. While the primary focus of the research will be on viral pathogens, the proposed work will have the potential to establish a new foundation for phylogeographic modelling in general. Besides developing methodology, the successful candidates will be involved in developing a new version of the BEAST software to include both phylogeographical modelling and visualization.

The research will be conducted in collaboration with Dr Marc Suchards research group in UCLA and the successful candidates will have the opportunity to spend up to one month each year in Los Angeles.

The successful candidates will have a background in applied mathematics, statistics, computer science or evolutionary biology.

Students will be affiliated with either the Bioinformatics Institute or the Department of Computer Science depending on their background and preference. Applications should be sent to Dr Alexei Drummond ([alexei@cs.auckland.ac.nz](mailto:alexei@cs.auckland.ac.nz)) by 3rd March 2009, and include a CV, and the names of two referees.

– Dr Alexei Drummond Associate Professor in Bioinformatics, Department of Computer Science The University of Auckland Private Bag 92019, Auckland, New Zealand Ph: +64 9 3737599 ext 88298 Email: [alexei@cs.auckland.ac.nz](mailto:alexei@cs.auckland.ac.nz) WWW: <http://compevol.auckland.ac.nz/> [alexei@cs.auckland.ac.nz](mailto:alexei@cs.auckland.ac.nz)

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## UEastAnglia EvolutionaryRiskAndCancer

Project title: Genetic conflicts in cancer: from evolutionary principles to mechanisms underlying increased cancer risk

SCHOOL OF BIOLOGICAL SCIENCES, UNIVERSITY OF EAST ANGLIA, NORWICH, UK

1 year POST-DOCTORAL RESEARCH ASSOCIATE POSITION

Salary: From GBP 29,704 per annum

A full time postdoctoral position, funded by the BigC Local Cancer Care (<http://www.thebigappeal.co.uk/>), is available for 12 months in the laboratory of Dr Tracey Chapman and Professor Dylan Edwards (see <http://www1.uea.ac.uk/cm/home/schools/sci/bio/people/Faculty>) in the School of Biological Sciences and Biomedical Research Centre at UEA.

An immediate start date is available and the position must be filled as soon as possible.

Synopsis: There is great value in applying principles of evolutionary biology to the study of cancer. It can explain the high prevalence of cancer in humans and why cancer genes are often positively favoured by selection. For example, genes with beneficial effects early in life can be strongly favoured, even if the cost in later life is cancer. Conflicts of interest, for example between males and females, may also be an important source for increased cancer risk. We have recently shown that the experimental application of increased

mating stress results in dysregulation in reproductive hormone signalling and microRNA biosynthesis genes. These changes were associated with significantly increased death rate and are potentially significant in the context of cancer. In this proposal we aim to build upon this work, to understand (i) whether microRNAs themselves are differentially expressed in response to mating conflict and (ii) the mechanistic basis of how changes in gene expression (and gene translation controlled by microRNAs) leads to loss of organismal integrity and increased death rate. The research is important because of the need to understand the fundamental principles of how evolution acts on genes that increase cancer risk.

More information about the School of Biological Sciences can be found at <http://www.uea.ac.uk/-bio/> Informal enquiries to Tracey Chapman ([tracey.chapman@uea.ac.uk](mailto:tracey.chapman@uea.ac.uk))

Closing date: 6th March 2009. Interview date: Week beginning March 16th 2009

Applications via: <http://www.uea.ac.uk/hr/jobs/ra/-ra553.htm> Please send a CV and cover letter in addition to the application form.

Tracey Chapman <[Tracey.Chapman@uea.ac.uk](mailto:Tracey.Chapman@uea.ac.uk)>

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## UEdinburgh ComputationalBiology

We are now recruiting bright, ambitious and numerate graduates for PhD studentships within the Medical Research Council (MRC) Human Genetics Unit at the Institute of Genetics and Molecular Medicine of the University of Edinburgh. We have up to 6 MRC Capacity Building studentships designed to fulfill national requirements for expertise in mathematical biology and statistics. These prestigious studentships support each student and their project for 4 years and include a £2K pa stipend supplement over the usual award (in 2009 the stipend is £15,290) and generous funding for research expenses and travel. Full details are available from: <http://www.findaphd.com/custadverts/-4year/mrc/hgucompmed.asp> Applications are encouraged from those combining a biological background with experience in computational analysis or from those with a mathematical/computer science background and a keen interest in biology. For general inquiries about the studentships please contact: [Pauline.Mcdonald@hgu.mrc.ac.uk](mailto:Pauline.Mcdonald@hgu.mrc.ac.uk). For informal or academic enquiries please contact: [Colin.Semple@hgu.mrc.ac.uk](mailto:Colin.Semple@hgu.mrc.ac.uk). Interviews will be held

at the MRC Human Genetics Unit on the 1st of April 2009. The closing date for applications is the 20th of March 2009.

– Dr Colin A. M. Semple Head of Bioinformatics MRC Human Genetics Unit Institute of Genetics and Molecular Medicine Edinburgh EH4 2XU, UK Tel: +44 (0)131 332 2471 x4034 Fax: +44 (0)131 467 8456 Email: [Colin.Semple@hgu.mrc.ac.uk](mailto:Colin.Semple@hgu.mrc.ac.uk) Web: <http://www.hgu.mrc.ac.uk/Users/Colin.Semple/> [colins@hgu.mrc.ac.uk](mailto:colins@hgu.mrc.ac.uk) [colins@hgu.mrc.ac.uk](mailto:colins@hgu.mrc.ac.uk)

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## UEdinburgh QuantGenet

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

We are currently recruiting a Ph.D. student to evaluate and apply novel techniques for diversity-based gene mapping in livestock species. 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, 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. En-

thusiasm, 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). For further information, please contact [pam.wiener@roslin.ed.ac.uk](mailto:pam.wiener@roslin.ed.ac.uk). We will begin reviewing applications on 15 March 2009.

Pam Wiener Roslin Institute and Royal (Dick) School of Veterinary Science University of Edinburgh Roslin, Midlothian EH25 9PS 0131 527 4464

[Pam.Wiener@bbsrc.ac.uk](mailto:Pam.Wiener@bbsrc.ac.uk) [Pam.Wiener@bbsrc.ac.uk](mailto:Pam.Wiener@bbsrc.ac.uk)

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## UExeter FlyEvolution

I am seeking an enthusiastic student with a background in evolution, genetics, ecology or zoology to study: Parallel evolution of insecticide resistance in flies Supervised by Dr Nina Wedell at the University of Exeter UK

Insecticide resistance is rapidly reaching global fixation in many insect pest populations, hence there is an urgent need to develop new approaches to the management of agricultural pests and vectors of diseases. We will examine the evolution of parallel insecticide resistance in two related fly species caused by two different retrotransposon (Accord and Doc) insertions into homologous cytochrome P450 genes, which confer DDT resistance in both species. This provides an unrivalled opportunity to examine the impact of a single gene on the population genetics of two cosmopolitan fly species. DDT resistant *Drosophila melanogaster* females are more fecund than susceptible females, but although resistance alleles were present before the use of DDT, they only occurred at low frequency, implying an unknown cost to carrying the DDT resistance allele in males. In *D. simulans*, the Doc insertion also confers DDT resistance, but the potential costs and benefits to males and females has not been examined. There is evidence of a selective sweep of both TE insertions in both species, and intriguingly, the endosymbiont *Wolbachia* has also rapidly spread through fly populations in recent times.

We will quantify the fitness consequences of DDT resistance on male and female fitness in both *Drosophila* species and examine the interaction between homologous resistance genes and *Wolbachia* infection, to eval-

uate their relative importance for fly fitness. This will provide valuable information about the impact of foreign DNA present in the genome of potential pest species directly regulating their fitness, which may be useful in developing future pest management plans.

For more information contact Dr Wedell ([N.Wedell@exeter.ac.uk](mailto:N.Wedell@exeter.ac.uk))

Dr N Wedell Centre for Ecology & Conservation School of Biosciences University of Exeter Cornwall Campus Penryn CORNWALL TR10 9EZ UK

[http://biosciences.exeter.ac.uk/staff/profiles/-profile.php?id=nina\\_wedell](http://biosciences.exeter.ac.uk/staff/profiles/-profile.php?id=nina_wedell)

DJ Hosken <[D.J.Hosken@exeter.ac.uk](mailto:D.J.Hosken@exeter.ac.uk)>

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## UExeter FungalTreeOfLife

PHD Studentship

Understanding the fungal tree of life.

Supervisors: Dr Thomas Richards, Dr Akbar Javadi, and Prof. Nick Talbot

Deadline for Application: Friday 13 March 2009

Project summary: Standard approaches have failed to resolve the ecological complexity and branching order of the fungal tree of life. Environmental DNA sequencing in combination with bioinformatic analysis has demonstrated that microbial life has vastly more evolutionary complexity than had previously been observed. This project will use whole genome sequences, in combination with sophisticated phylogenetic models, to identify the backbone of the fungal tree of life and understand ancient fungal cell evolution. The project will also use large-scale environmental DNA amplicon sequencing to identify novel phylo-groups and discover how these groups relate to the fungal tree of life. Together, these data will identify the evolutionary history and the ecological complexity of the fungal kingdom.

This project is ideal for a candidate interested in evolution and who wants to learn molecular and phylogenetic methods.

For informal enquiries contact Dr Thomas Richards at [T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk) or for more information about the project and application procedure see <http://biosciences.exeter.ac.uk/postgraduate/-newposts.php#fungal> [T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)  
[T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)

at ex.ac.uk

Alexie Papanicolaou <A.Papanicolaou@exeter.ac.uk>

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## UExeter InsectGenomeBioinformatics

Project title: Bioinformatics of next generation sequencing approaches: using 454 and Solexa data to look at insect genomes and transcriptomes

Three-year studentship: tuition fees (UK/EU rate) and annual stipend at current research council rate

This PhD will provide training in state of the art bioinformatics both at the genomic and transcriptomic level. It takes advantage of a) the large amount of non-model insect 454 sequence data generated by our laboratory, b) our participation in the Heliconius genome project (3 species being sequenced at Baylor College of Medicine), c) our ongoing collaboration with the Sanger Center with BAC mapping and DNA sequencing and, most importantly, d) our initiation of collaborations with ecology and evolution groups in Cornwall. The project aims to fill the gap generated by the purchase of the Illumina sequencer at Streatham and the analysis of the pump priming projects from non-molecular biologists at both Tremough and Streatham Campuses of the University of Exeter. The student will receive training in the assembly and analysis of large next-generation sequence data sets of both the genome (e.g. Heliconius) and the transcriptome. The student will learn how to annotate ESTs and genomic DNA and to mine the data for items of interest to non-molecular biologists e.g. SNPs and micro-satellite markers. Students with a computing background will be involved in creating state-of-the art software to analyse -omic data derived from non-model species. The exact nature of the project will be decided with the candidate. For example, SNPs will be used to look for gene flow between the different islands of the Scillies to test if gene flow relates to the standing differences seen in eye spot variation between islands in the Meadow Brown (with Dave Hosken). SNPs will also be used to look for gene flow and dispersal between the different populations of the endangered Marsh Fritillary in the South West (with Dave Hodgson and Melanie Smee). Candidates with a Computer Science background wishing to learn about biology, evolution and comparative genomics are especially invited to apply.

Full details are available at [www.exeter.ac.uk/-biosciences/postgraduate/newposts](http://www.exeter.ac.uk/-biosciences/postgraduate/newposts) For informal enquiries contact: Prof. Richard ffrench-Constant: rf222

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## UExeter InsectGenomeBioinformatics Update

Dear Colleagues, This is an update for our PhD scholarship advert: These Departmental studentships will cover the full fee & stipend for the successful candidates regardless of their nationality. Thus International applicants are also invited to apply.

many thanks alexie – Alexie Papanicolaou Richard ffrench-Constant group CEC-Biology Univ. Exeter in Cornwall Penryn TR10 9EZ United Kingdom

alpapan@googlemail.com

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## UFribourg EvolutionaryGenetics

PhD Position in Evolutionary Genetics

Project: The genetics of reproductive isolation and trait differences in European Populus

Supervision: Christian Lexer, University of Fribourg, Switzerland

A PhD position is available in the newly established lab of Christian Lexer. I am looking for a highly motivated candidate with interests in the fields of evolutionary biology, population genetics, and ecology. The PhD fellowship is university-funded, and the project will be tightly linked with a British NERC-funded research project on the ecological & evolutionary genomics of species isolation in European Populus, which involves a postdoc, two other PhD students, and several collaborating labs in the EU and USA.

The PhD project will address the genetics of reproductive isolation and ecological trait differences in Populus alba and P. tremula. It is based on molecular genetic data which my group has gathered over the last several years, and on recent advances in the use of admixed populations and hybrid zones for addressing key questions in ecology & evolution. Key aspects of the PhD



project will be (1) to study the molecular population genetics of loci involved in species isolation, (2) to study the genetic basis and ecological impact of trait differences among different genotypes in natural populations. The project involves both, experimental lab work (sequencing, microsatellites, SNPs, interactions with related transcriptomics project) and ecological field work (assessment of tree biotic interactions). Depending on the interests of the student, there can be a stronger focus either on the lab or on the field component. In any case, an interest in new methods in computational biology is essential.

The starting date is negotiable (any time from July 2009 onwards). Funding from the university is for three years (annual salary is ca. CHF 40'000). Knowledge of French or German is helpful in every day life, but the working language in the group is English. A Diploma or Masters degree (or equivalent) in biology or related subject is necessary for admission. Fribourg is a lively town with over a quarter of the population being students. It's ca. 30 minutes from the Alps, close to other cities such as Berne and Lausanne and just a little over an hour from Geneva.

To apply, please send an e-mail with the application materials in a single pdf file to Christian Lexer ([christian.lexer@unifr.ch](mailto:christian.lexer@unifr.ch)). Application materials should include a CV, a list of publications, and a short (less than one page) statement of research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 30 March will be given full consideration. Interviews will take place end of April or early May.

Further information and address for application: Dr. Christian Lexer, Associate Professor of Evolutionary Biology E-mail: [christian.lexer@unifr.ch](mailto:christian.lexer@unifr.ch), Tel: +41 26 300 8868 Web: <http://www.unifr.ch/biol/ecology/lexer/index.html> For more information about Ecology & Evolution in Fribourg see <http://www.unifr.ch/biol/ecology/> christian.lexer@unifr.ch [christian.lexer@unifr.ch](mailto:christian.lexer@unifr.ch)

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## UFribourg EvolutionPlantInvasions

1 PhD & 1 Post-Doc Position in Evolutionary Ecology of Plant Invasions, University of Fribourg, Switzerland

Rationale

The proposed project will be the first one that considers the importance of polyploidy and herbivores for invasions simultaneously. Our leading hypothesis is that herbivore pressure and assemblage will, at least partially, explain the predominance of specific cytotypes both in the native and introduced range. The *Centaurea stoebe* L. (syn. *C. maculosa* Lam.) (Asteraceae) system provides an excellent model system to study these interactions, and we take advantage of the large knowledge already available on this plant and its herbivores. Native to Europe where it occurs as a diploid (2x) and a tetraploid (4x) cytotype, the species is highly invasive in North America, where nearly exclusively only 4x plants have been found. Several specialist insect herbivores have been introduced to North America for its biological control, with only partial success so far.

We seek two highly motivated researchers to help clarifying underlying mechanisms of this most successful plant invasion as a complement to various presently ongoing studies that we carry out in collaboration with both national (through NCCR Plant Survival) and international partners. We plan to (i) explore the relationship between type and amount of herbivory and the occurrence of the two cytotypes of *C. stoebe* in its native range by a European-wide survey combined with a replant/transplant experiment, (ii) carry out a series of experiments to analyze interactions between two selected specialist herbivores and the *C. stoebe* cytotypes, and (iii) investigate more generally into the role of generalist herbivores for plant invasions (in collaboration with Urs Schaffner, CABI Europe-Switzerland and our US counterparts).

### Requirements

- PhD position: Master Thesis in Biology, preferentially in ecology and evolution
- Post-Doc position: doctoral degree in plant ecology and evolution

For both positions, knowledge of, and experience in one or several of the following areas of research is desirable: experimental (field) ecology and evolutionary biology, invasion biology, plant-herbivore interactions, experimental design and statistical analysis; furthermore, fluency in English and driver's license will be required.

### Salary and conditions

The positions are funded by the Swiss National Science Foundation, and start April 1, 2009. Salaries: PhD c. 43'000 SFr/year for 3 years; Post-Doc dependent on age and status, gross salary in the first year about CHF 70'000, for 2-3 years.

## Applications

Applicants should e-mail their CV and publication list, together with a short motivation letter and a summary of research experience and interests, and the names of two professional referees to [Heinz.mueller@unifr.ch](mailto:Heinz.mueller@unifr.ch). Please indicate your earliest possible, and your ideal start.

For further information, please contact:

Prof. Dr. Heinz Müller-Schärer, Département de Biologie, Unité Ecologie & Evolution, Université de Fribourg, Chemin du Musée 10; CH-1700 Fribourg, SWITZERLAND; tel: + (41) (0) 26-300 88 35/50 cf. my research website at <http://www.unifr.ch/biol/-ecology/muellerschaerer/group/mueller/> for further information and recent publications on this subject.

Heinz Müller-Schärer <[heinz.mueller@unifr.ch](mailto:heinz.mueller@unifr.ch)>

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## UGroningen EvolGenomics parasitoidhost

### PhD position in Evolutionary Genomics (1.0 fte)

The PhD position is available at the Centre for Ecological and Evolutionary Studies at the University of Groningen. The candidate will join a recently started research group that studies parasitoid-host interactions to unravel the evolutionary genomics of adaptations. The overall aim of the research group is to identify what genomic features (e.g., SNPs, transposons, epigenetic regulation) enable a rapid evolutionary response to adverse environmental conditions. The aim of the PhD project is to identify genomic variation among natural *Drosophila melanogaster* populations and associate it to immunological resistance against their parasitoids. The research will comprise a mix of field work, genomic techniques (tiling arrays and high-throughput sequencing), fly biology and genetics, as well as bioinformatics.

**Requirements and duties** We seek an energetic PhD student, to carry out this fundamental research project at the forefront of evolutionary genomics. The candidate has a master's degree or equivalent in biology, with a strong interest in evolutionary biology and a background in genetics, genomics, evolutionary ecology, molecular biology and/or bioinformatics. Good analytical skills and a positive attitude towards learning new methods are required. Objective of the temporary 4 years position is the production of a number of research articles in peer-reviewed scientific journals,

which together will form the basis of a thesis leading to a PhD degree (dr.) at the University of Groningen. Candidates will enrol in the education and supervision program of the Groningen Graduate School of Science. Teaching duties of 10% of the time are foreseen.

**Organization** The University of Groningen was founded in 1614 and is one of the best universities in Europe and the world. It houses a wide variety of disciplines, is socially active and is internationally oriented. The university is rooted in the North of the Netherlands. Our researchers and lecturers are inspired academics and our students are ambitious. We respect the differences in talent, ambitions and performance of the 25.000 students and members of staff. The university provides a career advisory service for partners of new staff who move to Groningen. The university is an equal opportunities employer. Because women are still under-represented in a number of fields, they are particularly encouraged to apply.

**Additional conditions of employment** The University of Groningen offers a salary of 2042 gross per month in the first year up to a maximum of 2612 gross per month in the fourth year. After the first year there is an evaluation for feasibility of successful completion of the PhD thesis within the next 3 years. The Centre for Ecological and Evolutionary Studies (CEES) at the University of Groningen provides a stimulating research environment, with good facilities and high quality training and teaching.

**Additional information** Additional information about the vacancy can be obtained from Dr. Bregje Wertheim, e-mail address: [b.wertheim@rug.nl](mailto:b.wertheim@rug.nl). Or additional information can be obtained through one of the following links. About the organization: <http://www.rug.nl> About the Evolutionary Genetics group: <http://www.rug.nl/biologie/onderzoek/-onderzoekGroepen/evolutionaryGenetics/index> Application Letters in English language, including a personal motivation (important!), curriculum vitae, and the names and addresses of three referees (including telephone number and E-mail address), to be sent before 12 March 2009 to: [vmp@rug.nl](mailto:vmp@rug.nl). Also send an electronic copy of your application to [b.wertheim@rug.nl](mailto:b.wertheim@rug.nl). When applying for this job always mentions the vacancy number AT209073.

Dr Bregje Wertheim Rosalind Franklin Research Fellow  
Evolutionary Genetics Biological Centre University of Groningen  
Postbus 14 9750 AA Haren The Netherlands  
[p254663@rug.nl](mailto:p254663@rug.nl) [p254663@rug.nl](mailto:p254663@rug.nl)

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## UHouston EvolutionaryBiology

### GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Biology and Biochemistry at the University of Houston (UH) is recruiting graduate students for its graduate program in Evolutionary Biology and Ecology for Fall 2009. The following faculty in the area of Evolutionary Biology and Ecology are seeking graduate students for their labs:

Blaine Cole (bcole@uh.edu) - Evolution and social behavior  
 Dan Graur (dgraur@uh.edu) - Theoretical molecular evolution  
 Diane Wiernasz (dwiernasz@uh.edu) - Ecological genetics  
 George Fox (fox@uh.edu) - Experimental evolution and origin of life  
 Rebecca Zufall (rzufall@uh.edu) - Genome and molecular evolution  
 Ricardo Azevedo (razevedo@uh.edu) - Evolution of development and behavior  
 Steve Pennings (spennings@uh.edu) - Community ecology  
 Tim Cooper (tcooper@central.uh.edu) - Experimental evolution  
 Tony Frankino (wafranki@central.uh.edu) - Evolution of development  
 Yuriy Fofanov (yfofanov@bioinfo.uh.edu) - Evolutionary bioinformatics

For more information regarding the Evolutionary Biology and Ecology graduate program at UH see:

<http://www.uh.edu/admissions/graduate/> The deadline for application of prospective students is April 1st, 2009, but students are encouraged to apply as soon as possible.

razevedo@uh.edu razevedo@uh.edu

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## UKiel CombJellyEvolution

The Leibniz Institute of Marine Sciences (IFM-GEOMAR) at the University of Kiel is one of the leading institutes in marine research worldwide. Its major goal is fundamental research in all areas of marine sciences. For more information please visit [www.ifm-geomar.de](http://www.ifm-geomar.de). We are offering a PhD position in

Evolutionary Ecology and Genetics of an Invasive Comb Jelly

in the research unit Evolutionary Ecology of Marine Fishes

### Job Description

The successful applicant will study the population genetics of the invasive comb jelly *Mnemiopsis leidyi* that has recently colonized North and Baltic Sea and may result in drastic ecosystem changes in the pelagic zone. Key goals are to (1) reconstruct the invasion history and sources (2) compare genetic diversity at neutral and selected markers over time and between populations (3) assess the importance of hybridization for invasion success. Moreover, genome scans using SNPs and microsatellites derived from EST libraries will be developed to address the potential role for rapid adaptation of invading *Mnemiopsis* to its new environment at the molecular genetic level. Through the cluster of excellence "The Future Ocean", our group has access to state-of-the-art molecular genetic and genomic tools (Q-PCR, Roche454 and solid sequencing, capillary sequencing and fragment analysis, array technology). The project will also involve a substantial effort in worldwide field sampling either from the coast or during research ship cruises for obtaining plankton samples. If the requirements are fulfilled, a doctorate of science, equivalent to a PhD degree, can be granted by the University of Kiel after 3 years. All PhD students are members of the graduate school ISOS = Integrated School of Ocean Sciences (<http://www.ozeander-zukunft.de/isos/ueber-uns/>)

### Qualification

We request a Master or Diploma degree in Biology, Evolution, Ecology, Genetics or a related subject. Basic experience with molecular genetic techniques is required. Preference will be given to candidates with one or more of the following areas of expertise, best demonstrated through their thesis work, or scientific publications: microsatellite genotyping, EST library construction, SNP genotyping, genome scans, evolutionary biology, population genetics, invasion biology, evolutionary bioinformatics.

This is a half time position is available for a period of 3 years, starting immediately. The salary is according to class 13 TV-L of the German tariffs for public employees and will be approximately 25 000 Euro gross /yr. Working language in the group is English. The Leibniz-Institute of Marine Sciences is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply. Please send your applications for this post no later than 10 March 2009 by e-mail using the keyword "invasion genetics" to Prof. Thorsten Reusch (treusch@ifm-geomar.de <<mailto:treusch@ifm-geomar.de>>). Please give name and address of two ref-

erences and add a short statement of your interest in this position.

Prof. Thorsten B. H. Reusch Professor of Marine Ecology Leibniz Institute of Marine Sciences IFM-GEOMAR 24105 Kiel Germany treusch@ifm-geomar.de

## UKiel FishStressEvolution

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

PhD position in fish stress evolution and transcriptomics in the newly founded research unit Evolutionary Ecology of Marine Fishes

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

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

This is a half time position is available for a period of 3 years. The salary depends on qualification up to the class 13 TV-L of the German tariffs for public employees. Working language in the group is English. The

Leibniz-Institute of Marine Sciences is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply.

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

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

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

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

Prof. Dr. Reinhold Hanel Leibniz-Institut für Meereswissenschaften IFM - GEOMAR Dienstgebäude Westufer Düsternbrooker Weg 20 D-24105 Kiel Germany ><((( $\hat{A}$ ) < $\hat{A}$ )))>< Tel: +49 431 600 4556 Fax: +49 431 600 4553 e-mail: rhanel@ifm-geomar.de [www.ifm-geomar.de](http://www.ifm-geomar.de) Reinhold Hanel <rhanel@ifm-geomar.de>

## ULouvain TetrahymenaBiodiversity

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

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

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

We are currently looking for a highly motivated student to start a Ph.D. within the framework of a new and stimulating project focusing on the experimental study of metapopulation dynamics and viability with microcosms of a unicellular microorganism, *Tetrahymena thermophila*. Such microcosms are simplified versions of real world systems, with a level of control and replication impossible to achieve on real populations. We intend to use such microcosms to unravel the complex links between life history traits, population struc-

ture and viability. More information on the project is available on <http://www.uclouvain.be/en-81937.html> (see also BMC Evol. Biol. 7, 133 for our previous work). This project nicely complements our ongoing research on threatened butterfly metapopulations.

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

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

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

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

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

Prof. Nicolas Schtickzelle Research Associate (FNRS) & Lecturer

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

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

[nicolas.schtickzelle@uclouvain.be](mailto:nicolas.schtickzelle@uclouvain.be)  
[www.uclouvain.be/quant-cons-biol](http://www.uclouvain.be/quant-cons-biol)

<http://->

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## UMontreal Bioinformatics

Graduate student position (PhD) in bioinformatics available

A position is available to identify (primary and secondary structure) motifs involved in a novel RNA trans-splicing process that we discovered recently (Marande & Burger 2007, Science 318:415). Predicted motifs and postulated mechanisms will be the basis for in vitro experiments, which, in turn, will help to narrow the search space of in silico analyses. More information about the laboratory's research program is available at <http://megasun.bch.umontreal.ca/People/burger/-research.html> Affiliation: Robert-Cedergren Centre for Bioinformatics and Genomics, biochemistry department, Université de Montréal, Montréal, Canada.

Training background: MSc in bioinformatics or interdisciplinary training in molecular biology & computer science. The candidate will enroll in the bioinformatics PhD program of the Université de Montréal.

Expertise: Methods and tools in pattern searching, motif prediction, RNA secondary structure prediction, gene prediction. Programming expertise in Perl, C(++), Java on the Unix/Linux platform.

Starting date: Immediately.

Application: Interested candidates are encouraged to send their CV, addresses for potential reference letters, student transcript, and Master thesis (electronic form) to

Gertraud Burger, PhD Robert-Cedergren Centre for Bioinformatics and Genomics Département de Biochimie Université de Montréal, Pavillon Roger Gaudry 2900 Blvd Eduard-Montpetit Montréal, Québec, H3T 1J4, CANADA Email: [jobs@bch.umontreal.ca](mailto:jobs@bch.umontreal.ca) (Subject: "PhD-bioinfo")

Gertraud Burger <[gertraud.burger@umontreal.ca](mailto:gertraud.burger@umontreal.ca)>

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## UMunich LMU EvolutionEcolSyst MasterProgram

Since 2007 the University of Munich (LMU) offers a 2-

year, international Master program in Evolution, Ecology and Systematics (EES).

The EES Master program contains many innovative elements such as a mentoring program, integrated skills courses and individual research training. We also apply a feedback and revision system instead of simple grading. All courses are offered in English. Classes are small and students have a lot of contact to the teachers. Thanks to funding by the Volkswagen Foundation, students can apply for their own research and travel money and for money to invite international speakers.

Applications to start in October 2009 are now welcome from highly motivated students who have a Bachelor's degree or equivalent in biology or a related subject. Application deadlines: 30th of April (for non-EU students) and 30th of June (for EU-students and others who don't need a visa to study in Germany).

For more information, please have a look at our website (<http://www.eeslmu.de>) or contact me by e-mail.

Best wishes, Elisabeth Brunner

\* Program Coordinator of the Munich Graduate School for Evolution, Ecology, and Systematics

Department Biologie II University of Munich (LMU)  
Großhaderner Str. 2 D-82152 Planegg-Martinsried

Tel: 0049 89 2180 74 208 <http://www.eeslmu.de/-eeswiki> brunner@bio.lmu.de

Elisabeth Brunner <brunner@biologie.uni-muenchen.de>

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## UNewOrleans ConservationBiology

### DOCTORAL FELLOWSHIPS IN CONSERVATION BIOLOGY UNIVERSITY OF NEW ORLEANS

The Department of Biological Sciences at the University of New Orleans announces two Doctoral Fellowships in Conservation Biology available for Fall 2009. The fellowships provide support for four years with an annual stipend of \$25-26,000 and a full tuition waiver. The Department of Biological Sciences offers exciting opportunities for graduate student research in ecology, evolution, systematics, genetics, physiology, molecular biology, and biochemistry. For more information on the Department, faculty research interests, and other resources, please see the website: <http://biology.uno.edu/> < <http://biology.uno.edu/> >

Applicants should indicate that they wish to be considered for a Fellowship on the standard application form for the Graduate Programs in Biological Sciences, which can be obtained online at <http://biology.uno.edu/phdprogram.aspx> or by writing to:

Graduate Coordinator Department of Biological Sciences  
University of New Orleans New Orleans, LA 70148

Applicants must also file a graduate application with University of New Orleans admissions (see <http://admissions.uno.edu/app.cfm>). Applicants must be U.S. citizens or permanent residents. Applications from minority groups under-represented in the sciences are especially encouraged. The deadline for review of applications has been extended to March 16, 2009. UNO AA/EEO.

Nicola M. Anthony, Assistant Professor, Department of Biological Sciences University of New Orleans 2000 Lakeshore Drive New Orleans LA 70148

Tel. (504) 280-1362 Fax. (504) 280-6121 Email: [nanthony@uno.edu](mailto:nanthony@uno.edu)

Nicola Mary Anthony <[nanthony@uno.edu](mailto:nanthony@uno.edu)>

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## UOttawa AntibioticEvolution

Applications are sought from outstanding candidates for a PhD position in evolutionary genomics of antibiotic resistance. This work is part of a Canadian Institutes of Health Research funded study to investigate the persistence of resistance to fluoroquinolone antibiotics in *Pseudomonas aeruginosa* infections associated with cystic fibrosis. The project demands a combination of skills including genome resequencing and bioinformatics, experimental evolution, and molecular microbiology. Experience in at least one of these fields is an asset. The successful candidate will work under the supervision of Rees Kassen (<http://www.science.uottawa.ca/~rkass574/> < <http://www.science.uottawa.ca/~rkass574/> > ) in partnership with researchers at the Ottawa Hospital and will join a growing community of evolutionary biologists at the University of Ottawa (<http://www.evolution.uottawa.ca/> < <http://www.evolution.uottawa.ca/> > ). The University is also host to the 2012 meeting of the Society for the Study of Evolution held in conjunction for the first time with the European Society of Evolutionary Biology.

Applications should include a cover letter and curriculum vitae, as well as the names and contact information (including e-mail) of at least two referees. All application materials must be submitted as a PDF in a single email to Rees Kassen (rees.kassen@uottawa.ca), to whom queries may also be addressed. The closing date for applications is March 10, 2009. It is anticipated that the successful candidate would take up the position as early as May 01, 2009 and no later than September 01, 2009.

Located at the confluence of English and French Canada, Ottawa is a vibrant national capital of approximately 1 million inhabitants (<http://www.ottawatourism.ca> < <http://www.ottawatourism.ca/> > ). The city offers a wide range of cultural activities in the visual and performing arts, as well as easy access to green spaces and wilderness. The University of Ottawa is located next to the historic Rideau Canal, steps from Parliament and within easy access to a wide range of research facilities of interest to evolutionary biologists including the Canadian Museum of Nature, the National Wildlife Research Center, Health Canada, and Environment Canada.

Rees.Kassen@uottawa.ca Rees.Kassen@uottawa.ca

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## UStAndrews Lichen2ryMetabolism

Dear Evoldir,

I am re-advertising this position, because it has recently become even better due to the addition of a new supervisor and institute.

We are seeking applicants for a PhD position at the University of St Andrews and the Royal Botanic Garden Edinburgh.

**SECONDARY METABOLISM IN LICHENS - LINKING GENES TO METABOLITES**

Supervisors: Dr Daniel Barker, Dr Terry Smith and Dr Shiela Unkles (University of St Andrews) and Dr Rebecca Yahr (Royal Botanic Garden Edinburgh)

Lichens are a symbiosis between a fungus and an alga or cyanobacterium. Lichens form a major component of many environments, particularly extreme environments such as desert and arctic regions. Secondary metabolites are chemicals produced by an organism that are not directly involved in growth, but are beneficial to its well-being, for example through interactions between

species such as competition and defense. Many secondary metabolites are useful to humans, for example as antibiotics or dyes.

Secondary metabolites are particularly common in lichen-forming fungi. An understanding of the biochemical detail of secondary metabolism, its regulation, and the evolutionary forces acting on these are often poorly understood. The gene families involved in secondary metabolism are often known, but the link between a specific secondary metabolite and the gene coding for the specific enzyme activity to make it, is often unknown.

This proposal aims to link specific secondary metabolites to their cognate genes. The project will focus on investigating the evolution of the polyketide class of secondary metabolites, and the underlying biosynthetic and regulatory genes, in *Porpidia*. *Porpidia* is a lichen-forming fungal genus in which secondary metabolites vary both between, and within, species. The student will carry out “wet” laboratory work and some fieldwork, and will develop and use novel bioinformatics algorithms to integrate data on secondary metabolites and genes.

Informal enquiries to Daniel Barker, db60@st-andrews.ac.uk

For further details, including how to apply, please see:

<http://biology.st-andrews.ac.uk/-projectProfile.aspx?psr=79&pid=163> IMPORTANT NOTE ON FUNDING

A successful candidate would receive funding (covering fees and stipend) as a Natural Environment Research Council CASE studentship. This funding is ONLY possible for candidates who meet NERC’s criteria:

<http://www.nerc.ac.uk/funding/application/-studentships/studentbook2008.pdf> In particular, please note the section “Residence” (pp. 3-6).

Best regards,

Daniel

– Daniel Barker <http://bio.st-andrews.ac.uk/staff/-db60.htm> The University of St Andrews is a charity registered in Scotland : No SC013532

db60@st-andrews.ac.uk db60@st-andrews.ac.uk

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## UWarwick ExperimentalEvolution

PhD studentship, Experimental evolution in *Chlamydomonas*, University of Warwick, UK

We have recently been awarded Leverhulme Trust funding for an exciting new project to study the experimental evolution of resistance to herbicides in the unicellular chlorophyte, *Chlamydomonas reinhardtii*. As part of this 3-year project we are looking to recruit a postdoctoral researcher.

There is increasing recognition that human activities are accelerating rates of global environmental change. There is a concern that these changes are driving increased rates of evolutionary change in the global biota. The emerging and vibrant discipline of experimental evolution offers the possibility to study such 'evolution in action' to address fundamental and applied questions in ecology and evolution. Our research uses *Chlamydomonas* as a model photosynthetic organism to study the dynamics of evolution of resistance to herbicides. This work addresses fundamental questions relating to the evolution of tolerance/resistance to a novel stress as well as practical issues surrounding the management of a significant constraint to global food production.

We are looking for enthusiastic and committed applicants with a strong academic record in disciplines related to ecology and evolution. The project will start in September 2009 and will be supervised by Dr Paul Neve (Warwick HRI, University of Warwick) and Dr Nick Colegrave (Institute of Evolutionary Biology, University of Edinburgh). The positions will be based at University of Warwick, though it is expected that successful applicants could spend some time in Edinburgh.

Indicative areas of research for the PhD student are: evolution of resistance in simple (one herbicide) and complex (multiple herbicide) environments, impact of cycling different herbicides on evolution of specialist and generalist resistance types, impacts of simulated gene flow and habitat structure on resistance evolution.

For further details please contact Paul Neve: Email: p.neve@warwick.ac.uk Tel: +44 24 7657 5843.

Dr Paul Neve Warwick HRI University of Warwick Wellesbourne Warwickshire CV35 9EF

Tel: +44 2476 575843 Fax: +44 2476 574500

"Neve, Paul" <P.Neve@warwick.ac.uk>

WAGNER Andreas, Prof. aw@bioc.uzh.ch six digit code:010000

\*PhD thesis in computational evolutionary biology\*

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study robustness and evolvability in large metabolic networks, using computational approaches. The successful candidate will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also necessary is a strong background in biology. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further. We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently. The working language in the laboratory is English. German skills are not essential.

The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects range from laboratory evolution experiments in yeast to human population genomics. A sample of our research can be found at <http://www.bioc.uzh.ch/wagner/>. \*Lab members are a group with very diverse backgrounds, research projects, and nationalities. They are unified by their interests in evolution and /or fundamental organizational principles of life. \*\*

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

To be considered, please send a single (!) PDF file merged from the following parts to jobs\_aw@bioc.uzh.ch: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references. Please include the word COMP09 in the subject line. The application deadline is March 30, 2009. The earliest starting date is August 1, 2009.

—  
Christiane Gujan Administrative Assistant of Prof. A. Cafilisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 Fax 0041 (0)44 635 68 62

Christiane Gujan <gujan@bioc.uzh.ch>



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### AarhusU Bioinformatics

Associate professorship in bioinformatics

A position as associate professor in bioinformatics is available starting July 1, 2009 at the Bioinformatics Research Center (BiRC), Aarhus University, Denmark. BiRC is an interdisciplinary research center that employs about 35 researcher and PhD students.

The successful candidate must have strong scientific qualifications and a broad and well documented knowledge of the field of bioinformatics. Applicants with a biological background who can contribute to the theoretical foundation of bioinformatics, and who have experience with empirical work in the applications areas of bioinformatics, will be preferred.

The successful candidate is expected to establish his or her own research group and profile, as well as participate actively in collaborations with other researchers at BiRC and Aarhus University. Applications must be in English and include a curriculum vitae, a complete list

of publications, a statement of future research plans and information about research activities, teaching qualifications and management experience, all in 4 copies (see <http://www.nat.au.dk/default.asp?id=7842&la=UK> for the recommended level of detail). If the applicant wants other material to be considered in the evaluation (publications and other documentation of research and teaching qualifications, as well as management experience) such material must be clearly specified and must either be enclosed in hardcopy (3 copies) or must be available electronically.

The Faculty refers to the Ministerial Order No. 92 of 15.02.2008 (<http://science.au.dk/default.asp?id=7839&la=UK>) on the appointment of teaching and research staff at the universities under the Ministry of Science, Technology and Innovation. Salary depends on seniority as agreed between the Danish Ministry of Finance and the Confederation of Professional Unions. Applications should be addressed to The Faculty of Science, University of Aarhus, Ny Munkegade, Building 1520, DK-8000 Aarhus C, Denmark, and marked 212/5-268.

The deadline for receipt of all applications is March 16,

2009, at 12,00 noon. For more information please contact the director of BiRC, Christian NÅrgaard Storm Pedersen, e-mail [cstorm@birc.au.dk](mailto:cstorm@birc.au.dk), phone +45 8942 3121. For information about BiRC in general, see <http://www.birc.au.dk> . Aarhus University offers a good and inspiring education and research environment for 35,000 students and 8,500 members of staff, who produce academic results of a high international standard. The budgeted turnover for 2009 amounts to EUR 700 million. The university's strategy and development contract are available at [www.au.dk](http://www.au.dk) . "Mikkel H. Schierup" <[mheide@daimi.au.dk](mailto:mheide@daimi.au.dk)>

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### AngersFrance ConservationBiol

National Institute of Horticulture and Landscape (INHP) Angers, France

The National Institute of Horticulture and Landscape in Angers (France) invites applications for a tenure track position in insect ecology and conservation biological control. The position is at the Assistant Professor level. Expected starting date is September 1, 2009.

For complete job description, visit [http://www.emploi-scientifique.info/esf\\_view\\_offre.php?id\\_offre=4042&retour\\_bureau=1](http://www.emploi-scientifique.info/esf_view_offre.php?id_offre=4042&retour_bureau=1) The candidate is expected to teach and to contribute to the education and training of undergraduate and graduate students. Research will be conducted in collaboration with the UMR BiO3P. Our team is interested in the evolution of plant-animal interactions as a basis for more sustainable pest and crop management.

Ph.D. required and a post-doctoral experience is desirable.

[josiane.lecorff@agrocampus-ouest.fr](mailto:josiane.lecorff@agrocampus-ouest.fr)

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### ArizonaStateU ResearchSpecialist ConservationGenetics

The Dowling lab in the School of Life Sciences at Arizona State University invites applications for a Research Specialist. The individual will assist with multiple aspects of research focused on conservation of native fishes of the southwestern United States. Applicants

are expected to have a B.Sc. degree or higher in biology, with laboratory experience preferred. The principal duties of the individual pertain to the collection and organization of data and lab management. Applicants should be proficient with basic molecular procedures (DNA/RNA extraction, PCR, electrophoresis, molecular cloning, sequencing). Precision and reliability are essential. Duties will also include contributing to lab management such as oversight of undergraduate student workers, safety awareness, ordering, chemical inventories and the repair of minor equipment. Computer literacy is expected.

Salary will be commensurate with experience. Additional information on the position and instructions for application are provided at the following web address:

< <https://www.asu.edu/go/employment/?auth=guest>  
><https://www.asu.edu/go/employment/?auth=guest>

Go to job #22266. The closing date is 24 February 2009. If you have any additional questions email me at [thomas.dowling@asu.edu](mailto:thomas.dowling@asu.edu).

Thomas Dowling <[thomas.dowling@asu.edu](mailto:thomas.dowling@asu.edu)>

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### ArizonaStateU Undergraduate AvianEvolution

SEEKING UNDERGRADUATE RESEARCH ASSISTANT FOR STUDY OF AVIAN COLORATION AND SEXUAL SIGNALING We are seeking a qualified undergraduate to participate in a Research Experience for Undergraduates (REU) opportunity, funded by the National Science Foundation, to study coloration and sexual signaling in birds. The research experience will involve up to 10 weeks of full-time work during the summer of 2009 (approx. June-August) at Arizona State University. The REU student will work closely with Professor Kevin McGraw and Dr. Melissah Rowe (post-doctoral associate) on this project. The program includes a weekly stipend, and some travel funds will be available to help defray the cost of traveling to Tempe, Arizona. The research project will involve working with captive populations of two species of waterfowl V mallard (*Anas platyrhynchos*) and northern pintail (*Anas acuta*). The student will gain hands-on experience working with birds and will utilize a suite of biochemical, immunological, nutritional, and color-analysis techniques in the lab. In addition, the student will be involved in data entry, analysis, and interpretation. The student is also strongly encouraged to de-

velop an independent research project throughout the summer. We seek students with strong credentials, a general background in biology and chemistry, and an interest in ecological, evolutionary, physiological and/or immunological research. Preference will be given to students planning to attend graduate school in animal behavior or a related field. Women and ethnic minority students are especially encouraged to apply. Interested students should submit the following application materials electronically (as attachments, preferably in a single PDF) to Melissah Rowe (melissah.rowe@asu.edu): i) Curriculum Vitae, ii) grades (unofficial transcripts are fine) and a list of relevant courses, iii) names and contact details for three references iv) a cover letter that describes any previous research and a brief statement explaining your interest in obtaining research experience in animal behavior.

melissah rowe

School of Life Sciences Arizona State University Tempe, AZ 85287-4501

phone: 480/ 727-9094 email: melissah.rowe@asu.edu

melissah rowe <Melissah.Rowe@asu.edu>

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### BernU FieldAssist AvianEvolution

Ubern: field assistants bird evolutionary ecology

We are seeking 4 enthusiastic field assistants interested in taking part in a field study in Bern, Switzerland. Applicants will be part of the evolutionary ecology team (Zoological Institute, Bern University). Our study model is a passerine bird, the great tit. The tits are a good model system as they are hole nesting birds, breeding in forests near Bern, and as they can be easily manipulated. We are part of a 10 people lab team, all working with great tits in natural conditions. We work with about 300 nest boxes for each, disposed in several forests close to Bern. The study aims to investigate the effect of oxidative stress on sperm quality as well as a potential heritability of these traits in the great tit. This experiment will be conducted by Sylvain Losdat (PhD).

We will require 2 field assistants that will help with all the aspects of the work, including checking nests, ringing the birds, catching adults, performing treatments, and more. Applicants with a Msc in Biology/Ecology and/or with bird handling experience would have an advantage. Supervising for potential Msc analysis and

report would be assured by PhD and Post-doc people from the lab. Motivation will play a key role: the work is hard and demanding, may take place in changing weather and requires long hours at times. The study will start at the end of March 2009 until the beginning of June 2009. Fluent English or French speaking is required as well as a valid European driving license.

Applicants can send us a letter + CV and ask for further details or questions on the following email address:

\*Sylvain Losdat\* Evolutionary Ecology Group, Zoological Institute University of Berne Baltzerstr. 6 3012 Bern Switzerland Email: sylvain.losdat@iee.unibe.ch Phone: +41316313020 Mobile: +41774565214

Sylvain Losdat <sylvain.losdat@iee.unibe.ch>

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### BlackHills FieldAssist Avian

FIELD ASSISTANTS needed for a field study in the Black Hills National Forest of South Dakota starting roughly at the beginning of April and running through the end of July 2009 (dates flexible). The research is part of an ongoing study by DR. ELLEN KETTERSON on the breeding biology of Dark-eyed juncos. Responsibilities may include locating birds on their territories, finding nests, targeted and passive mist-netting, bird measuring and blood sampling, nest monitoring, behavioral observations, lab work and data entry. Applicants must be able to distinguish colored leg bands in the field, enjoy working outdoors (even in bad weather), be self-motivated and demonstrate a willingness to learn new skills, be able to work well with others, and be willing to do minor manipulative research with animals. Experience strongly preferred but not absolutely necessary. However, motivation is a primary consideration: the work is sometimes hard and demanding and can require long hours. The work is very rewarding if you are interested in animal behavior and like to be outdoors. Room, board, transportation allowance and stipend will be provided. An independent research project may also be available for a particularly promising undergraduate applicant. Questions and applications should be sent to Christy Bergeon Burns, Department of Biology, Indiana University, 1001 E. 3rd St., Bloomington, IN, 47405 or email (preferred) cbergeon AT indiana.edu. Please include a summary of your background and your reasons for applying for this position, as well as the names and email addresses of 2-3 people who might evaluate your work or potential. Re-

view of applications will begin immediately, but applications will be accepted until positions are filled.

cbergeon@gmail.com

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## Edinburgh BlueTitResTech

Post title: Blue Tit Research Technician

A vacancy has arisen at the University of Edinburgh, UK, for a research technician to work as part of a NERC funded project to understand the evolutionary ecology of Blue tits, and in particular the underlying genetics of family interactions. From April-June the successful candidate will assist with data collection in a wild population of Blue tits under the supervision of Dr Jarrod Hadfield. Outside of the field season the successful candidate will be involved in genotyping microsatellites and sex-specific markers under the supervision of Dr Jarrod Hadfield, Prof Josephine Pemberton & Prof Mark Blaxter. Experience with handling birds and/or molecular techniques would be preferred but is not essential, as full training will be given.

Salary range: 17,519 to 19,645

Applications are to be submitted on-line at <http://www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=vacancies.viewnew> (reference number: 3010510) by the 6th March.

Jarrod Hadfield

Jarrod Hadfield <J.Hadfield@ed.ac.uk>

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## Hagerman ID ConservationGenetics

Position Title: Conservation Geneticist - Genetic Stock ID Specialist Agency/Dept: Columbia River Inter-Tribal Fish Commission, Fishery Science Classification: Full-time (contingent upon funding), Regular Location: Hagerman, Idaho Starting Salary: \$50,000 - \$60,000 depending on qualifications and experience Application Deadline: March 6, 2009 (applications will be considered until position is filled)

Job Summary:

We are seeking a fishery scientist experienced in genetic

stock identification (GSI) methods. The position is part of CRITFCs Fishery Science Department, but will be based at the Hagerman Fish Culture Experiment Station located in Hagerman, ID. The research group is involved in testing conservation, evolution, and ecological theories related to Pacific salmon. The employee will work under the Lead Geneticist, in association with CRITFC geneticists and technicians, as well as staff of the Fishery Science Department in Portland, OR. Efforts will focus on conservation genetics and genetic stock identification of Chinook, steelhead, sockeye, and coho salmon.

Essential Functions:

Specific duties of this position include, but are not limited to:

1. Conduct genetic laboratory analyses including microsatellite and SNP genotyping.
2. Perform data analysis with heavy emphasis on mixed stock analysis.
3. Develop sampling designs and protocols for mixed stock analysis.
4. Execute research in accord with developed proposals.
5. Produce reports and peer reviewed publications of key scientific results.
6. Develop research proposals to attract extramural funding.
7. Participate in inter-agency workgroups, as necessary.
8. Provide technical advice and reviews in the areas of genetics and conservation biology to tribal staff, attorneys and policy.
9. Other duties as assigned and as appropriate to CRITFC goals and purposes.

Qualifications: The Conservation Geneticist - Genetic Stock ID Specialist is required to have a Ph.D. or M.S. (with three years experience) in the field of molecular biology, genetics, fishery biology, ecology and/or a related discipline. In addition, the scientist must have demonstrated skills in the following areas. 1. Research experience related to population/conservation genetics and mixed stock analysis. 2. In depth knowledge of current molecular genetic techniques, laboratory methods and equipment (i.e., Tecan Evo200 automated pipettor, ABI 3730 capillary sequencer, ABI 7900 HT, Fluidigm EP1, or similar equipment). 3. Excellent understanding of theoretical/statistical population genetics. 4. Experience in statistical analysis, computer modeling and the relevant software. 5. Proven ability to publish research in peer-reviewed publications. 6. Good writing and oral communication skills. 7. Interpersonal skills, including the ability to develop, guide, and work within inter-disciplinary teams. 8. Strong skills with common computer software for word processing, spreadsheet, database, and statistics use.

The following qualifications, although not required, are desirable: 9. Demonstrated technical competence in fishery biology or a closely related discipline. 10.

Database management, computer programming skills.

Supervision Received/Given: The incumbent must be an effective team member and may assist in supervision of technicians. The Conservation Geneticist - Genetic Stock ID Specialist must have the ability to work independently, but coordinate and communicate well with Lead Geneticist in Hagerman, and staff in the Fishery Science and Fishery Management departments in Portland, OR.

Working Conditions: Most of the work is performed in a laboratory or office setting. There may be opportunity to participate in field sampling and attend regional meetings, conferences and workshops. Must be able to travel occasionally, by auto and air.

Application procedure: Email cover letter, CV/resume, completed job application (available at <http://www.critfc.org/text/jobann.html>) and a list of three professional reference contacts to:

Columbia River Inter-Tribal Fish Commission Attn: Human Resources 729 NE Oregon, #200 Portland, OR 97232 Email: [andj@critfc.org](mailto:andj@critfc.org) Fax: 503-235-4228

[NARS@critfc.org](mailto:NARS@critfc.org)

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## INRA France InvasionDynamics

Permanent research position at INRA, the French National Agricultural Research Institute

Population dynamics of invading populations

Description

The success or failure of biological invasions depends on intrinsic demographic factors (demographic stochasticity, Allee effects), indirect demographic processes (the effect of population size on genetic variability and evolution in the novel environment), or genetic processes which reflect on demography (inbreeding depression). In order to limit accidental invasions or to optimize introduction strategies (biocontrol, reintroductions), it is important to understand the nature and consequences of such processes. In this perspective, we are recruiting a research scientist with skills in population dynamics and a strong motivation to work on invasive phenomena. We seek someone being able to develop an approach based on experiments, but with a serious theoretical background concerning processes at work in small populations. One objective is to develop researches combining academic approaches of invasion bi-

ology - based on concepts from population biology and evolutionary ecology - with the more applied research field of biological control. The recruited researcher will bring a new competence in a team already involved in population genetics and behavioral ecology (4-5 researcher scientists, 4 research assistants and 4 PhD students and postocs). There will also be some opportunity to develop research programs with the technical assistance of the local biological control research unit (a dozen of research assistants including 3 PhD).

Practical Information

The position is open at the INRA Research Institute located in Sophia-Antipolis, South-East of France (N43.612611; E7.077860). A PhD is mandatory, a post-doc is a plus. The annual starting salary is 26000 32000 depending on experience. The deadline for submitting the application (administrative) package is February 27<sup>th</sup> 2009. Applications by non-French citizens are welcome!

More information can be found on the following web sites:

Practical information in English: <http://www.inra.fr/-drh/js2009/informations.htm> Official job announcement on the national website of INRA: <http://www.inra.fr/drh/js2009/bdd/cr2/profil-cr2.php?codeprofil=CR2-2009-4-SPE-4>

Host team: Biology of Interacting Populations: <http://bpi.sophia.inra.fr/index2.html> Biological Control Research Unit: [http://www.sophia.inra.fr/-les\\_unites\\_et\\_les\\_equipes\\_de\\_recherche/-unite\\_experimentale\\_de\\_lutte\\_biologique](http://www.sophia.inra.fr/-les_unites_et_les_equipes_de_recherche/-unite_experimentale_de_lutte_biologique)

Person to contact 1rst: Christian Boucher ([Christian.Boucher@toulouse.inra.fr](mailto:Christian.Boucher@toulouse.inra.fr)) Person to contact 2nd: Xavier Fauvergue ([Xavier.Fauvergue@sophia.inra.fr](mailto:Xavier.Fauvergue@sophia.inra.fr))

[xavier.fauvergue](mailto:xavier.fauvergue)

Equipe Biologie des Populations en Interaction UMR IBSV 1301 INRA-UNSA-CNRS 400 Route des Chappes - BP 167 06 903 Sophia-Antipolis Cedex France

tel 33 4 92 38 64 63

Personal web page: <http://www2.sophia.inra.fr/-perso/fauvergue> [xavier.fauvergue@sophia.inra.fr](mailto:xavier.fauvergue@sophia.inra.fr)  
[xavier.fauvergue@sophia.inra.fr](mailto:xavier.fauvergue@sophia.inra.fr)

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## INRA France InvasionPopDynamics

Permanent research position at INRA, French National

Institute of Agriculture

Population dynamics of invading populations

Description

The success or failure of biological invasions depends on intrinsic demographic factors (demographic stochasticity, Allee effects), indirect demographic processes (the effect of population size on genetic variability and evolution in the novel environment), or genetic processes which reflect on demography (inbreeding depression). In order to limit accidental invasions or to optimize introduction strategies (biocontrol, reintroductions), it is important to understand the nature and consequences of such processes. In this perspective, we are recruiting a research scientist with skills in population dynamics and a strong motivation to work on invasive phenomena. We seek someone being able to develop an approach based on experiments, but with a serious theoretical background concerning processes at work in small populations. One objective is to develop researches combining academic approaches of invasion biology - based on concepts from population biology and evolutionary ecology - with the more applied research field of biological control. The recruited researcher will bring a new competence in a team already involved in population genetics and behavioral ecology (4-5 researcher scientists, 4 research assistants and 4 PhD students and postocs). There will also be some opportunity to develop research programs with the technical assistance of the local biological control research unit (a douzen of research assistants including 3 PhD).

Practical Information

The position is open at the INRA Research Institute located in Sophia-Antipolis, South-East of France (N43.612611&deg;; E7.077860&deg;). A PhD is mandatory, a postdoc is a plus. The annual starting salary is 26000&#8364; &#8211; 32000&#8364; depending on experience. The deadline for the application package (administrative) is February 27th 2009.

More information on the following web sites: Practical information in English Job announcement on the national website of INRA Host team: Biology of Interacting Populations Biological Control Research Unit

Person to contact 1st: Christian Boucher(Christian.Boucher@toulouse.inra.fr)

Person to contact 2nd: Xavier Fauvergue(Xavier.Fauvergue@sophia.inra.fr)

xavier fauvergue

Equipe Biologie des Populations en Interaction UMR IBSV 1301 INRA-UNSA-CNRS 400 Route des Chappes - BP 167 06 903 Sophia-Antipolis Cedex France

Tel 33 4 92 38 64 63

xavier.fauvergue@sophia.inra.fr

xavier.fauvergue@sophia.inra.fr

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## INRA Gif-sur-Yvette PlantQuantGenet

Brief position description: Within the Plant Genetics and Breeding Division of INRA (French national institute for agronomical research), develop and evaluate new methods for association genetics and related approaches to investigate genetic determinism of traits of interest in agricultural plants, in view of molecular breeding applications. These methods include the combination of Linkage and Linkage Disequilibrium mapping to map determinants of quantitative traits. Application to maize within the research group and other crops in cooperation with other groups of the division. The position is permanent (equivalent to tenure) at the Associate Research Scientist (CR2) level and is located in Gif-sur-Yvette (near Paris). Applicants should have a PhD or equivalent. The candidate should have a strong background in statistical, quantitative genetics and/or population genetics, and programming skills in standard languages.

Contacts: Further scientific information before formal application: Alain Charcosset: charcos@moulon.inra.fr , tel: +33 1 69 33 23 35 (in case of absence, please send email to arrange a phone meeting); in case of possible difficulties with address charcos@moulon.inra.fr, please use: acharcosset28@gmail.com General hiring process information and documents for application: <http://www.inra.fr/drh/js2009/informations.htm> Attention, complete application package (including CV, 8 to 10 pages report, publication list) must be sent between January 15th and February 27th.

Alain Charcosset <charcos@moulon.inra.fr>

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## KansasStateU ScienceEducation

Program Manager Kansas State University, Manhattan, Kansas

Program Manager sought for a newly funded, five-

year program designed to integrate graduate students in the biological sciences, physics and geosciences into science courses at Junction City High School, Junction City, Kansas. The program theme emphasizes the nature of scientific inferences about objects or events that we cannot directly experience or manipulate. The successful candidate will take a leadership role in developing and implementing this new graduate training program. Specific responsibilities include leading a one-credit course for the graduate student fellows during the academic year and providing ongoing feedback to the students, facilitating graduate student involvement with teachers and administrators in the Junction City school district, overseeing research experiences for teachers, assisting with development of a summer training institute and a spring capstone meeting, designing several additional training activities during the academic year, and participating in program assessment activities. Opportunities for scholarly research in science education are possible.

Required Masters or Ph.D. in one of the science content areas or in education or bachelors degree plus five years of experience in scientific research and/or science education. Desirable experience in any of the following areas: scientific research, teaching at the high school level, involvement with K-12 school districts, web development. We seek an individual who is highly motivated, ambitious, possessing excellent communication and organizational skills, and who is able to work in a collegial manner with a diverse group of colleagues as well as independently within the project parameters established by the principal investigators and project collaborators. Salary will be nationally competitive, commensurate with qualifications. Desired start date: May 2009.

Kansas State University is located in Manhattan, Kansas ([www.ci.manhattan.ks.us](http://www.ci.manhattan.ks.us)), a pleasant community of ca. 50,000 located in the Flint Hills of northeastern Kansas, about two hours from Kansas City. Local recreational opportunities include a large lake/park system, diverse outdoor activities, athletic events, and a rich program in the performing arts. Manhattan also serves as the regional center for education, health care, commerce, entertainment and communications.

Candidates should submit a letter of interest, curriculum vitae and representative reprints, and arrange to have letters of recommendation sent by three academic and/or professional references. It is preferred that the application be submitted electronically to: [biolgy@ksu.edu](mailto:biolgy@ksu.edu). If electronic submission is not feasible, materials may be mailed to: Dr. Carolyn J. Ferguson, Division of Biology, 104 Ackert Hall, Kansas State University, Manhattan, KS 66506-4901 (phone: 785-

532-3166). Review of applications will begin 23 March 2009, and continue until the position is filled.

Kansas State University is an Equal Opportunity/Affirmative Action Employer and actively seeks diversity among its employees. Background check required.

Carolyn J. Ferguson Assoc. Professor and Curator of the Herbarium (KSC) Division of Biology, Ackert Hall 313 Kansas State University Manhattan, KS 66506-4901

Office ph: 785-532-3166 Herbarium ph: 785-532-6619  
Fax: 785-532-6653

[www.ksu.edu/biology/faculty\\_pages/ferguson.html](http://www.ksu.edu/biology/faculty_pages/ferguson.html)

[www.ksu.edu/herbarium](http://www.ksu.edu/herbarium) [www.biodis.ksu.edu](http://www.biodis.ksu.edu)

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

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## LabTech UKansas EvolutionaryGenetics

Research Assistant/Technician: Evolutionary Genetics

A research assistant position in the field of evolutionary genetics is available in the Blumenstiel lab (<http://www.people.ku.edu/~jblumens/>) at the University of Kansas. The overall goal of the lab is to describe the evolutionary dynamics of genetic and epigenetic systems, with special interest in the evolution of the RNAi machinery. We use species in the *Drosophila* genus and research is performed at the interface between theoretical and evolutionary genetics and molecular genetics. The research assistant will directly contribute to both lab management and the lab research program. Salary range \$26,000–\$32,000/ year, depending on experience.

Responsibilities include:

Assisting in the daily operation of the lab including ordering supplies, preparation of reagents and maintaining fly stocks.

Standard molecular biology laboratory procedures: DNA and RNA extraction, PCR, RT-PCR, cloning, fly genetics, and immunocytology.

Contributing to the lab research program by working as a team member and contributing intellectually to the group

Qualifications:

A strong work ethic, the ability to work independently

and enthusiasm for research in molecular and evolutionary genetics.

A Bachelors degree in biological sciences or related field and some experience in lab research.

Strong organizational skills and attention to detail.

Special consideration will be given to applicants that also possess any of the following skills or experience:

Laboratory research experience in molecular genetics.

Experience in Drosophila genetics research.

Familiarity with bioinformatics and a computer programming language such as PERL.

To apply, please apply online at: <https://jobs.ku.edu/> and search for Research Assistant, Position Number: 00061001.

Contact [jblumens@ku.edu](mailto:jblumens@ku.edu) for inquiries.

tions being equal, precedence will be given to candidates with disabilities. Salary will be according to TV-L. Benefits correspond to those of employees in public service. The position will ideally begin in spring/summer 2009. The scientific language at the institute is English. Complete applications should be submitted by March 30, 2009 to Dr. Michaela Hau at the address below, and should include your CV, a 2-page visionary research statement, and a list of three references. For further details, please contact Dr. Michaela Hau.

Dr. Michaela Hau Max Planck Institute for Ornithology Vogelwarte Radolfzell Schlossallee 2 D-78315 Radolfzell, Germany Phone: ++49-(0)7732-150113 Email: [mhau@orn.mpg.de](mailto:mhau@orn.mpg.de) Website: <http://orn.mpg.de/mitarbeiter/hau.html>

Michaela Hau <[mhau@orn.mpg.de](mailto:mhau@orn.mpg.de)>

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## MaxPlanckInst Radolfzell EvolutionaryBiol

Research scientist position in evolutionary biology

The Max Planck Institute for Ornithology, Vogelwarte Radolfzell, is an internationally renowned research institution working in the field of Eco-Immunology and Migration. We have recently established a new research group in ecological and evolutionary physiology and are inviting applications for a Research Scientist position.

The successful candidate will be an excellent, highly motivated and productive postdoctoral scientist. Successful applicants will have demonstrated the ability to perform top international research in evolutionary biology, ideally using integrative approaches to study evolutionary questions. The position is available for 5 years and will be hosted by the research group on ecological and evolutionary physiology (group leader Dr. Michaela Hau). The researcher can expect an outstanding scientific environment and excellent support at this newly re-established department of the Max Planck Institute of Ornithology in Radolfzell, Baden-Württemberg, at Lake Constance. This department has close ties with the nearby University of Constance (a cluster of excellence university).

The Max Planck Institute is an equal opportunity employer. Women and members of minority groups are strongly encouraged to apply. In addition, qualifica-

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## OregonStateU LabManager PopGenetics

Mike Blouin is looking for a lab manager/head technician. The main projects in lab currently involve:

(1) DNA-based pedigree work on steelhead trout. In particular, we are now studying why hatchery-raised fish have lower fitness than wild fish (includes studying which traits might be under selection, and the loci involved).

(2) Interactions between parasites and hosts. In particular, we are studying selection on loci that snails use to defend themselves against infection by Schistosomes. This is part of an NIH-funded project we do in collaboration with Chris Bayne's lab.

The lab work will involve lots of genotyping (microsatellites and other loci) and sequencing, and possibly some gene expression work. Maintaining a large genotype database error free will be an essential part of the work. So I'm looking for someone who is well organized and methodical. Good computer skills are essential. Someone who has some statistical skills and/or bioinformatics experience would be great.

For more about our work see <http://oregonstate.edu/~blouinm/> The official job ad is below. To find out more or to apply, go to the OSU jobs website and use the posting number below. Applications must be in by March 15th. Feel free to email or phone me for more



info. Thanks, Mike

Faculty Research Assistant (lab technician, genetics), Dept. Zoology, Oregon State University. Appointee will conduct population genetics research in Michael Blouin's lab. Responsibilities include basic molecular biology procedures, database management, working with students, and ordering and managing supplies. Required qualifications include BA or BS, database management skills and basic RNA and DNA molecular biology skills such as nucleic acid extractions, PCR, and working with cDNA or DNA libraries. Preferred qualifications include experience with bioinformatics or population/evolutionary genetics. This is a full-time, 12-month fixed-term position with renewal at the discretion of the supervisor. To review complete posting and apply, go to <http://oregonstate.edu/jobs> Posting #0003855. Closing Date: 03/15/09. Start date after 04/01/09. Feel free to contact Michael Blouin for further info at [blouinm@science.oregonstate.edu](mailto:blouinm@science.oregonstate.edu). OSU is an AA/EOE.

Michael Blouin Dept. Zoology, Oregon State University Corvallis, OR 97331-2914 <http://oregonstate.edu/~blouinm/> Tel: 541-737-2362 Fax: 541-737-0501

[blouinm@science.oregonstate.edu](mailto:blouinm@science.oregonstate.edu)  
[blouinm@science.oregonstate.edu](mailto:blouinm@science.oregonstate.edu)

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## Peruvian Amazon Field Assist Avian Speciation

Field Assistant Position Peruvian Amazon Summer 2009

Species diversification and coexistence in antbirds

A field assistant is required to work with a PhD student on a project investigating the roles of rivers and habitat mosaics in driving population differentiation, by acting as barriers to gene flow, in populations of 3 species of antbird. Based at the Los Amigos research centre, SE Peru, the position requires extensive mist-netting and bird ringing experience, and would suit someone with an interest in avian ecology and evolutionary biology, happy to live and work at a remote site in difficult field conditions.

Day to day duties would include assisting in locating birds using playback, mist-netting individuals for ringing and bleeding, recording songs and subsequent individual identification. Therefore experience with identifying individuals based on colour rings would be ad-

vantageous, as this is extremely challenging in the dense forest understory.

The position would be for 2-4 months with dates to be finalised (June-September 2009). Field station costs will be covered but flights would be the responsibility of the assistant. Peruvian applications are encouraged, and a basic salary will be offered in these instances.

For further information please contact [Claire.salisbury@zoo.ox.ac.uk](mailto:Claire.salisbury@zoo.ox.ac.uk) To apply please send a covering letter, CV, and contact details for 2 referees. Deadline 1st March 2009.

Asistente de Campo (Aves) Amazonia Peruana

Diferenciación de especies y coexistencia en hormigueros

Se necesita asistente de campo para trabajar con una estudiante de doctorado de la Universidad de Oxford. El proyecto consiste en investigar los roles de los ríos y hábitats, como una barrera para el flujo genético, en la diferenciación de tres poblaciones de hormigueros. El trabajo se realizará en el Centro de Investigación y Capacitación Río Los Amigos (CICRA), Madre de Dios, Perú. El candidato debe tener un fuerte interés en ecología de aves y biología evolutiva, además de amplia experiencia en el uso de redes de neblina y anillado de aves.

El candidato exitoso deberá localizar a las aves mediante uso de "play-back", manejo de redes de neblina para anillar y tomar muestras de sangre, hacer grabaciones de los cantos y localizar e identificar individuos por lectura de anillos de color. Debido a que las aves de estudio viven en un denso sotobosque es ventajoso que el candidato tenga experiencia previa leyendo bandas de color.

Esta posición sería por 2 - 4 meses (Junio - Setiembre 2009). Están cubiertos todos los costos de alimentación y hospedaje, pero los vuelos hasta Puerto Maldonado tendrán que ser cubiertos por el asistente. Se alienta a postulantes peruanos a aplicar, ya que en estos casos se puede proveer de un salario básico.

Para mayor información contactarse con: [Claire.salisbury@zoo.ox.ac.uk](mailto:Claire.salisbury@zoo.ox.ac.uk)

Para aplicar por favor mandar una Carta de intención, CV y contacto de 2 referencias.

Fecha de cierre de aplicaciones: 1ero de Marzo del 2009

[claire.salisbury@zoo.ox.ac.uk](mailto:claire.salisbury@zoo.ox.ac.uk)  
[claire.salisbury@zoo.ox.ac.uk](mailto:claire.salisbury@zoo.ox.ac.uk)

valentin amrhein <pca.recherche@orange.fr>

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## UBasel FieldAssist BirdMigrationEvolution

Field assistants and bird ringers in evolution of bird migration

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

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

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

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

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

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

Valentin Amrhein, [pca.recherche@orange.fr](mailto:pca.recherche@orange.fr) Steffen Hahn, [steffen.hahn \[at\] vogelwarte.ch](mailto:steffen.hahn@vogelwarte.ch)

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## UExeter 5 SystemsBiology

As is our practice, we have very broad definitions of suitable areas of research:

Five New Academic Posts in Systems Biology at Exeter

The result of the 2008 Research Assessment Exercise confirms Exeter's position as one of the UK's leading research-intensive universities. Almost 90% of our research is at internationally recognised levels and every single subject submitted was assessed as including world-leading (4\*) research. When adjusted for the 95% of staff submitted, Exeter ranks among the top 15 in the UK for research out of 159 higher education institutions. The Times Higher Education described Exeter as 'a rising star among research-intensive institutions'.

As 2007/08 THES University of the Year, Exeter also rose four places to 13th in the Times league table of UK universities and ranks 14 to 19 in tables published by the Guardian, Sunday Times and Independent. Our Streatham campus is widely regarded as one of the most attractive in Britain, and the new purpose-built Cornwall Campus is superbly equipped to meet the challenges of the 21st century. In April 2008 the University of Exeter announced plans to invest £80 million in science, engineering and medicine, building on existing areas of excellence. An initial £30 million of existing funds will be spent on new appointments, infrastructure and studentships in five groundbreaking interdisciplinary research themes.

Systems Biology is one such theme. Our vision is for a multidisciplinary approach to understanding biological processes through the application of integrative and predictive biology.

The Systems Biology Theme brings together the research of over 50 academics in the disciplines of Applied Mathematics, Biosciences and Informatics across both campuses. It will benefit from synergies with the recently announced Environment and Sustainability Institute to be based on the Cornwall campus.

As part of this major research initiative in Systems Biology, the School of Engineering, Computing and Mathematics (SECaM) and the School of Biosciences seek highly motivated individuals for four new lectureships.

Two Lectureships in Applied Mathematics - Systems

Biology (Ref 1881/1882)

The School of Engineering, Computing and Mathematics (SECaM) seeks highly motivated individuals who will bring modelling skills from Control Theory, Dynamical Systems and/or Bayesian Statistics to catalyse inter-disciplinary research collaboration in Systems Biology.

We encourage applications from Applied Mathematicians with modelling experience at any level of biological organisation - from genomes to cells to organisms to population and community dynamics. Informal enquiries should be directed to Prof. Stuart Townley (s.b.townley@ex.ac.uk), SECaM.

Two Lectureships/Senior Lectureships in Cell Biology (Ref 1907/1908)

Two Lectureships/Senior Lectureships in Cell Biology are available to applicants with a research focus in either Mammalian Molecular Cell Biology or Plant Cell Biology. The School has excellent facilities for contemporary biological investigation including a new Bio-imaging centre (Cryo and Transmission EMs, LSM, live cell imaging workstations). We particularly encourage applications from individuals with interests in cell polarity, cytoskeleton, motors or membrane trafficking. We seek motivated individuals who can form effective collaborative linkages within and outside the School. Informal enquiries should be directed to Prof. Gero Steinberg (G.Steinberg@exeter.ac.uk).

One Lectureship/Senior Lectureship in Biochemistry (Ref 1906)

A Lectureship/Senior Lectureship is available in biochemistry. We seek applicants with interests and expertise in protein biochemistry, protein-protein interactions and analytical biochemistry who is able to make linkages with existing strengths within the School, particularly in plant and microbial sciences, microbial infection, cell biology or biocatalysis. Informal enquiries should be directed to Prof. Nicholas Talbot (N.J.Talbot@exeter.ac.uk).

Full details of all of these posts, including the application procedure, may be found on our website at [www.ex.ac.uk/jobs](http://www.ex.ac.uk/jobs). Generous relocation assistance will be available for all of these posts. Full details of all of these posts, including the application procedure can be found on our website at [www.ex.ac.uk/jobs](http://www.ex.ac.uk/jobs). Applications should be submitted electronically to [hradmin@exeter.ac.uk](mailto:hradmin@exeter.ac.uk)

The closing date for applications is noon on Friday 27th March 2009.

All of these posts are available from 1st September 2009

or earlier by negotiation, with a start date by mutual agreement. Appointments will be made within the following salary range:

Lecturer £31,513 - £35,469 pa with access to further contribution points rising to £38,757 Senior Lecturer £38,757 - £44,930 pa with access to further contribution points rising to £52,086

Allen J. Moore

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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/evodir.html>

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## UNevada LabTech PopulationGenetics

POSITION AVAILABLE: I am anticipating the hire of a Molecular Lab Technician, full or part-time.

QUALIFICATIONS: A degree is required, may be bachelor's or master's.

WHERE: Dr. Forister's lab, Department of Biology, University of Nevada, Reno (<http://web.me.com/mforister/GreatBasinBugLab/Home.html>)

WHEN: Both starting date and duration of position are flexible. I would like the starting date to be not later than June of 2009, but will consider a later date if necessary. The ideal duration would be 11 months, with possibility of extending beyond that.

SALARY: Dependent on education and experience.

CONTACT: If you're interested, please contact me, Matt Forister, via email: [mforister@unr.edu](mailto:mforister@unr.edu)

OTHER DETAILS: I am looking for someone with a range of molecular- genetic skills. Candidate must be reliable, independent, and able to juggle multiple projects. Most work will include sequencing of mitochondrial and nuclear DNA, as well generation of AFLPs. Depending on prior experience or skills, duties may include editing of sequences and processing of fragment data.

For especially motivated people, I am open to collaborations in areas relevant to my lab, particularly population genetics, phylogeography, and QTLs. Thus this position could serve as an effective bridge between Master's and PhD work, or between undergrad and grad.

Housing in Reno is affordable, and a number of outdoor activities are in our backyard. You can be at an alpine trailhead in an half hour, or you can kayak in the river running through downtown. The Department of Biology is a friendly and collaborative environment with people working in both ecology/evolution as well as cell/molecular biology.

mforister@unr.edu mforister@unr.edu

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## UOxford PopulationGenetics

University of Oxford

Wellcome Trust Centre for Human Genetics

3X Post Doctoral Scientists in Evolutionary and Population Genetics Academic-related Grade 8: £34,793 - £41,545 depending on qualifications and experience, but if no suitable applicants are identified at this grade the positions may be offered at grade 7: £27,466 - £33,780 with an appropriate change of duties

Up to two posts (3 years) are available to work within the 1000 Genomes Project ([www.1000genomes.org](http://www.1000genomes.org)) on experimental design, the development of statistical methodology for the analysis of whole-genome low-coverage short-read sequencing data, and population-genetic analysis of fundamental evolutionary processes including recombination, natural selection and demographic history. The posts would be working primarily within the group of Gil McVean (who co-chairs the analysis group of the 1000 Genomes Project).

One post (2 years) is available to work in the group of Chris Spencer on the use of genome-wide variation data in population and evolutionary genetics.

More details about the projects are given in the detailed job descriptions available on request.

Candidates should have an existing background in population or evolutionary genetics, statistics, or modern computational statistics and its application. Candidates from the mathematical and physical sciences wishing to move in the field of genetics are encouraged to apply. Good computational skills are essential. Candidates should have a doctorate in statistical genetics, population genetics, statistics, mathematics or computer science.

To obtain more details of the positions, please contact the Personnel Officer (email: [personnel@well.ox.ac.uk](mailto:personnel@well.ox.ac.uk), tel: 01865 287508 or from our web

page [www.well.ox.ac.uk /vacancies](http://www.well.ox.ac.uk/vacancies)), quoting reference H5-08-043-GM. Applications, in the form of a full and detailed CV together with the names and addresses of two referees, should be sent to the Personnel Officer at the Wellcome Trust Centre for Human Genetics, Roosevelt Drive Oxford, OX3 7BN, or by email to; [personnel@well.ox.ac.uk](mailto:personnel@well.ox.ac.uk), or fax; 01865 287516. Please quote the reference number on your application. If candidates do not wish to be considered for all of the positions, please state clearly which posts you are applying for within your application. The closing date for applications is 27th February 2009. Interviews will be held on March 12th.

Gilean McVean Professor of Statistical Genetics Department of Statistics 1 South Parks Road Oxford OX1 3TG UK

Tel: +44 1865 281881 Fax: +44 1865 281333  
web: <http://www.stats.ox.ac.uk/~mcvean>  
[mcvean@stats.ox.ac.uk](mailto:mcvean@stats.ox.ac.uk) [mcvean@stats.ox.ac.uk](mailto:mcvean@stats.ox.ac.uk)

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## UOxford ResFellows PlantEvolution

Research Fellowships in Plant Evolution, Oxford

The University of Oxford Plant Sciences Department is an internationally leading centre of excellence in plant evolution (ranked equal 3rd of 52 UK Biological Sciences research institutions in RAE2008) and is based in the central multidisciplinary science area of Oxford. We seek applications from outstanding researchers who would like to be Independent Research Fellows within our Department. Those already holding or intending to apply for such Fellowships may apply to attend a two-day Departmental Independent Research Fellows Event at the Department 5th - 6th May 2009. If invited to this Event you will be asked to present a talk about your proposed area of research, and have the opportunity to discuss your proposals, the future development of your group and your future career plans in depth with senior departmental academic staff.

Following the Event, selected candidates will be mentored in the writing of Fellowship applications and/or offered the opportunity to move existing Fellowships to the Department of Plant Sciences.

Further details and particulars can be found <http://www.plants.ox.ac.uk/> see Vacancies

Please e-mail a 2-page summary of your research plan, a copy of your CV and arrange for

two letters of recommendation to be emailed to sandie.hardaker@plants.ox.ac.uk by noon on Friday 13 March 2009

John Pannell <john.pannell@plants.ox.ac.uk>

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## URostock MolecularEvolution

Summer Sabbatical (3-6 months) Molecular Ageing / Bioinformatics / Evolution, University of Rostock, Baltic Coast

A 3-6 month Summer Sabbatical is available for a life scientist with experience in molecular ageing research. Remuneration will depend on qualification; we seek a postdoc or a senior scientist. You will work in a dry-lab environment, with bioinformatics & systems biology folks who have an intense interest in ageing & collaborations with experimentalists across the University.

The University of Rostock is building up and strengthening expertise in Ageing research, e.g. within the department 'Ageing Sciences and Humanities' that is part of the newly established 'Interdisciplinary Faculty', in line with the state focus area 'Gesundheitsland Mecklenburg-Vorpommern' and in cooperation with the Max-Planck- Institute for Demographic Research. More specifically, you will be hosted in the 'Institute for Medical Informatics and Biometry' which is supposed to be renamed into 'Institute for Biostatistics and Informatics in Medicine and Ageing Research'. The new director of the institute is a bioinformatician with a focus on phylogeny/evolution and a strong interest in Ageing Research. The 'Molecular Ageing special interest group' in Rostock also includes the well-known systems biology group of Olaf Wolkenhauer, and several wet-lab groups. Depending on your qualification and experience, your roles and duties may include:

+ to define and pursue a data analysis task in a collaborative effort of wet-lab ageing research and in-silico analysis, for example of microarray and other high-throughput data, of population genetics data, and/or of signalling network / molecular pathway data, + to connect your research program in molecular ageing to bioinformatics / systems biology, + to co-supervise 1-2 graduate students in their startup phase, with the perspective of a long-term collaboration, + to provide support towards establishing a long-term perspective for experimental and/or clinical molecular ageing research in Rostock.

Resources allocated to the sabbatical also include a reimbursement of reasonable travel expenses.

In the summer, the Baltic Coast is the number one (!) vacation area in Germany, with a very pleasant climate and a wide variety of recreational opportunities.

Review of applications (in one pdf file if possible) will begin February 15 and will continue until the position is filled.

Kind Regards Georg Fuellen

Prof. Dr. Georg Fuellen Director, Institute for Medical Informatics and Biometry University of Rostock, Medical Faculty Rembrandtstr. 16/17 18055 Rostock, Germany Phone + 49 381 494-7360 Fax + 49 381 494-7203 <http://www.imib.med.uni-rostock.de/> fuellen@alum.mit.edu fuellen@alum.mit.edu

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## USheffield EvolutionaryZooology Lecturer

Lecturer in Zoology (Fixed-term)

Department of Animal & Plant Sciences, The University of Sheffield

Ref No R07015

Closing Date: 15th March, 2009

Salary: UKpound36,532 - 43,622 per annum with the potential to progress to UKpound49,096

This post offers an exciting opportunity to join a vibrant department that excels in both teaching and research. Animal and Plant Sciences, along with its sister departments of Molecular Biology and Biotechnology and Biomedical Sciences, received top marks in the last Teaching Quality Assessment (24/24) and was ranked 3rd in the UK for Biological Sciences in the 2008 Research Assessment Exercise. The appointee will contribute to undergraduate teaching and will extend our collaborative research programme in one of the following areas: evolutionary developmental biology, ecological/evolutionary genomics, disease and immunity, A PhD (or equivalent experience) in a relevant discipline, teaching experience, willingness to work as part of a team, and demonstrated ability to undertake high quality research and to produce publications that contribute to the department's research reputation are essential. This post is available from July 2009 for a period of 4 years.

See <http://www.shef.ac.uk/jobs/> for further details  
 r.k.butlin@sheffield.ac.uk r.k.butlin@sheffield.ac.uk

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### UTexasBrownsville 4 EvolutionaryBiol

Lecturer (4 positions) Position Number: FY 09-82 Reports to: Chairperson of Biological Sciences Scope: Responsible for teaching undergraduate Anatomy and Physiology, General Biology and other introductory courses in the biological sciences. These are four full-time, non-tenure track positions offered for 2009/2010 Academic Year. These positions are contingent upon funding. Education/Experience: Master's Degree in Biology or related field is required. A doctoral degree is preferred. Student advising, academic services and scholarship are also expected to fulfill position requirements. Salary: Commensurate with experience and qualifications. Deadline: Applications will be reviewed upon receipt and continue until the position is filled.

Please send applications with indication of position number to: The University of Texas- Brownsville and Texas Southmost College Human Resources Cortez Building - Suite 129 80 Fort Brown Brownsville, Texas 78520 Phone: (956) 882-8205 Fax: (956) 882-7476

Human Resources website: <http://www.utb.edu/ba/hr/Pages/default.aspx> UTB website: <http://www.utb.edu> Andrea.Schwarzbach@utb.edu

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### UVienna 2FieldAssist AvianBiodiversity

Dear colleague, I would like to offer these positions and enclose you the announcements. Thank you very much for posting it in the mailing list,

cheers and sincerely, Sabine Hille

Two field assistants in Behavioural Ecology of Birds and in Avian Biodiversity including one bird ringer

Two field assistant positions are available in an international research project on reproductive biology and distribution patterns of hole nesting birds. This study is part of the alpine biodiversity project run by Dr.

Sabine Marlene Hille at the Institute of Wildlife Biology and Game Management <http://www.dib.boku.ac.at/iwj.html> at the University of Natural Resources and Applied Life Sciences in Vienna, Austria <http://www.boku.ac.at/>

Fieldwork will be done from April to July 2009, at the Alpine field site at the Ötscher mountain and in the Viennan forest in Austria.

We are looking for two field assistants, one with ringing experience in small passerines and one with intensive knowledge on identifying forest bird species. Candidates should preferably have a background in biological sciences. Field assistants will participate in systematic monitoring of breeding forest bird community, surveys of territory settlement of coal tits and assist bird ringers in capturing and banding the birds at nest boxes. Field work will include intensive hiking through mountain forests, leader climbing to reach nest boxes and field assistants are expected to work in the mountain only in groups and also in the early morning. Work includes also entering data in a database.

Field assistants will receive 1000-1500 euros per month, depending on qualification. Applicants are expected to stay for the entire field season (spring time of beginning depending on snow cover) from mid April to end of July 2009. The language at the study sites will be English. Accommodation during fieldwork is provided at the field station hut at Ötscher mountain.

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

Closing date: 10. March 2009

prvs'4a3242c=sabine.hille@boku.ac.at

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### UVienna 2FieldAssist MammalBiodiversity

Dear colleague, I would like to offer these positions and enclose you the announcements. Thank you very much for posting it in the mailing list,

cheers and sincerely, Sabine Hille

Two field assistants in small mammal biodiversity:

Two field assistant positions are available in an international research project on reproductive biology of small mammals in the Alps. This study is part of the alpine biodiversity project run by Dr. Sabine Marlene Hille at the Institute of Wildlife Biology and Game Management <http://www.dib.boku.ac.at/iwj.html> at the University of Natural Resources and Applied Life Sciences in Vienna, Austria <http://www.boku.ac.at/>

Fieldwork will be done from April to July 2009, at the Alpine field site at the Ötscher mountain and in the Viennan forest in Austria.

We are looking for two field assistants, one at least with intensive skills in trapping, identifying and handling small mammals and one who assists the former in a survey of small mammal populations in different altitudes at the Ötscher mountain. Candidates should preferably have a background in biological sciences. Field assistants will establish a trapping set of trip trap and Sherman traps in a mountain forest, will handle, measure, mark and release the mammals. Work includes also entering data in a database. Field work will include intensive hiking through mountain forests and field assistants are expected to work in the mountain only in groups and also in the early morning and at night.

Field assistants will receive 1000 - 1500 euros per month depending on qualification. Applicants are expected to stay for the entire field season (depending on snow cover in spring) from beginning May to end of August 2009. The language at the study sites will be English. Accommodation during fieldwork is provided at the field station hut at Ötscher mountain.

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

Closing date: 10. March 2009

prvs'4a3242c=sabine.hille@boku.ac.at

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**UVirginia AssistantProfessor**

We are initiating a job search, and although we've entitled the position "Ecologist," the definition of research areas are broad enough that we would hope to attract applications from many of the users of EvolDir.

David E. Carr Research Associate Professor, Environmental Sciences Director, Blandy Experimental Farm

Date: 27 February 2009

Institution: University of Virginia

Position: Research Assistant Professor in Ecology

The University of Virginia's Blandy Experimental Farm seeks to hire an Ecologist at the Research Assistant Professor level.

Academic appointment is within the University's Department of Environmental Sciences, and the position is based at Blandy, an environmental field station located in Virginia's Shenandoah Valley. The position's distribution is 50% research and 50% administration. The successful candidate is expected to establish an extramurally funded research program, attract and mentor successful graduate students, and mentor undergraduate researchers. Area of research is open but should complement existing strengths at Blandy and strengthen connections with the Departments of Environmental Sciences and Biology. Possibilities include (but are not limited to) invasive species ecology, restoration ecology, landscape ecology, and agroecology. Administrative responsibilities include oversight of Blandy's undergraduate and graduate research programs and working with other faculty to make Blandy a leader in environmental research and outreach.

Ph.D. in biology, environmental science, or a closely related discipline is required. Postdoctoral experience is preferred. Applicants must provide evidence of high-quality research. For more detailed information about the position refer to [www.virginia.edu/blandy/-ecologist.htm](http://www.virginia.edu/blandy/-ecologist.htm). This is a non-tenure track position with an initial three year contract, renewable pending successful review.

To apply, please complete a Candidate Profile on-line through Jobs@UVA (<https://jobs.virginia.edu>) and attach a cover letter briefly highlighting your research experience and potential as a research administrator, curriculum vitae, and a statement of research interests. Search for Posting Number 0603195. Please arrange for three letters of recommendation to be sent to Dr. David Carr, Search Committee Chair ([dec5z@virginia.edu](mailto:dec5z@virginia.edu)). Review of applications will begin on March 31, 2009, however the position will remain open until filled.

Questions regarding the position can be sent to Dr. Carr, and questions regarding the candidate profile pro-

cess or Jobs@UVa should be directed to Judy Masi (jmasi@virginia.edu).

The University of Virginia is an equal opportunity/affirmative action employer. Women and members

of underrepresented groups are strongly encouraged to apply.

“David E. Carr” <dec5z@virginia.edu>

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## Other

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### Alberta 3FieldVolunteers GroundSquirrel

Field Assistants Required Columbian ground squirrels  
Sheep River Provincial Park, Alberta, Canada

We are looking for 3 volunteers to assist with fieldwork from April 01 to May 15, 2009, with the possibility of

extension to July 15. The project investigates the evolutionary ecology of Columbian ground squirrels. As a member of the study, assistants will be involved with monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, behavioural observation and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal. All fieldwork is carried out in the spectacular Rocky Mountains



of western Alberta, Canada.

We will be staying at the University of Calgary's field station in Sheep River Provincial Park, Alberta. You will interact with other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, the field station is home to a number of other researchers working on a variety of projects, ranging from insects to large mammals.

Food and accommodation costs are covered as are travel costs to the field station.

Training will be provided and no experience is necessary, but candidates should have an interest in ecology and evolutionary biology, enjoy the outdoors and be optimistic.

If you wish to apply for a post then please send a CV with a cover letter and contact details of three references (with e-mail address) to Jeff Lane (contact info below), by February 28, 2009

Contact: Dr. Jeffrey Lane

E-mail: [Jeff.Lane@ed.ac.uk](mailto:Jeff.Lane@ed.ac.uk) Institute of Evolutionary Biology Kings Buildings University of Edinburgh Edinburgh EH9 3JT

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

[Jeff.Lane@ed.ac.uk](mailto:Jeff.Lane@ed.ac.uk) [Jeff.Lane@ed.ac.uk](mailto:Jeff.Lane@ed.ac.uk)

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## AMP concentration

Dear all

Would anyone happen to know:

- 1)The concentration of AMP (and other adenine nucleotides) in mesophyll cells of C4 plants (maize, sorghum, etc.)
- 2)What are Reduced ferredoxin/Oxidized ferredoxin ratios?

Thanks in advance

Ben

Benjamin Walter <[benwalter44@gmail.com](mailto:benwalter44@gmail.com)>

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## Articles about Evolution and Pathology/Immunology

dear friends,

we are discussing in my department how to teach some subjects using more applied approaches and some colleagues teaching pathology and immunology are from a health school what can be a problem because they dont have a strongbackground in evolutionary theory.

we are trying to help them finding articles including evolution and pathology and immunology issues but.... i am feeling that this is not very easy because there is not many publications like that.

thats why i am here requesting some help!

if you have articles like that please send me and i will share them with my colleagues here.

thanks for any help !!!

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamiferos (ECOMAM) UNITAU, Depto. Biologia, Taubate, SP. 12030-010. Grupo de pesquisa ECOMAM: <http://jcvoltol.sites.uol.com.br/> Fotos de projetos e cursos: <http://jcvoltol.fotoblog.uol.com.br/> Exemplo de um curso de ecologia de campo: <http://trabiju.blogspot.com/> Fotos artisticas: <http://voltolini.fotos.net.br/texturas> VOLTOLINI <[jcvoltol@uol.com.br](mailto:jcvoltol@uol.com.br)>

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## Articles about Evolution and Pathology/Immunology 2

Dear friends,

After two weeks I have all the articles people sent me about evolution and areas like pathology and immunology. Some friends of mine more experienced in this area selected the most interesting articles to be used in Biology undergrad courses and I would like to thanks who help us and also to share the articles. If you are interested, send me an email and I will send the articles for you by email!

Thanks for helping us to improve our courses!!!

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamíferos (ECOMAM) Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br Website do grupo de pesquisa ECOMAM: <http://jcvoltol.sites.uol.com.br/> Fotos de Projetos e Cursos: [http://jcvoltol.fotoblog.uol.com.br/-Amostra de um Curso de Campo de Ecologia:](http://jcvoltol.fotoblog.uol.com.br/-Amostra-de-um-Curso-de-Campo-de-Ecologia:) <http://trabiju.blogspot.com/> Currículo Lattes: <http://lattes.cnpq.br/8137155809735635> Fotos Artísticas: <http://voltolini.fotos.net.br/texturas> 'Siamo tutti angeli con un'ala e possiamo volare soltanto se ci abbracciamo'

jcvoltol@uol.com.br

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### BAC-end sequencing

Dear all,

I would like to sequence the ends of some BAC-clones that are positive for a gene of interest. As I have understood this is a standard procedure, but I can't seem to find any good protocols for this on the internet. I will use both T7 and Sp6 primers, and I guess the idea is to culture the positive clones over night, extract the DNA (miniprep) and use this as a template for the Cycle-Seq reaction for sequencing (we use Beckman Seq 8000 capillary sequencer).

Does anyone have any hands on tips and good protocols for this? I'm particularly interested in knowing how much template I will need for CycleSeq reaction (otherwise I plan to use different amounts to find the optimal). I guess the DNA extraction of the culture will fragment the template, will this be a problem?

Thanks in advance!

/Petri

Dr. Petri Kemppainen, Tjärnö Marine Biological Laboratory, 45296, Strömstad, Sweden Tel: +46 526 686 83 Fax: +46 526 686 07 Mob: +46 709 360 124

Petri Kemppainen <petri.kemppainen@marecol.gu.se>

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### BigDye dilutions for ABI310

Dear EvolDir members,

I'd be grateful to anyone who could tell me about their experiences of diluting BigDye for the ABI 310 capillary sequencer.

I'd also be interested to hear from anyone who has tried the "dLUTE SEQ DNA Sequencing BigDye Dilution Reagent" on the ABI 3130.

Thanks,

Paul

Paul Bloor Coordinador Grupo de Identificación de Especies Silvestres Instituto de Genética Universidad Nacional de Colombia Bogotá D.C - COLOMBIA

Tel.: +57-1-3165-000 Ext. 11611

pbloor@gmail.com

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### Bonferroni and GENEPOP

Other:

Dear all,

I am currently dealing with some microsatellite data and I am computing whether the markers are in Hardy-Weinberg Equilibrium for my population and whether they present Linkage Disequilibrium, using GENEPOP. I would like to apply the sequential Bonferroni correction to my analyses, but do not really know if I can do it within GENEPOP, and, if not, how I could compute it. Is it possible to calculate it with some other software? Should I calculate it "by hand"?

Thank you for your answers!

Luis

- Luis Cadahía Lorenzo PhD

Current address: Molekulare Systematik Naturhistorisches Museum Wien +43 152 177 332 / +43 (0) 680 126 73 74

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## Combining diversity indices

Dear Evoldir members,

I was wondering whether someone could be having/knowing of an index combining diversity indices (haplotype or nucleotide diversity), signals of expansion (theta, tajimas D, Fu's Fs etc), uniqueness of haplotypes and the number of mutations between haplotypes as determined from network analysis that could be combined with archaeological dates (of bones for instance) to provide an indication of the time of either arrival or expansion of particular haplotypes/haplogroups/clades in different geographic regions of interest such as continents.

Any suggestions would be highly welcome

Thank you

Mwacharo JM

– Four stages of acceptance: i) this is worthless nonsense; ii) this is an interesting, but perverse, point of view; iii) this is true, but quite unimportant; iv) I always said so. J.B.S Haldane, *Journal of Genetics* 1963

Joram Mwacharo <mwacharo@gmail.com>

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## Darwin 200th birthday

We hope all have had a nice Birthday Celebration for Charles Darwin on 12 February. We invite you to view the SSE YouTube birthday greetings at the following link:

<http://www.youtube.com/watch?v=jn7zLGJE9EY>

Other details of the SSE Darwin 200 outreach projects can be found at:

<http://www.happybirthdaydarwin.org> Enjoy!

Robert Pennock, Chair, SSE Education Committee  
Thomas Meagher, Chair, SSE Darwin 200 Working Group

Judy Stone <jstone@colby.edu>

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## DNA from larvae

Hi,

I have samples of very tiny parasitoid larvae (smaller than 0.5mm) that I want to sequence. Most of them are Tachinidae and some are Hymenoptera (probably Ichneumonidae), and they were all obtained from Lepidoptera larvae. Some of the samples are three-years old, but others are less than one-year-old. They are stored in 100% ethanol, at 4°C, so I suppose that the DNA is still good. Unfortunately I still didn't manage to get the right protocol for DNA extraction, specially in the case of the Tachinidae. I have already tried one of Qiagen's extraction kits and also using promega extraction solutions, but it doesn't work. Since the larvae is so small, I can't even squash it, so I don't know if this can also influence the result. I would be very grateful if someone could give me any suggestions on how to extract DNA from such tiny insects.

Regards,

Ana Santos

– Ana M. C. Santos (PhD student) Imperial College London Silwood Park Campus Buckhurst road, Ascot SL5 7PY, UK Tel.: +44 (0)2075942446

a.santos05@imperial.ac.uk a.santos05@imperial.ac.uk

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## DNA from schistosoma eggs

Dear Evoldir members,

I have a problem with extracting DNA from schistosoma eggs. The eggs of these flatworm parasites are passed out in the urine and faeces and if you expose them to sunlight they will hatch to miracidia, the free-living larva. We collected individual miracidia and eggs on Whatman FTA cards. If you extract the DNA out of the FTA punches, it yield good results for the miracidia but not for the eggs. I have a feeling that the enzymes which are released from the FTA card upon addition of the sample (chemicals that lyse cells, denature proteins and protect nucleic acids from nucleases), cannot pass through the egg shell. We tried chitinase (2hrs at 42C)

but no result.

Does anyone has experience with this? Protocols for DNA extraction of eggs stored in ethanol rather than FTA are very welcome as well.

Thank you in advance,

Sarah Geldof Laboratory of Animal Diversity and Systematics Ch. Deberiotstraat 32 3000 Leuven Belgium phone. 32 16 323918 fax. 32 16 324575 Website: <http://bio.kuleuven.be/de/dev/> Sarah Geldof <sarah.geldof@bio.kuleuven.be>

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## Ecology Immunity

Philosophical Transactions of the Royal Society B have just published: Ecological Immunology compiled and edited by Hinrich Schulenburg, Joachim Kurtz, Yannick Moret and Mike T Siva-Jothy- <http://publishing.royalsociety.org/ecological-immunology> A specially discounted price of £47.50 is available by contacting Debbie Vaughan at the Royal Society direct (debbie.vaughan@royalsociety.org) or by contacting Portland Customer Services (quoting reference TB 1513) via the Portland Press website.

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## Extracting tree info

Dear colleagues,

I am wondering if anyone knows of software, or has written code, that can extract clades from Newick trees. Given a text tree file, I want to get a list of all the sets of taxa that cluster together at any level.

Thanks, Martha

– Martha T. Hamblin Senior Research Associate Institute for Genomic Diversity Cornell University 607-254-4849

[mth3@cornell.edu](mailto:mth3@cornell.edu) [mth3@cornell.edu](mailto:mth3@cornell.edu)

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## Frequency data software

Hi All,

Does anyone know of a software package that can take allele frequency data, e.g. from multiple allozymes, and use these to calculate Fst values? I am trying to make use of data from some older papers that include a table of allele frequencies in each population, but never calculated pairwise Fst between populations. I know that Arlequin takes frequency data, but the frequency infile format is not something I can figure out how to use with multiple loci as given in these types of tables.

Thanks for you thoughts, Amy

Amy Baco-Taylor <[abaco@ocean.fsu.edu](mailto:abaco@ocean.fsu.edu)>

---

## Frequency data software answers

Hi All,

Thanks to those who responded quickly. Just to clarify on this (original post below), the data in the tables is total allele frequencies for each population. There is no information on which individuals had which alleles or which alleles for a given locus occurred with which alleles for another locus, so the types of infiles used for e.g. Fstat, Genepop and Genetix would not be possible to make. Data example:

```
Locus Allele Pop1 Pop2 pgm A 0.5 0.3 B 0.5 0.7 Pgi A
0.3 0.5 B 0.7 0.5
```

Arlequin has a “frequency” data option, that takes frequency data by population for a single locus, but to enter multiple loci, you need to know the multilocus haplotypes, i.e. which alleles go together from different loci, e.g. the frequency of PgmA with PgiA is one line, PgmB/PgiA the next, etc for all combinations. Not something that can be derived from these tables.

Thanks again for your thoughts and suggestions, Amy

–

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

Phone: (850) 645-1547 Fax: (850) 644-2581  
abaco@ocean.fsu.edu

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

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### Gel extraction advice

Hi evoldir

Can anyone recommend a really good kit for extracting DNA from gels? The kits we have are frankly rubbish, and we seem to lose way more of the DNA than we should. I am interested in both info on kits that are good for HMW DNA (>20kb) and LMW DNA (100-20kb) - they need not be the same kit of course.

Thanks in advance

Tom Gilbert

Dr Tom Gilbert Associate Professor Department of Biology University of Copenhagen

mtpgilbert@gmail.com +45 51 89 13 30

Tom Gilbert <mtpgilbert@gmail.com>

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### Gel extraction advice answers

Dear Evoldir

A few weeks ago I posted a query on Gel extraction kits. Thanks to all the replies, especially Robert Marra, Luiz Marquez, Rossana Giordano, Karen Osborn, Will Fairbrother, Violeta Munoz and Carla Hurt.

I promised several people a summary of what I found, it follows right now,

Yours

Tom Gilbert

For DNA fragments <10kb:

QIAquick gel extraction kit - specifically one user found 80% recovery of a 1.5kb fragment and 60% of a 4kb fragment.

Millipore Montage Gel Extraction Kit with Ultrafree-DA centrifugal filter was recommended

A further reply indicated that a comparison of kits

showed Zymoclean Gel DNA recovery kit was best, Zymo Research Cat #D4001, for DNA from 75kb-23kb

There were a couple of more detailed replies that are also of interest:

The enzyme Gelase was recommended. Specifically:

I used to use Promega gel purification column kit but recently I've switched to using Gelase followed by ethanol/ammonium acetate purification. The protocol is very easy. You don't have to change tubes or mess with columns which is where much of the DNA loss occurs. I find that the yield is very good and usually very clean so long as the digestion is complete. I've tried it on DNA up to 2kb but I suspect it would work with any size.

Modified protocol 1.)Melt the gel at 75 degrees 2.)Cool it to 45 and then add the enzyme 3.)Let the gel digest at 45 degrees overnight (shorten the time by adding more enzyme) 4.)Add 200ul 5M ammonium acetate and 800 ul absolute ethanol 5.)Centrifuge at high speed for 30 minutes 6.) Wash with 70% ethanol 7.) Evaporate the ethanol and rehydrate in water .....

And then some useful insights followed in this message:

My experience is the lower percentage gel you can use the better the whole thing works. But I can't say I have found anything that I am all that happy with. I like the old school Crush n' Soak method (Maniatis) - it gives you about 50% recovery but the DNA is very clean.

The kits are not that great. I feel like I have tried many and The Squeeze and Freeze (Biorad) is quick and easy. It sometimes gives you 70% but is dirty. you have to do a phenol chloroform precip afterwards. Make sure you cut the gel into little pieces.

Invitrogen's kit was bad. I found the quiagen gel extraction kit better if the initial digestion is done longer than the recommended time with lots of mixing.

Colleagues swear by electrophoresis based elution methods. There are combo UV boxes/horizontal electrophoresis apparatus were you cut cubes out of gels in front of the band, watch the DNA go in there, and suck it out with a pipet and extract. In grad school I cut out a cube with the band in it. Put the whole thing in a dialysis tube and chucked it back in the gel rig. That was efficient and you could see the ethidium stained DNA in a crease in the tubing but recovery was a hassle. It was hard getting DNA out in a small volume.

Tom Gilbert <mtpgilbert@gmail.com>

---

## Guppy Genome Project

Dear all,

I looked around at NCBI if there is a guppy (*Poecilia reticulata*) genome project, but did not find it. Considering the many people who do research on this fish I was irritated that there is nothing on it yet. I am considering this fish as a model in a new proposal but therefore I would like to know if there is at least a whole genome sequencing project initiated, or will be initiated soon.

I would be happy if anybody who know's about anything about a possible guppy genome project could contact me.

Cheers, Robert

Robert H. KRAUS PhD student Wageningen University Resource Ecology Group Droevendaalsesteeg 3a 'Lumen' Building, Number 100 6708 PB Wageningen The Netherlands

Phone +31 317 4 83530/83944 Fax +31 317 419000  
Email robert.kraus@wur.nl

<http://www.reg.wur.nl/UK/Staff/Kraus/>  
robert.kraus@wur.nl

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## HaplotypeNetwork Software

Dear Evoldir members, does anybody know a free software for drawing high quality haplotype networks? Thanks in advance, Romina

Dr. Romina Piccinali Lab. de Eco-epidemiología Facultad de Ciencias Exactas y Naturales Universidad de Buenos Aires Argentina

rpicci@ege.fcen.uba.ar rpicci@ege.fcen.uba.ar

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## HaplotypeNetwork Software answers

Dear all, Thanks to all the members that answered my question: Does anybody know a free software for drawing high quality haplotype networks?

Below I compile the main ideas:

- To use Network software (<http://www.fluxus-engineering.com/sharenet.htm>)
- To use TCS (<http://darwin.uvigo.es>)
- To use SplitsTree (<http://www.splitstree.org>)
- To use any graphics software such as Illustrator or Corel Draw
- To use Network and import the wmf file to Illustrator to touch it up/improve the colour/resolution. Basic functions in Network are free, though for more spiffy/efficient things you need to buy it.
- To use Export the TCS network as a postscript and improve with Illustrator, Inkscape, CorelDraw, etc.

Dra. Romina Piccinali Lab. de Eco-epidemiología Facultad de Ciencias Exactas y Naturales Universidad de Buenos Aires Argentina

rpicci@ege.fcen.uba.ar rpicci@ege.fcen.uba.ar

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## Independence of academics

Dear colleagues, Here is a link to an international call to sign-up for the defense of the independence of French (and other) researchers/academics who face particularly hard times at the moment. Though the text shows clumsy (chauvinistic) aspects, I think most of you would agree with the general idea. Best regards,

<http://math.univ-lyon1.fr/appeal/spip.php?article2>  
(you have to select "See the international call" to see the text)

Frantz Depaulis (phD CR1 CNRS)

Laboratoire d'Ecologie Ecole Normale Supérieure 46 rue d'Ulm 75230 Paris cedex 05 France (Pièce 426) tel +33 (0)1 44 32 23 44 Telex +33 (0)1 44 32 38 85

[http://ecologie.snv.jussieu.fr/eem/frantz\\_depaulis](http://ecologie.snv.jussieu.fr/eem/frantz_depaulis)  
Frantz DEPAULIS <depaulis@biologie.ens.fr>

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## LiCOR plates

Dear Evoldir

we have recently discovered, after months of painful

trouble-shooting, that there are multiple different kinds of glass for LiCOR 4200 and 4300 DNA analyzers, some of which are useless with certain models of machine.

If you use the wrong plates or a mixture, you will get focus errors, stalled runs after about 6 minutes, gels that are focussed on one side but not the other and a host of other incapacitating problems.

A brief summary:

1. Borofloat glass plates come in two completely different kinds, pre-2003 and post-2003. They have the same product name and same product number, yet the early ones work well with 4200 machines, the latter ones are USELESS. It remains a mystery why they would not be given different names and product codes. It has been extremely debilitating for us.

The older and newer kinds of Borofloat are distinguishable only by subtle differences in colour (the older ones, which work on 4200, are yellowish, the newer ones, which don't work on 4200s, are nearly colourless).

2. Starphire glass plates are now the suggested ones for 4200s. They probably do not work as well as old Borofloat, particularly in the 700 channel, on reactions that are not very strong, but may be OK. Older Borofloat is not made any more, so even if they are better, they are not really an option unless you have a big stash. Starphire are bluish, and have two corners dubbed (c.f. only one on Borofloat).

3. 'New' Borofloat are suggested for the newest machines, the 4300s.

I have a summary document about all this, which includes a photographic field guide to cryptic LiCOR glass plates, which was not publicly released even though it was intended to be, as far as I understand. I will pass it along if you email me.

I would love to hear your stories if you have been on the pointy end of these unhighlighted differences in glass composition. At the least I would like LiCOR to have a summary of the trouble it has caused to have good vs useless versions of the same product, yet not have that indicated and indeed highlighted in their materials.

thanks Paul

- Dr Paul Sunnucks Reader in Zoology School of Biological Sciences and Australian Centre for Biodiversity Monash University, Melbourne Clayton Campus 3800 Victoria Australia ph + 61 3 9905 9593 fax + 61 3 9905 5613

email paul.sunnucks@sci.monash.edu.au

webpage: <http://www.biolsci.monash.edu.au/-staff/sunnucks/index.html>

[www.biolsci.monash.edu.au/research/acb/-index.html](http://www.biolsci.monash.edu.au/research/acb/-index.html) paul.sunnucks@sci.monash.edu.au  
paul.sunnucks@sci.monash.edu.au

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## Long term pedigrees

Dear Evoldir readers,

I would like to compile a list of long-term animal population datasets that include pedigree information. By long-term I mean datasets that span 10 years or more.

If you know of any please can you let me know:

1) Species 2) Location (place name and lat/long) 3) Start and (if applicable) end dates

It would also be useful if you could provide a reference so I can read a bit about the project.

Best wishes and thanks!

Owen

- Dr Owen Jones Imperial College London  
jonesor@gmail.com

---

## MantelTest weighted by phylogenetic uncertainty

Hi Everyone

I am trying to make ideally a partial Mantel tests but otherwise two normal mantel tests analysing the relationship between genetic distance and two sets of environmental variables.

The phylogeny is only known with uncertainties and I wish to make the mantel tests based on the 1000 most likely trees weighted by their probability.

Do anyone know a program which can perform this analysis, given the data.nex.parts file and two environmental matrices?

Kind regards, Søren (soren.faurby@biology.au.dk)

---

## Measures of diversity Jost2008

Members of Evoldir,

I've written some software to calculate the new measures of diversity described in Jost 2008. It's web accessible at <http://www.ngcrawford.com/django/jost/> and takes files in GENEPOP format. I haven't independently verified my calculations, so if someone's worked them out by hand (e.g., in excel) and could let me know if my calculations agree with theirs, that would be most helpful.

- Nick

Citations:

Jost L. 2008. GST and its relatives do not measure differentiation. *Molecular Ecology* 17(18), 4015 - 4026.

Nicholas Crawford PhD Track Graduate Student Ecology, Behavior and Evolution Boston University Biology Department 5 Cummington Street Boston, MA 02215 Phone: 617-358-0252 Office: Brb 507 Blog: [www.ngcrawford.com](http://www.ngcrawford.com) Nicholas Crawford <ngcrawfo@bu.edu>

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## Netherlands AvianRadioTracking

Field assistant needed for radio tracking Great tits (Parus major) The Netherlands

In the end of February we will equip 60 female great tits (Parus major) with radio-transmitters. We will follow them up until egg laying using radio tracking equipment. Our main interest is where female great tits forage in the period before egg laying. This is a time consuming task and therefore I would like some assistance. The main work will be radio tracking the individuals, however, we might also take branch samples to find out what they are eating. Fieldwork will take place at 2 populations around Arnhem and Nijmegen.

Unfortunately there is no payment involved. We can discuss about covering of costs of course.

Do you have nothing to do in March and the beginning of April, and would you like to develop radio tracking

skills?

Please contact Luc te Marvelde

[l.temarvelde@nioo.knaw.nl](mailto:l.temarvelde@nioo.knaw.nl)

"Marvelde, Luc te" <[L.teMarvelde@nioo.knaw.nl](mailto:L.teMarvelde@nioo.knaw.nl)>

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## NIH Evolution Resource for Educators

NIH's National Institute of General Medical Sciences (NIGMS) announces the release of a special, evolutionary-themed issue of Findings, a student-oriented magazine that puts a face on science. This issue celebrates the 200th anniversary of Charles Darwin's birth and the 150th anniversary of the publication of his book *On the Origin of Species* by featuring the exciting work of two evolutionary biologists and short articles that highlight the role of evolution in medical research. This magazine is an excellent classroom resource for showcasing innovative, creative, and interesting scientists and is offered at no cost to teaching professionals, educators, and students in the science field.

Find even more on Findings Online (<http://www.nigms.nih.gov/findings/>): \* A Jeopardy!-style game on evolution you can use during class \* An online "Who Wants to be an Evolutionary Biologist?" trivia game your students can use to learn more about evolution \* A video interview with one of the featured scientists and a podcast with the other \* Links to a free image database \* Links to other free science education material from NIGMS

This special evolution issue of Findings will be available in late February. If you are a subscriber you will automatically get a copy. If not, subscribe for free now at <http://publications.nigms.nih.gov/findings/subscribe.asp> to ensure that you receive the issue (single copies or class sets available). You can also order a free, new full-color poster for your classroom!

If you do not want to subscribe at this time but would like to receive just this issue of Findings, please send an e-mail to [info@nigms.nih.gov](mailto:info@nigms.nih.gov) with the subject line "Request for February 2009 Issue of Findings - EvolDir" and your name and address in the body of the message.

For questions or help contact Alison Davis, Findings editor, at [alison.davis@nih.gov](mailto:alison.davis@nih.gov) <[mailto:davisa@mail.nih.gov](mailto:mailto:davisa@mail.nih.gov)> .

Victoria Butz Contractor NOVA Research



Company 4600 East-West Highway, Suite 700  
Bethesda, MD 20814-3415 941-383-5742 (Office)  
vbutz@novaresearch.com

Vicki Butz <VButz@novaresearch.com>

Elizabeth Salas PhD student Universidad del  
Valle Cali-Colombia dayesale@univalle.edu.co  
eliza.3176@hotmail.com

Elizabeth L <eliza.3176@hotmail.com>

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## Question on Kingroup Software

Dear all,

I am having problems since last Monday for accessing the Kingroup software webpage at [www.kingroup.org](http://www.kingroup.org). Does anyone know if it has been moving to another address?

Thank you very much, Sincerely

Carolina I. Miño, MSc. Doctoral Student Laboratório de Genética de Aves Departamento de Genética e Evolução Universidade Federal de São Carlos Rodovia Washington Luis km 235 SP-310 CEP: 13565-905 Monjolinho. São Carlos, SP, Brazil. Phone number: +55 16 3351 8391 (Work) Fax: +55 16 3351 8377 Mobile: +55 16 91190380

Carolina Minio <carolinaianido@yahoo.com.ar>

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## R and F statistics question

Dear all,

I am working with plant microsatellites trying to know about the genetic structure of a mangrove species. I've analyzed my data set using F and R statistics. I've compared both Fst and Rst using spagedi software in order to know which one is the best option for my study. According to Hardy et al (2003) criteria, I found that Rst explain better than Fst my data. So, now I know that mutations have contributed to the genetic differentiation in my species, which means that I have to assume SMM. Assuming SMM model implies that I have to work with Ris as a fixation index. Could someone tell me what software can I use to obtain Ris per population (spagedi just does global Ris calculations)? Or could I continue using Fis taking into account that is calculated on Heterozygosity basis? I need a clue how I can face this problem since Fixation index is very important to explain my results.

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## Redimensioned BIOSYS-2 software

Hi All

Many thanks to the EvoDir community for providing me with the BIOSYS-2 software following my previous post. As it happens, my version was not corrupt and merely needed to be redimensioned and recompiled. However, not knowing the second thing about compiling, and unable to find the suggested compiler (Microsoft FORTRAN Compiler 5.1) or a living FORTRAN expert, I have spent two months struggling with it. Would anyone perhaps have a version of BIOSYS-2 that has already been redimensioned (essentially I need the number of alleles it can handle to be increased from 10 to 22)? Appreciate anyone's help (or a borrowed copy of the compiler).

Many thanks!

Gavin

South African Institute for Aquatic Biodiversity Private Bag 1015 Grahamstown 6140 South Africa

Tel: +27 (0)46 603 5843 Fax: +27 (0)46 622 2403

<http://www.saiab.ac.za> Alternative e-mail: gavingouws@gmail.com <mailto:gavingouws@gmail.com>

Gavin Gouws <g.gouws@saiab.ac.za>

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## Sample size bias

Hello, Can anyone point me in the direction of a paper where issues of bias in estimating heterozygosity as a function of sample size are addressed quantitatively? Thanks much! – Laura T. Carney

Doctoral Student Department of Biology San Diego State University San Diego, CA 92182 Office phone (619) 594-8157 Fax: 619-594-5676 <http://www-rohan.sdsu.edu/~kelplab/> lcarney@sciences.sdsu.edu

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## Scoring MHC genotypes

I hope someone working with MHC genes in Salmonid fishes could help me with a mixture of protocol and software problems.

I have been genotyping trout from infection challenge experiments in three loci, which together code for classical MHC function of both MHCI and MHCII in rainbow trout (*Oncorhynchus mykiss*).

Genotyping cDNA has generally gone well, although I have trouble finding software that will align sequences from the MHCI locus (onmy-UBA), since this locus contains insertion/deletion heterozygotes. I am currently using CodonCode, but I end up doing very much of the aligning and genotyping by hand, which takes forever. I have also tried SeqScape from ABI and an older version of Sequencher.

The gDNA genotyping has proven very difficult in general, with many individuals not producing readable sequence at all, although there is no reason my primers shouldn't work on gDNA.

I would very much like to discuss this with people who have experience with software, which can align sequence with indel heterozygotes, or people who have good experience with gDNA sequencing protocols for MHC genes.

Thank you for any ideas or suggestions

Best regards

Mette Hansen Projektforsker / Project scientist

AARHUS UNIVERSITET / UNIVERSITY OF AARHUS  
Det Jordbrugsvidenskabelige Fakultet / Faculty of Agricultural Sciences  
Inst. for Genetik og Biotechnologi / Dept. of Genetics and Biotechnology  
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Tel: +45 8999 1900 Direct: +45 8999 1095 Mobile: +45 E-mail: MetteH.Hansen@agrsci.dk  
<mailto:MetteH.Hansen@agrsci.dk> Web: www.agrsci.dk <<http://www.agrsci.dk/>>

“Mette H. Hansen” <MetteH.Hansen@agrsci.dk>

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## SmallRead StatsPackages

Dear fellow EvolDir'ers,

I am wondering if anyone knows of any statistical packages which can process mega-base sequences, generated from parallel sequencing, within a phylogeographic/population genetics framework? If not, perhaps you are aware of a research group who are thinking along the same lines?

Much thanks in advance!

– Jack Lighten Ph.D. candidate Bentzen Lab Room 6078 Department of Biology, Dalhousie University Halifax, NS, B3H 4J1

Email: Jackie.Lighten@Dal.Ca

Jackie Lighten <jc807177@DAL.CA>

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## SocIntegCompBiol boycott NewOrleans

Witty article on the matter from New Orleans...

Mad scientists

Wednesday, February 18, 2009 James Gill

Perhaps you did not know that the Society for Integrative and Comparative Biology had New Orleans in mind for its 2011 annual meeting in New Orleans.

Perhaps you are not even familiar with the Society for Integrative and Comparative Biology. Well, you've missed your chance. Although New Orleans “has been a popular venue of us in the past,” society president, Richard Satterlie, has advised Gov. Bobby Jindal that the 2011 meeting will go to Salt Lake City instead.

In his letter to Jindal, Satterlie says the society will be urging other scientific organizations to “reconsider any plans to host meetings in Louisiana.”

The American Society for Biochemistry and Molecular Biology is already committed to New Orleans for this year, but that will be it. Its president Gregory Pet-sko has declared, “No future meeting of our society will take place in Louisiana as long as that law stands.”

“That law” is the Louisiana Science Education Act, which is named for what it is designed to destroy. Jindal signed it last year, clearing the way for creationism to be taught in biology class.

Satterlie wants Jindal to work for a repeal of the act in this year’s session, but parting the Red Sea would be child’s play by comparison. The bill received only three nay votes in the House last year, and none at all in the Senate, so even if Jindal were prepared to heed the voice of reason, he could probably never twist enough arms in the corridors of the Capitol to engineer a repeal.

But the voice of reason cuts no ice with Jindal anyway, at least on this issue. He refused to veto the bill last year, ignoring the pleas not only of Satterlie’s group, but the American Association for the Advancement of Science, a slew of other learned bodies and even his old genetics professor from Brown University.

The force behind the bill was the Louisiana Family Forum, a group of Christian soldiers that few politicians would wish to cross, given that polls suggest a startlingly high number of Americans refuse to accept that mountains of scientific evidence prove the truth of evolution.

While some politicians might kowtow to the forum out of expediency, Jindal does not appear to be one of them. He actually appears to believe this stuff. Darwin or Genesis? You pays your money and you takes your choice, so far as the Louisiana Science Education Act is concerned.

This legislation is straight out of the Dark Ages, but it will remain on the books even if every scientist in the land joins in the boycott.

The Family Forum has this administration in its clutches. Not only has Jindal, in his ostentatious Catholicism, voiced doubts about evolution, but his chief of staff, Timmy Teepell, is an old friend of Forum director, Gene Mills. Jindal’s labor secretary, Tim Barfield, is a founding member of the Forum.

Satterlie’s letter to Jindal included a somewhat heavy-handed and superfluous reminder that conventions “can contribute to the economic regime of any community.” His society’s convention held in Boston this year “brought over 1,850 scientists and graduate students to the city for five days,” Satterlie wrote.

Dependent though this city is on the extravagance of strangers, Forum zealots are not going to be deterred by such mundane considerations. If the intellectual, and therefore economic, health of the state were of any concern, they wouldn’t be so eager to lumber us with generations of scientific ignoramus.

Their own intellectual honesty may be measured through their repeated denials that the Louisiana Science Education Act had a religious purpose in allowing the introduction of “supplemental materials” in science class.

How they squawked when a Board of Elementary and Secondary Education task force called their bluff and included a ban on “the teaching of creationism or intelligent design” in rules it drew up to implement the act. The board licked Mills’ hand and removed the ban.

So scientists are going to be thin on the ground around here. What economic effect the Louisiana Science Education Act will have, however, is hard to say, since maybe there will be an influx of fundamentalists to take up the slack.

The city economy might still suffer a net loss anyway, since, when it comes to cocktail time, one biologist is probably worth at least six Bible literalists.

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James Gill is a staff writer. He can be reached at 504.826.3318 or at [jgill@timespicayune.com](mailto:jgill@timespicayune.com).

[clarroux@sib.uq.edu.au](mailto:clarroux@sib.uq.edu.au) [clarroux@sib.uq.edu.au](mailto:clarroux@sib.uq.edu.au)

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## Software Nemo 2.1 released

Dear EvolDir members,

I am happy to announce a major update of Nemo, version 2.1.0, available on SourceForge ( <http://nemo2.sourceforge.net> ).

Nemo is a forward-time, individual-based, genetically explicit, and stochastic simulation program designed to study the evolution of life history/phenotypic traits and population genetics in a flexible (meta-)population framework.

The two major updates for this release are:

- Temporal parameter modifiers (change simulation settings during a the course of a simulation) and population fission/fusion, bottlenecks, etc.
- Data saving and loading from text files (e.g. FSTAT files for neutral markers), allows to use field genetic data in simulations, for instance.

General presentation:

Nemo implements many different life cycle events and genetic traits. It also allows to model species interac-

tion between a parasite and its host (i.e. Wolbachia). All this is framed within a flexible metapopulation model that allows for patch-specific carrying capacities, dispersal rates, and extinction/harvesting rates, etc. Populations can be dynamically modified during a simulation, allowing for population bottlenecks, patch fusion/fission, and expansion, etc.

Nemo's interface is a simple text file containing the simulation parameters and their values. It is run on the command line. Each parameter can have several argument values thus allowing to run many simulations from a single init file. Parameters can also be set with temporal values that will automatically modify the simulation settings during its run.

Nemo is also intended as a C++ developing framework. The complete code documentation and coding guidelines for the development of new evolutionary models using Nemo are available at <<http://nemo2.sourceforge.net>>. Binaries for Mac OS X and Win32 are available for download at <http://sourceforge.net/project/nemo2>. The complete source code and user documentation are available at the same address.

Nemo v2.1.0 includes the following features:

- customizable sequence of life cycle events (breeding, dispersal, aging, selection, etc.)
- temporal parameter modifiers (in the configuration file, check the manual!)
- flexible population model, from the Island Model to explicit spatial structure with dynamic population sizes
- several mating systems:
  - o random mating (promiscuity)
  - o polygyny
  - o monogamy
  - o selfing / hermaphroditism
  - o cloning
- the available individual's traits are:
  - o sex-specific dispersal
  - o deleterious mutations
  - o neutral markers (bi- or multi-allelic)
  - o cytoplasmic incompatibility inducing endosymbiotic parasite (Wolbachia)
- lots of statistics for each trait and the population dynamic, including:
  - o F-statistics (Gst, theta, heterozygosities, etc.), Nei's D
  - o coancestry analysis for the neutral trait
  - o inbreeding load dynamics (mutation frequencies, fixation rate, heterosis, genetic load, lethal equivalents, etc.)
  - o dispersal rates
  - o population demography and kinship analysis
  - o population fitness and survival
  - o and more...
- data saving and loading in binary mode or from text files (FSTAT files for neutral markers)
- please have a look at the user manual for more features and details

Nemo allows to run simulations in batch mode by running several simulations from the same input parameters file or from several such files. Nemo also runs in parallel computing environments by using the MPI standard.

This is an open-source, free software project, so feel free to contribute!

and enjoy...

Frederic Guillaume

Frédéric Guillaume Post-doctoral Fellow Dpt. of Zoology University of British Columbia 6270 University Boulevard Vancouver, BC, V6T 1Z4

office: ++1 604 822 3366 cell: ++1 604 760 6277

guillaum@zoology.ubc.ca guillaum@zoology.ubc.ca

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## SouthAfrica VolunteerFieldAssist SmallMammalEvolution

Volunteers needed as field assistants for the project:

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

>From May 2009 onwards, especially for July/August to December 2009

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

Project: We study the evolutionary and ecological reasons 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 group.

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field; maintenance of the research station.

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 750 (around 65 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 2000 or 170 Euro/month). Including extras, you should expect costs of about 250 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 to start in April / May 2009 and several volunteers that want to come during the period July/ August to December 2009. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months 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@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch).

More information under [www.strippedmouse.com](http://www.strippedmouse.com) Contact via e-mail: [carsten.schradin@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch)

Dr. Carsten Schradin Research Assistant, Zoological Institute, 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 and curtains quickly added to our daily field work activities.

It was never boring in Goegap! There was always something to do: studying the striped mouse, listening to the interesting and funny

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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/evodir.html>

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## SSB ErnstMayrAward

Society of Systematic Biology Awards Available

Ernst Mayr Award (Graduate Student Award)

The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meetings of the Society of Systematic Biologists. The award consists of \$1000 and a set of available back issues of Systematic Biology.

Who is Eligible. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to: <http://systbio.org/?q=node/6>). Previous Mayr award winners are not eligible. Application

Procedure. Applications should be sent to the current SSB Awards Committee Chair (Sydney Cameron), at [ssb-apps@life.illinois.edu](mailto:ssb-apps@life.illinois.edu). E-mail submissions are required. In the subject line of the email, please indicate the SSB award category as "Mayr Award".

Applicants should:

Submit a 400-word abstract of their talk to the SSB Mayr Awards Committee ([ssb-apps@life.illinois.edu](mailto:ssb-apps@life.illinois.edu)) by March 15, 2009. All candidates will be notified of their status no later than March 30, 2009. If selected as a Mayr candidate, during the meeting registration process (<http://evolutionmeetings09.org>) enter a note about being a Mayr candidate in the field concerning participation in a specific session. The deadline for the meeting submission is the same as for all other talks, i.e., April 5.

Judging. Based on the submitted abstracts, the Mayr Awards Committee (appointed by the Awards Chair) will select a maximum of 15 applicants for inclusion in the Ernst Mayr session at the 2009 Moscow, Idaho meetings, which will be held at a single venue in a separate session. Talks will be judged on creativity, quality, excellence of research, and quality of presentation. Abstracts should clearly indicate methods used, conclusions, and the relevance to systematics. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

Co-Authors. The paper may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenter, and the intention is that the student presenter will be senior author on the published version of the paper.

Notification of Winner. The winner of the award will be announced at the SSB business meeting in Moscow, again during the banquet or awards ceremony at the conclusion of the Evolution Meetings, and an announcement will be published in *Systematic Biology*.

Sydney Cameron <[scameron@life.illinois.edu](mailto:scameron@life.illinois.edu)>

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## SSB GradStudentResearchAwards

Society of Systematic Biology Awards Available

Awards for Graduate Student Research

The Society of Systematic Biologists (SSB) announces

the 2009 annual Graduate Student Research Awards competition. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbio.org/?q=node/6>). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards will range between \$1,200 and \$2000 and approximately seven awards will be made.

All application materials must be in electronic format. Applicants and their recommenders are strongly encouraged to use pdf format, rather than Word or some other application, to minimize difficulties in file transfer. We strongly recommend that applicants send all materials (except letters of reference) in a single pdf file. Letters of recommendation should be sent separately by the referees in pdf format or in the text of an e-mail; please include the full name of applicant in letters of recommendation. Applicants must submit 1. curriculum vitae (one page) 2. brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3. budget and budget justification (1 page) 4. two letters of recommendation; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. Please include e-mail contacts for the applicant in the application itself. Both Masters and Ph.D. students are eligible. Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work. Please email all application materials and queries to SSB Award Committee [ssb-apps@life.illinois.edu](mailto:ssb-apps@life.illinois.edu). In the subject line of the email, please indicate the SSB Student Research.

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2009.

Sydney Cameron <[scameron@life.illinois.edu](mailto:scameron@life.illinois.edu)>

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## SSE International travel awards

The Society for the Study of Evolution (SSE) announces International Travel Awards for 2009, to foster international relationships between evolution societies and SSE members with particular focus on students and young scientists. The committee sponsors annually a series of activities/awards to reach this goal: international travel awards for meeting attendance, international symposia awards, and other international events awards. For details and eligibility requirements, see the SSE awards webpage (<http://www.evolutionarysociety.org/awards.asp#sseic>). Deadline for application is March 31, 2009.

Thanks, Judy, SSE secretary

Judy Stone <jstone@colby.edu>

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## Stenamma ant samples

Dear Evolutionary Biologists,

I am a graduate student at the University of California, Davis and I work on the systematics of the ant genus *Stenamma*. One of my goals is to produce a broad-scale phylogeny of the genus. However, I have not been able to obtain fresh specimens from Europe or Asia. If you have any recently collected specimens preserved in 90-100% etoh I would be very grateful if you could send me a few. The genus is a cold hardy cryptic group, whose members are most often encountered in forest leaf litter samples (Winkler or Berlese). Please let me know if you can help in any way.

Best regards, Michael

– Michael G. Branstetter Department of Entomology  
University of California, Davis One Shields Ave Davis,  
CA 95616 lab ph. 530-752-9977

Michael Branstetter <mbranstetter@ucdavis.edu>

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## Texas creationism

Please forward the following appeal for help to EvolDir members. Thanks! -Dan Bolnick danbolnick@mail.utexas.edu

Begin forwarded message:

Click to view this email in a browser

Dear Colleagues,

The Texas State Board of Education is considering several changes to the state science curriculum that will undermine effective coverage of evolution in high-school biology classes. Proposed anti-evolution language will also put pressure on textbook publishers to incorporate creationist criticisms of evolution or else risk being excluded from the monolithic Texas textbook market.

The board members are receiving thousands of emails from creationists supporting the current curriculum draft. To keep scientifically unfounded arguments out of our schools' biology classes, we need help from each and every one of you. Please email the 15 members of the State Board and urge them to

- (1) adopt the scientifically sound curriculum standards drafted by a working group of teachers and scientists in December, and
- (2) reject amendments to these standards that have been proposed by anti-evolution members of the State Board of Education.

Below, we provide instructions on how to contact State Board of Education members. Although we include a form letter below, we encourage you to personalize the email. Below, we also provide a succinct explanation of the current status of curriculum revision in Texas.

Sincerely,

The 21st Century Science Coalition  
([www.texasscientists.org](http://www.texasscientists.org))

Dr. D.I. Bolnick University of Texas at Austin  
Dr. R.E. Duhrkopf Baylor University  
Dr. D. Hillis University of Texas at Austin  
Dr. B. Pierce Southwestern University  
Dr. S. Sarkar University of Texas at Austin

PS If you know of colleagues who have not yet signed the 21st Century Science Coalition statement, please forward them this e-mail or direct them to [www.texasscientists.org](http://www.texasscientists.org). What you can do to help

Please email members of the State Board Of Education, encouraging them to adopt the original draft of the standards proposed by working groups in December.

You can email the entire SBOE directly at [sboeteks@tea.state.tx.us](mailto:sboeteks@tea.state.tx.us).

Here is a template for an email to the SBOE (we encourage you to personalize this):

To the Texas State Board of Education,

As a scientist and active researcher and educator, I am writing to urge you to support sound science education in Texas. In particular, I request that you adopt the Biology and Earth Sciences TEKS draft as originally proposed by the Working Groups. These working groups are composed of educators and scientists with deep expertise in science, and their proposed TEKS drafts should be given unreserved support without amendment.

In particular, I object to the recent changes made to the highschool TEKS (subchapter C) section 112.34 (c) 7.B: “analyze and evaluate the sufficiency or insufficiency of common ancestry to explain the sudden appearance, stasis, and sequential nature of groups in the fossil record;” This language inaccurately insinuates that the fossil record supports long-standing creationist arguments that existing species were created as they exist today. The present wording is misleading. I also object to changes to section 112.36 (c) 8.A, which now read: “evaluate a variety of fossil types, proposed transitional fossils, fossil lineages, and significant fossil deposits and assess the arguments for and against universal common descent in light of this fossil evidence” ; Transitional fossils are not “proposed” - they are clearly documented based on detailed anatomical measurements. Also, the phrase “arguments for and against universal common descent” is a common creationist phrase that inaccurately suggests that there is credible scientific data arguing against common ancestry.

In conclusion, please revert to the original working group version of the science TEKS, and resist additional changes that are not approved by the working groups of scientists and educators.

Sincerely,

YOUR NAME

YOUR QUALIFICATIONS

YOUR AFFILIATION/POSITION

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Some suggestions for emailing the SBOE

1. You can specify in your email to [sboeteks@tea.state.tx.us](mailto:sboeteks@tea.state.tx.us) that you wish your message to reach particular SBOE members. It may help if you take advantage of this and vary your tone depending on which members you are writing to. For instance, the Science Supporters [Bob Craig; Mary Helen Berlanga; Pat Hardy; Rene Nunez; Mavis Knight] cast difficult votes to support evolution in the TEKS, and are being hammered by angry emails from creationists. When emailing these members, please be sure to thank these five for their consistent support of the science standards AS WRITTEN BY THE WORKING GROUPS, and urge them to continue to oppose amendments to the standards or efforts to revert to problematic language that

— / —

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>

## Turin ESEB JMaynardSmithPrize

Announcement of the 2009 John Maynard Smith prize of the ESEB

The European Society for Evolutionary Biology has established The John Maynard Smith Prize to be awarded to outstanding young researchers in the field of evolutionary biology.

The prize is named after John Maynard Smith (6 January 1920 - 19 April 2004), eminent evolutionary biologist, and author of many books on evolution, both for scientists and the general public. He was professor emeritus at University of Sussex, UK, Fellow of the Royal Society, winner of the Darwin Medal, and laureate of the Crafoord Prize of the Swedish Academy of Sciences.

Starting from 2009 the Prize also includes a Junior Fellowship of generally 3 months at the Wissenschaftskolleg zu Berlin, Germany. Information about the fellowship can be found under <http://www.eseb.org> Further Junior Fellows for the Wissenschaftskolleg, may be selected from the other applicants. For more information on Junior Fellowships at the Wissenschaftskolleg zu Berlin, or information on this institution, contact Paul Schmid-Hempel, ETH Zurich, Switzerland.

The seventh prize winner will be announced at the 2009



congress of the society in Turino, Italy.

The previous winners are introduced on the ESEB webpage [www.eseb.org](http://www.eseb.org) Nomination:

The prize is open to any field of evolutionary biology. Candidates for the prize must be nominated by a senior colleague; the nomination must be accompanied by the candidate’s CV, a list of publications, a short description of future research plans, the names and addresses of two referees, and a letter from the candidate approving the nomination. Candidates for the 2009 prize must have received a PhD (or equivalent) degree no earlier than January 2007.

The nominations should be received by email and sent to:

Mauro Santos Departament de Genetica i de Microbiologia Facultat de Biociencias, Edifici Cn Universitat Autònoma de Barcelona 08193 Bellaterra (Barcelona) SPAIN Fax: +34 93 581 2387 e-mail: mauro.santos@uab.es or msantos@colbud.hu

They should arrive no later than March 15, 2009. Please take care to limit the size of attachments (total < 5 MB) in any one email (use sequels if necessary). The winner is expected to attend the 2009 congress, where he or she will deliver the John Maynard Smith Lecture. The society will pay registration, accommodation, and travel expenses (economy fare).

Dieter Ebert Secretary ESEB Universität Basel, Zoologisches Institut, Evolutionary Biology Vesal-

gasse 1, CH-4051 Basel, Switzerland <http://-evolution.unibas.ch/> Email: dieter.ebert@unibas.ch Tel. +41-(0)61-267 03 60 FAX +41-(0)61-267 03 62

dieter.ebert@unibas.ch dieter.ebert@unibas.ch

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## Yellowtail Kingfish sampling

Dear EvolDir members,

I’m a PhD student at the University of Stellenbosch, South Africa and I’m looking for Yellowtail Kingfish (*Seriola lalandi*) samples for a phylogeography study over its entire distribution range. If you have any samples or are interested in collaboration please e-mail me at [bls@sun.ac.za](mailto:bls@sun.ac.za)<<mailto:bls@sun.ac.za>>.

Looking forward to hear from you!

Thanks in advance,

Belinda Swart

PHD Student Molecular Aquatic Research Group Department of Genetics JC Smuts Building Stellenbosch University Private Bag X1 Matieland SOUTH AFRICA 7602 Tel: +27 (0)21 808 5837

“Swart, BL, Mej <[bls@sun.ac.za](mailto:bls@sun.ac.za)>” <[bls@sun.ac.za](mailto:bls@sun.ac.za)>

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## Auckland PopGenetics

Postdoctoral Scientist Molecular Ecology of Speciation  
Plant & Food Research Location: Mt Albert, Auckland, New Zealand We are seeking a molecular ecologist/population geneticist to investigate the genetic basis of speciation in a group of endemic New Zealand moths. Applicants will have a PhD in molecular ecology or molecular phylogenetics with an interest in speciation, experience in collecting and analysing molecular population data, and a passion for addressing basic questions in evolutionary biology. The successful applicant will become an active participant of the Allan Wilson Centre for Molecular Ecology and Evolution (<http://www.allanwilsoncentre.ac.nz>)

This two year fixed term position offers an exceptional opportunity to develop and apply your skills within a friendly, professional environment.

If this sounds like you, please visit our website [www.plantandfood.com](http://www.plantandfood.com) for more information including application details. Enquires about the position to Richard Newcomb ([rnewcomb@hortresearch.co.nz](mailto:rnewcomb@hortresearch.co.nz))

To apply, send your application details, C.V. and a covering letter to Plant & Food Research, Human Resources, Private Bag 92 169 Auckland, or [vacancies@hortresearch.co.nz](mailto:vacancies@hortresearch.co.nz) Please quote vacancy number 015 Applications close 20 February 2009

Richard Newcomb <[RNewcomb@hortresearch.co.nz](mailto:RNewcomb@hortresearch.co.nz)>

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## Canberra 2 PhylogenomicsMolPhylogeny

Two postdoctoral fellowships in Molecular Evolution

and Phylogenomics are available at CSIRO Entomology (Canberra, ACT, Australia).

1 ' Phylogenomics: A Comparative Study of the Cotton Bollworm Genome for further details, please go to

> [https://recruitment.csiro.au/asp/-job\\_details.asp?RefNo=3D2009%2F37](https://recruitment.csiro.au/asp/-job_details.asp?RefNo=3D2009%2F37)

2 ' Molecular Phylogeny: Inference of Ancestral DNA and Protein for further details, please go to

> [https://recruitment.csiro.au/asp/-job\\_details.asp?RefNo=3D2009%2F38](https://recruitment.csiro.au/asp/-job_details.asp?RefNo=3D2009%2F38) Closing date: 22 Feb. 2009.

— Assoc. Prof. Lars Jermiin Biological Science, Bldg A08 University of Sydney NSW 2006, Australia

+61-2-9351-3717 (phone) +61-2-9351-4119 (Fax)  
[lars.jermiin\[at\]usyd.edu.au](mailto:lars.jermiin[at]usyd.edu.au)

Patience is a priceless commodity...

[lars.jermiin@usyd.edu.au](mailto:lars.jermiin@usyd.edu.au)

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## Duesseldorf 2 GenomeEvolutionaryNetworks

Duesseldorf.GenomeEvolutionaryNetworks.2postdocs

The Institute of Botany III, University of Düsseldorf, laboratory of Dr. William Martin, is currently seeking to fill two full-time postdoctoral positions to study the application of networks in genome evolution.

The Institute offers a modern and supportive working environment with solid funding and has recently received an Advanced Grant from the European Research Council to investigate the properties and utility of networks in genome evolution, specifically as it applies to non-treelike processes of microbial evolution, lateral gene transfer among prokaryotes and endosymbiosis among eukaryotes in particular. Information about our ongoing research ac-

tivities can be found at <http://www.molevol.de/lab/-publications.html>. 1. Prokaryotes. Postdoctoral position (biologist/bioinformatician/computer scientist; three years with possibility of extension for additional two years). Candidates should have a PhD in Mathematics or Informatics with a good working knowledge of biology or a PhD in Biology with a good working knowledge of computer science (programming skills). Experience with networks, experience using MatLab or related tools and ideally a basic working knowledge of genome biology and will be advantageous. Salary is the standard for university postdoctoral researchers according to E14, the position can be filled immediately. The project aims to investigate modularity in prokaryote gene sharing patterns, hierarchical manifestations thereof, and network attributes of prokaryote genome evolution at various taxonomic levels (including strains). Candidates should be able to work independently and to should show an interest in co-supervision of PhD students.

2. Eukaryotes. Postdoctoral position (biologist/bioinformatician/computer scientist; three years with possibility of extension for additional two years). Candidates should have a PhD in Mathematics or Informatics with a good working knowledge of biology or a PhD in Biology with a good working knowledge of computer science (programming skills). Experience with networks, experience using MatLab or related tools and ideally a basic working knowledge of genome biology and will be advantageous, as will familiarity with genome sequences and the role of endosymbiosis in eukaryote evolution. Salary is the standard for university postdoctoral researchers according to E14, the position can be filled immediately. The project aims to identify and investigate the nature of gene sharing patterns between prokaryotes and eukaryotes using network approaches, and the network properties of the data. Candidates should be able to work independently and to should show an interest in co-supervision of PhD students.

Interested candidates should send their application as a single pdf file including c.v. with publication list and contact details of two potential references to Prof. William Martin ([w.martin@uni-duesseldorf.de](mailto:w.martin@uni-duesseldorf.de)). Initial deadline for applications is March 31 but applications will be accepted until both positions are filled.

– Prof. Dr. William Martin Institut fuer Botanik III Heinrich-Heine Universitaet Duesseldorf Universitaetsstr. 1 40225 Duesseldorf

Germany

Tel : ++49-211-811-3011 Fax : ++49-211-811-3554 e-mail : [w.martin@uni-duesseldorf.de](mailto:w.martin@uni-duesseldorf.de) web :

<http://www.molevol.de> [W.Martin@uni-duesseldorf.de](mailto:W.Martin@uni-duesseldorf.de)  
[W.Martin@uni-duesseldorf.de](mailto:W.Martin@uni-duesseldorf.de)

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## Institut Pasteur Bioinformatics Microbial Pop Genomics

Post-doctoral position in bioinformatics: next-generation sequencing (NGS) analysis for population genomics of microorganisms, Institut Pasteur.

The objective is to develop analysis strategies for NGS data in the framework of population genomics or genomic epidemiology studies, for example to trace back strain microevolution based on nucleotide polymorphism or recombination events. Our group participates in projects aimed at characterizing the genome-wide diversity within emerging or epidemic infectious agents, in collaboration with Institut Pasteur laboratories and National Reference Centers. The successful applicant will be involved in the development and use of innovative methods for handling, analyzing and interpreting NGS data in this context.

The “Genomic Integration and Analysis” team belongs to the “Genomes and Genetics” department, it has developed the GenoList database framework (Lechat et al., NAR, 2008). Institut Pasteur, where NGS was recently installed, is a leading institute both in the study of infectious diseases and in genomics.

The candidate should have a background in genomics and computing science (PhD degree), including programming capabilities and skills in bioinformatics methods – expertise in statistics, microbiology or population genetics would be a plus.

Duration: 2 years, available immediately.

Salary: depending on qualifications.

Application (detailed CV, cover letter, references): Dr. Ivan Moszer - [ivan.moszer@pasteur.fr](mailto:ivan.moszer@pasteur.fr) Intégration et Analyse Génomiques - <http://genopole.pasteur.fr/PF4>  
Institut Pasteur, Paris, FRANCE

Sylvain Brisse <[sylvain.brisse@pasteur.fr](mailto:sylvain.brisse@pasteur.fr)>

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## LaurentianU ForestQuantGenetics

QUANTITATIVE GENETICIST: POST-DOCTORAL RESEARCH ASSOCIATE

Location: Laurentian Forestry Centre and Laval University, Quebec City, Quebec, Canada

Earliest Starting Date: April 1, 2009

Application Closing Date: For full consideration, apply by March 1, 2009

Context: The postdoctoral research associate will work on association studies within the Arborea project ([www.arborea.ulaval.ca](http://www.arborea.ulaval.ca)), a large multi-organization team that is funded mainly by Genome Canada and Genome Quebec, whose mission is to contribute to the durable development of forests through innovative solutions. Its multidisciplinary research team develops tools for the genetic selection of trees, advances the discovery of new knowledge and helps to train young scientists. The research associate will focus on quantitative genomics research aimed at discovering associations between genetic markers (SNPs) of several hundreds of candidate genes for wood formation and wood traits of white spruce and carrying out genome-wide identification of loci that control gene expression polymorphism (eQTLs) of candidate genes involved in the same traits.

Responsibilities: The incumbent will (1) develop analytical approaches and carry out statistical analyses for identification of genetic markers associated with wood traits, (2) develop analytical approaches and carry out analyses to find genotyped loci which together best explain the variability of target gene expression in an association population, and (3) communicate results orally and in writing via scientific meetings and peer-review papers.

Required qualifications: Qualified candidates will have a Ph.D. in quantitative genetics, statistics or genomics. They will possess a thorough understanding of genetics and statistical software (e.g., SAS, R). Moreover, they will have demonstrated their ability to write peer-reviewed papers, communicate fluently in English, and work collaboratively with a team of research scientists.

Desired qualifications: Experience with association analysis, QTL analysis, molecular markers, bioinformatics, genomics and tree breeding is desirable.

Fellowship: The fellowship is \$43,724 (CDN) per year, for an initial term of one year, renewable for up to two more years. The selected candidate will be required to apply to the NSERC- Visiting Fellowships in Canadian Government Laboratories Program. For additional information, visit the NSERC website at [http://www.nserc-crsng.gc.ca/Students-Etudiants/-PD-NP/Laboratories-Laboratoires/index\\_eng.asp](http://www.nserc-crsng.gc.ca/Students-Etudiants/-PD-NP/Laboratories-Laboratoires/index_eng.asp) . For

additional information: Contact Jean Beaulieu, Canadian Wood Fibre Centre, 1055 du P.E.P.S., Quebec City, Quebec, Canada G1V 4C7, Email: [Jean.Beaulieu@nrca.gc.ca](mailto:Jean.Beaulieu@nrca.gc.ca) or John MacKay, Université Laval, Quebec City, Quebec, Canada, G1K 7P4, Email: [John.Mackay@sbf.ulaval.ca](mailto:John.Mackay@sbf.ulaval.ca).

Application procedure: Qualified applicants are required to provide the following three documents: (1) curriculum vitae, (2) letter summarizing qualifications for this position, and (3) name and contact information for three professional references. They must be sent via email to Pascal Poulin at [info@arborea.ulaval.ca](mailto:info@arborea.ulaval.ca) .

Pascal Poulin <[Pascal.Poulin@sbf.ulaval.ca](mailto:Pascal.Poulin@sbf.ulaval.ca)>

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## MainzGermany ProteinEvolution

Postdoc: Protein Evolution; Institute of Anthropology, Mainz, Germany A POSTDOCTORAL FELLOW position is available at the Institute of Anthropology, University of Mainz, Germany, for an highly motivated individual interested in protein evolution of mammals. The project aims at studying the evolution of phosphorylated sperm-proteins of human and bovine and includes both laboratory and molecular evolution analysis components. Applications are invited from candidates with elaborated skills in the field of proteomics, in particular in 2D-gel electrophoresis and the interpretation of mass spectra. Candidates with a proven publication record will be preferred. Experience in phylogenetics and evolutionary analyses of molecular data is welcomed. The position is funded by the German research foundation (DFG). The initial appointment is for two years and is available immediately. To apply, please send a CV, a statement of research interests (one page maximum) and contact information for three references to Dr. H. Herlyn, [herlyn@uni-mainz.de](mailto:herlyn@uni-mainz.de). The successful candidate will benefit from a variety of laboratory, sequencing and computational resources at the Institute of Anthropology, Mainz. The group of H. Herlyn focuses on phylogenetics and the molecular evolution of reproductive proteins, both at the genome and proteome level. For more information see [http://www.uni-mainz.de/-FB/Biologie/Anthropologie/holger\\_herlyn.php](http://www.uni-mainz.de/-FB/Biologie/Anthropologie/holger_herlyn.php) . Application deadline is 28/02/2009. Please note that if you have not heard from me two weeks after the deadline, you have not been shortlisted for an interview.

Von: Herlyn, Dr. Holger Gesendet: Montag, 2.

Februar 2009 15:22

“Herlyn, Dr. Holger” <hherlyn@uni-mainz.de>

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## MaxPlanck Leipzig PrimateEvolution

Researchers in the department of Primatology of the Max Planck Institute for Evolutionary Anthropology in Leipzig study various aspects of the evolution of social systems, culture, ecology, and behavior in primates, with a particular emphasis on great apes. Apes live in a variety of social systems, within which we can examine reproductive strategies, aspects of cognition and cultural variation, and behavioural diversity within and among social units. Particularly interesting are the differences between apes and humans in fundamental social-cognitive processes involving communication, cooperation, social interactions, behaviors used to resolve conflict, and social learning.

Two post-doctoral research positions Or: One post-doctoral research position and one assistant professor position

are currently available. Ideal candidates preferably should have research experience related to the topics addressed in the department, but it is not necessary to have previous research focused on primates, and should be able to play an important role in consolidating and linking theoretical approaches with empirical data. Applicants should have a Ph.D. in Biology, Anthropology, Ecology or Mathematics and at least 2 years of post doc experience. Prior experience with modeling or comparative methods is a plus. The positions will initially be offered for 2 years with possible extensions to 5 years. Some research and student funding can be provided with the position.

Applications will be considered until the positions are filled but for full consideration a CV, statement of research interests and names of references should be received by March 15, 2009. Please email to Prof. Christophe Boesch (nebel(at)eva.mpg.de)

The Max Planck Society is an equal opportunity employer. For more information on the work of the department got to <http://www.eva.mpg.de/primat/> Claudia Nebel

Max-Planck-Institute for Evolutionary Anthropology  
Department of Primatology - Assistant to Prof.  
Christophe Boesch -

Deutscher Platz No 6 phone ++49 (0) 341 3550  
200 D-04103 Leipzig fax ++49 (0) 341 3550 299  
Germany e-mail nebel@eva.mpg.de Internet <http://www.eva.mpg.de> Wild Chimpanzee Foundation:  
[www.wildchimps.org](http://www.wildchimps.org) Save the Great Apes! Sign  
mAn: <http://www.apesmanifesto.org> Claudia Nebel  
<nebel@eva.mpg.de>

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## McMasterU Astrobiology

McMaster University Origins Institute Hamilton, Ontario

Postdoctoral Fellowship in Astrobiology

Applications are invited for an Origins Institute (OI) Astrobiology Postdoctoral Fellowship to commence on, or after Sept. 1, 2009 for an initial period of 2 years, with the possibility of renewal for a third year. The OI is involved in a wide range of astrobiological research including several major national and international collaborative efforts (please see our website <http://origins.mcmaster.ca/>). Funds will also be available to cover travel and research expenses.

Areas of interest include: the formation and delivery of biomolecules to terrestrial planets; the formation, physical properties, and characterization of SuperEarths and terrestrial exoplanets; phylogenetics and prebiotic conditions that gave rise to life on Earth; microbiology in extreme environments on Earth including polar microbiology and microbial energetics in extreme environments, and interpretation of biosignatures as the basis of understanding early life on Earth and as the foundation for the search for life on Mars. OI researchers are working at several Mars analogue sites and are associated with solar system exploration for signatures of microbial life. The OI has a strong complement of faculty members in a number of related fields and the OI Astrobiology Postdoctoral Fellow will have many opportunities to collaborate with OI faculty and OI collaborative research programs.

McMaster has a number of outstanding research facilities available to OI Fellows. These include SHARC-NETs high performance computing systems with over 8000 parallel CPUs (the applicant will be eligible for priority access and programming support) as well as excellent biological and geochemical laboratory facilities.

McMaster University is committed to Employment Eq-

uity and encourages applications from all qualified candidates, including aboriginal peoples, persons with disabilities, members of visible minorities, and women.

Applicants should send a CV, bibliography, a two page summary of their research interests, and arrange for letters of recommendation from three referees (these can be submitted as signed pdf attachments via email) to:

Origins Institute Astrobiology PDF c/o Ms. Rosemary McNeice  
Origins Institute Secretary ABB 241 McMaster University  
1280 Main Street West Hamilton, Ontario, CANADA L8S 4M1

Email: mcneicer@mcmaster.ca FAX: (905) 546-1252

Further information may be obtained from the OI director, Dr. Ralph Pudritz: pudritz@mcmaster.ca Tel: (905) 525-9140 ext. 23180

Deadline: All materials, including letters from referees, must arrive no later than March 2, 2009.

“J. R. Stone” <jstoner@mcmaster.ca>

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## Milan ComputationalBiology

Dear all,

The IFOM-IEO campus has launched the “International post-doctoral program”. The program is designed to boost the career of post-docs and to encourage them to become successful and independent biomedical scientists. Competitive salary and a series of short courses on topics of immediate and future relevance will be offered. Positions are intended for outstanding and highly-motivated applicants of any nationality. For info and application please visit: <http://www.semm.it/PostDoc.php> In particular, there is an open position in my group, which is interested in detecting the genotypic determinants of cancer through the analysis of genes, proteins and of non-coding portions of the human genome. The main expertise of the group is in computational biology. However, we are also involved in data production using next generation sequencing technologies as well as testing our dry predictions in wet lab. A tight collaboration with the many wet labs in the campus is a major trait of the job.

The successful candidate will deal with data analysis through the development of ad-hoc computational tools. Applicants must have a PhD in bioinformatics, theoretical biology, genetics or equivalent. Computational skills (Perl, R or Matlab, C/C++) are manda-

tory. A background in evolutionary biology and biostatistics would be favorable.

The IFOM-IEO Campus hosts more than 400 researchers and offers an international and interactive research environment. It results from the integration of two leading Institutes in cancer research: the IFOM (FIRC Institute of Molecular Oncology) and the IEO (European Institute of Oncology). The campus offers the state-of-the-art technologies in the field of molecular and cellular biology and hosts the International PhD program of the European School of Molecular Medicine.

– Francesca D. Ciccarelli, PhD Biocomputing IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303-053 fax +39-02 94375990 web: <http://ciccarelli.group.ifom-ieo-campus.it/fewiki/> –

Francesca D. Ciccarelli, PhD Biocomputing IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303053 fax +39-0294375990 web: <http://ciccarelli.group.ifom-ieo-campus.it/> Francesca Ciccarelli <francesca.ciccarelli@ifom-ieo-campus.it>

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## MuensterGermany HostParasiteCoevolution

Postdoc: Muenster (Germany) V Host-Parasite Coevolution and Ecological Immunology

A postdoctoral research associate position is available in the group of Animal Evolutionary Ecology at the Institute for Evolution and Biodiversity, University of Muenster, Germany (<http://ieb.uni-muenster.de/>) from April 2009. The position is initially for three years, with potential extension (up to six years).

We invite applications for a research associate to establish a vigorous research group in the evolutionary ecology of immune defense and/or host-parasite coevolution. Requirement for the position is a PhD degree and research experience in a biological field. A background in evolutionary ecology and experience with molecular techniques are advantageous. We are particularly interested in candidates who want to work with the flour beetle *Tribolium castaneum* as a model organism. Current projects of the group focus on the evolution of specific memory and phenotypic plasticity in immune responses and the adaptation of host immune defenses to parasites and vice versa. Working language of the lab is English.

Successful candidates will develop externally funded

research programs, direct graduate students and contribute to teaching in the fields of evolution, ecology and biodiversity of animals. The position will include some teaching and administrative duties. The position is paid according to TV-L 13.

The University of Muenster seeks to increase the proportion of female staff members and therefore strongly encourages interested female candidates to apply. In addition, preference will be given to qualified disabled applicants.

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

Interested candidates should send applications (preferentially as E- mail attachment) containing a CV, a list of publications, a research statement and the addresses of 3 potential referees to:

Prof. Joachim Kurtz

Institute for Evolution and Biodiversity, University of Muenster, Huefferstr. 1, DE-48149 Muenster, Tel. +49 251 83 24 661, [joachim.kurtz@uni-muenster.de](mailto:joachim.kurtz@uni-muenster.de)

Closing date is February 22nd, 2009.

Joachim Kurtz <[joachim.kurtz@uni-muenster.de](mailto:joachim.kurtz@uni-muenster.de)>

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## Philadelphia CaribbeanFishDiversity

### POSTDOCTORAL FELLOWSHIP POSITION - MARINE ICHTHYOLOGY

The Chaplin Postdoctoral Fellowship for the study of Caribbean Fish Diversity and Conservation The Academy of Natural Sciences, Philadelphia in collaboration with the Global Marine Species Assessment ([www.sci.odu.edu/gmsa/](http://www.sci.odu.edu/gmsa/)) announce a postdoctoral fellowship position in marine ichthyology to begin in 2009 and named for the Charles and Gordon Chaplin family. Past work in the Bahamas undertaken by the Chaplin family and Academy scientists has produced uniquely important specimen collections, field notes, photographs and films, books and journal publications that document the marine life of the Bahamas as it was a half-century ago. Conservation International (CI) and the International Union for Conservation of Nature (IUCN) launched a Global Marine Species Assessment

in 2005. A primary goal of GMSA is to complete IUCN Red List Assessments (RLAs) of all marine vertebrates.

The Chaplin Postdoctoral Fellowship provides an opportunity to further document and understand faunal and habitat change in the Caribbean region. The Chaplin Fellow will coordinate collection of data relevant to RLAs for Caribbean shore fishes and compilation of this information in the IUCN Species Information System. The fellow will refine species distribution information through original museum collection-based research, literature search, and consultation with relevant taxonomic experts. The fellow will also participate in fund raising, coordinate and help complete three RLA 5-day workshops on approximately 1,800 Caribbean fish species. Opportunities will be available to conduct self-selected taxonomic revisions of Caribbean shore fish taxa and to conduct targeted field collections that will improve knowledge of distributions and abundance of Caribbean fishes for the purpose of reducing Data Deficient RLAs.

See <http://www.ansp.org/about/employment.php> or for further information contact Dr. John Lundberg ([lundberg@ansp.org](mailto:lundberg@ansp.org)) or Dr. Kent Carpenter ([kcarpent@odu.edu](mailto:kcarpent@odu.edu)).

To apply send CV, statement of research interests and experience, and the names and email addresses of three references to: [hrjobs@ansp.org](mailto:hrjobs@ansp.org). Position number 984 must appear in the subject line. Review of applications begins on February 15, 2009. The Academy of Natural Sciences is an Equal Opportunity Employer. Minorities, women, disabled or veterans are encouraged to apply.

John G. Lundberg Department of Ichthyology Academy of Natural Sciences 1900 Benjamin Franklin Parkway Philadelphia, PA 19103 USA

phone 215 405-5069

<http://clade.acnatsci.org/lundberg/> <http://-catfishbone.acnatsci.org/> <http://silurus.acnatsci.org/>  
John Lundberg <[lundberg@acnatsci.org](mailto:lundberg@acnatsci.org)>

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## QueensU EvolutionaryTheory

Postdoctoral Fellowship in Evolutionary Theory/Mathematical Biology

Applications are sought from outstanding researchers for a 2-year postdoctoral position in evolutionary

theory, working in the lab of Dr. Troy Day in the Departments of Mathematics and Statistics and the Department of Biology at Queen's University ([www.mast.queensu.ca/~tday](http://www.mast.queensu.ca/~tday)). The specific research topic is open, with current projects in the lab focusing on developing theory for kin selection and spatial models of evolution, host/parasite epidemiology and (co)evolution, evolutionary immunopathology, genomic imprinting and nongenetic inheritance, and coral bleaching. The successful applicant will be free to conduct research in any of these or other related areas of interest. Ideally the position will be taken up by Sept. 1, 2009 but there is some flexibility in start date. Salary will be C\$40,000 per year.

Information about the Department of Mathematics and Statistics, the Department of Biology, and Queen's University can be found at [www.mast.queensu.ca](http://www.mast.queensu.ca), <http://biology.queensu.ca> and [www.queensu.ca](http://www.queensu.ca) respectively.

To apply, send a current CV and a statement of research interest to Troy Day via email ([tday@mast.queensu.ca](mailto:tday@mast.queensu.ca)). Please include the names of 2-3 potential referees, but applicants need not solicit reference letters at this stage. Review of applications will begin on March 15, 2009 and continue until the position is filled.

Troy Day Departments of Mathematics & Biology  
Jeffery Hall Queen's University Kingston, ON, K7L 3N6, Canada  
Phone: 613-533-2431 Mobile: 613-539-1540 Fax: 613-533-2964  
[tday@mast.queensu.ca](mailto:tday@mast.queensu.ca) <http://www.mast.queensu.ca/~tday/> [troy.day@mac.com](mailto:troy.day@mac.com)

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### Roscoff France TheoreticalPopGenetics

Post-doc: Genetic hitchhiking in spatially structured populations

Supervision: Denis Roze (CNRS, Roscoff) and Nicolas Bierne (CNRS, Montpellier)

A post-doctoral position is opened at the Institut des Sciences de l'Evolution, (CNRS-Université Montpellier), Montpellier, France, and at the Station Biologique de Roscoff (CNRS-Université Paris 6), Brittany, France.

The proposed work consists in the development of theoretical population genetics models to study genetic hitchhiking in spatially structured populations. Recent methods use measures of genetic differentiation ( $F_{st}$ ) at neutral loci in order to locate genes that are se-

lected differently in different regions of a species distribution range (genome scans). However, the theory on the effects of selection on linked, neutral variation in spatially structured populations remains little developed. A combination of mathematical and simulation approaches will be used to explore the effects of different adaptive/demographic scenarios on patterns of neutral variation (allele frequency spectra, linkage disequilibrium...) in spatially structured populations. These models will be used to identify whether some statistics (if not at the level of a single locus, at the level of a whole scan) may be used to discriminate between these scenarios. Genome scan data from different species of marine invertebrates will be available in order to test these methods. Once this first work accomplished, a second subject will be to develop models of speciation in spatially structured populations, focusing on the interaction between heterogeneous selection and the evolution of endogeneous (Dobzhanski-Muller) incompatibilities.

Candidates should have a strong background in theoretical population genetics. Strong motivation, communication skills and commitment are expected. Although knowledge of French is helpful in every day life, the working language will be English.

The position starts with a first period of 14 months at the Institut des Sciences de l'Evolution (Montpellier-Sète, France, <http://www.isem.cnrs.fr>), starting between April and September 2009, and will be expandable to a second period of 14 months at the Station Biologique de Roscoff (Brittany, France, <http://www.sb-roscoff.fr>). The salary will range from 1800 to 2500 per month depending on the experience of the candidate.

Applicants should send a CV including summary of past research, current interests and motivation for the present project, as well as contact information for three references to Denis Roze ([roze@sb-roscoff.fr](mailto:roze@sb-roscoff.fr)) and Nicolas Bierne ([n-bierne@univ-montp2.fr](mailto:n-bierne@univ-montp2.fr)).

Denis Roze Adaptation et Diversité en Milieu Marin  
Station Biologique de Roscoff Place Georges Teissier,  
BP 74 29682 Roscoff Cedex, France Ph: (+33) 2 98 29 23 20 Fax: (+33) 2 98 29 23 36

[roze@sb-roscoff.fr](mailto:roze@sb-roscoff.fr)

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### TulaneU EvolutionOfFrogMorphology



\*Postdoctoral position in amphibian biology, Tulane University\*

A postdoctoral position is available to work in Corinne Richards-Zawackis lab at Tulane University on either (1) the evolution of morphological variation among poison dart frogs or (2) the roles of environmental and behavioral heterogeneity in shaping amphibian host-pathogen interactions.

The position is available from September 1, 2009 and is offered for one year, with the possibility of renewal.

For more information on this position and research in the Richards-Zawacki lab see Corinnes website (<http://coririchards.googlepages.com/home>) or contact her directly at [cori@tulane.edu](mailto:cori@tulane.edu).

Applicants should email a short statement of research interests, CV, and contact information for three references to Corinne at [cori@tulane.edu](mailto:cori@tulane.edu). Review of applications will begin March 15, 2009 and continue until the position is filled.

Corinne L. Richards-Zawacki, Ph.D.  
email:[cori@tulane.edu](mailto:cori@tulane.edu) <[email%3Acori@tulane.edu](mailto:email%3Acori@tulane.edu)>  
Assistant Professor (fall 2009) Tulane University,  
Department of Ecology and Evolutionary Biology

Cori Richards <[clrichar@umich.edu](mailto:clrichar@umich.edu)>

is funded by the NCCR Plant Survival, and will be for a period of 2.5 years, starting 1 April 2009.

Requirements for the position include a PhD in biology, a proven record of research, experience with large experiments, a drivers license and strong statistical skills.

For more information on this position and research in our lab contact Mark van Kleunen at [vkleunen@ips.unibe.ch](mailto:vkleunen@ips.unibe.ch) <<mailto:vkleunen@ips.unibe.ch>> or Markus Fischer at [markus.fischer@ips.unibe.ch](mailto:markus.fischer@ips.unibe.ch).

Applicants should e-mail a short statement of research interests, curriculum vitae, and contact details of three references to both Mark van Kleunen at [vkleunen@ips.unibe.ch](mailto:vkleunen@ips.unibe.ch) <<mailto:vkleunen@ips.unibe.ch>> and Markus Fischer at [markus.fischer@ips.unibe.ch](mailto:markus.fischer@ips.unibe.ch). In addition, they should also apply through the NCCR homepage (<http://www2.unine.ch/nccr/page26549.html>). The application deadline is 22 February 2009.

– Dr Mark van Kleunen Institute of Plant Sciences University of Bern Altenbergrain 21 CH-3013 Bern Switzerland

Tel. +41 (0)31 631 4923 Fax +41 (0)31 631 4942 e-mail: [vkleunen@ips.unibe.ch](mailto:vkleunen@ips.unibe.ch)  
<http://www.staff.unibe.ch/vkleunen/> <http://www.botany.unibe.ch/planteco/index.php> Mark van Kleunen <[vkleunen@ips.unibe.ch](mailto:vkleunen@ips.unibe.ch)>

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## UBern ConservationBiol

We are seeking a highly motivated postdoc to work in a project on determinants of invasiveness and rarity of plants.

The work will involve meta-analysis of existing studies, and field and garden experiments on a large number of confamilial groups, each including an invasive alien species, a non-invasive alien species, a common native species, a species that has been rare for a long time and a species that has become rare recently.

The position will be with Prof. Dr Markus Fischer and Dr Mark van Kleunen in the Plant Ecology group at the Institute of Plant Sciences of the University of Bern (<http://www.botany.unibe.ch/planteco/index.php>), Switzerland.

We offer a stimulating research environment in a beautiful city close to the Alps. In addition to projects on invasive and rare plants, our group is involved in projects on evolutionary and molecular plant ecology, plant population biology and community ecology. The position

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## UBritishColumbia Marine Protist Diversity

Institute: Centre for Microbial Diversity and Evolution, Departments of Zoology & Botany, University of British Columbia, Vancouver, BC, Canada.

Subject: Biodiversity, evolution and single cell barcoding of marine microeukaryotes.

Number of Postdoctoral Research Positions: Two positions are available.

Tasks: The research post-docs will examine the diversity of several groups of marine microeukaryotes (including excavates, chromalveolates, rhizarians and meiofaunal animals) from global marine samples using molecular markers. Selected markers (barcodes) will be developed from available culture collections and compared with sequence diversity from natural marine samples. The PDFs will also participate in development of protocols for high throughput sequencing of bar-

code genes from single cells linked to microscopy. The PDFs will be part of the Centre for Microbial Diversity and Evolution at UBC ([www.cmde.science.ubc.ca/](http://www.cmde.science.ubc.ca/)) as well as the International Barcode of Life initiative ([www.dnabarcoding.org/](http://www.dnabarcoding.org/)). The following UBC laboratories will support and supervise one PDF each; however, collaborative work between the two labs is expected.

Laboratory webpages: The Leander Lab ([www.botany.ubc.ca/bleander/](http://www.botany.ubc.ca/bleander/)) The Keeling Lab ([www.botany.ubc.ca/keeling/](http://www.botany.ubc.ca/keeling/))

Required skills: The successful candidates will have completed a PhD with a focus on barcoding, microbial biodiversity, protist molecular evolution/systematics, or a relevant field. The candidates must have a strong record of productivity, skills in molecular biology and analysis of sequence data. Skills in microscopy and background knowledge of marine biology and protist diversity are also highly desirable.

Starting date and duration: The appointments may begin as early as Sept. 2009. The appointments will be for one year initially, with continuation to four years depending on performance.

Application deadline: March 31, 2009.

Contact: Applicants should send a letter of application, current curriculum vitae, and contact information of two references to both Patrick Keeling and Brian Leander: [bleander@interchange.ubc.ca](mailto:bleander@interchange.ubc.ca) and [pkeeling@interchange.ubc.ca](mailto:pkeeling@interchange.ubc.ca).

Brian S. Leander Associate Professor Departments of Zoology and Botany University of British Columbia #3529-6270 University Blvd. Vancouver, BC V6T 1Z4 CANADA

Web: <http://www3.botany.ubc.ca/bleander/-index.html> Email: [bleander@interchange.ubc.ca](mailto:bleander@interchange.ubc.ca)  
Tel: 604 822-2474 (office), 604 822-4892 (lab) Fax: 604 822-6089

[bleander@interchange.ubc.ca](mailto:bleander@interchange.ubc.ca) [bleander@interchange.ubc.ca](mailto:bleander@interchange.ubc.ca)

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## UChicago TranscriptionEvolution

Applications are invited for a postdoctoral research associate with Ilya Ruvinsky in the Department of Ecology & Evolution and the Institute for Genomics and Systems Biology at The University of Chicago.

The project will focus on understanding the mechanisms responsible for evolutionary and physiological robustness of transcriptional networks. We are using *C. elegans* as a primary model system. The unique opportunities of this position include a close collaboration with research groups of Richard Morimoto (molecular biology of heat-shock response) and Luis Amaral (computational analysis of gene networks) at Northwestern University as well as interactions with a dynamic group of researchers affiliated with the Institute for Genomics and Systems Biology (<http://www.igsb.anl.gov/>).

Candidates must have a Ph.D. in Genetics, Molecular or Evolutionary Biology or related field. The ideal candidate will be creative, energetic and have excellent communication skills. All candidates are expected to have a background or interest in molecular evolutionary genetics. In addition, the candidates should have expertise in molecular biology, particularly using genetics in model organisms, and computational skills.

To apply, please submit applications (by e-mail to I. Ruvinsky), including (1) a CV, (2) a 1-page statement of past accomplishments and PDFs of most relevant publications, (3) research interests and (4) names and contact information of three referees. Review of applications will begin immediately and will continue until the position is filled.

– Ilya Ruvinsky, Ph.D. Assistant Professor of Genetics and Evolution Department of Ecology & Evolution The University of Chicago 1101 East 57th Street Chicago, IL 60637

e-mail - [ruvinsky@uchicago.edu](mailto:ruvinsky@uchicago.edu) Office - (773) 702-1533 [http://pondside.uchicago.edu/ecol-evol/faculty/ruvinsky\\_i.html](http://pondside.uchicago.edu/ecol-evol/faculty/ruvinsky_i.html) Ilya Ruvinsky <[ruvinsky@uchicago.edu](mailto:ruvinsky@uchicago.edu)>

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## UCopenhagen EvolutionOfInteractions

Two post docs on interactions between plants, herbivores and pathogens

Department of Agriculture and Ecology and Department of Plant Biology and Biotechnology, University of Copenhagen, Denmark, wishes to appoint 2 post docs from 1 July 2009 to 31 December 2011 on a cross disciplinary research project on ecological, evolutionary, chemical and molecular interactions between a plant, an insect herbivore, and a pathogen.

Job description Post doc no 1 will focus mainly on ecological and evolutionary aspects. Place of work: The Dept. of Agriculture and Ecology. This postdoc will be involved in experimental crosses between plants, controlled manipulations with insects and pathogens, molecular marker analyses, assessment of plant fitness, and data integration.

Post doc no 2 will focus mainly on the chemical and molecular processes. Place of work: The Dept. of Plant Biology and Biotechnology. This postdoc will be involved in metabolite profiling and expression analysis of plants from experiments, and bioinformatic analysis of expressed genes.

Both posts may include teaching to a limited extent.

The positions are financed by The Danish Research Council for Technology and Production Sciences

Qualification requirements In connection with the appointment to the post special importance will be attached to the applicant having the professional and personal qualifications stated below:

For both post docs Documented scientific qualifications such as a Ph.D. or equivalent in relation to the above subject area(s) Fluency in English. Life generally encourages employees who do not speak Danish to acquire a working knowledge of the language. Documented research qualifications and publications Fluency in both written and oral English. Faculty of Life Sciences generally encourages employees who do not speak Danish to acquire a working knowledge of the language. Broad curiosity in biological questions and open-mindedness to cross-disciplinary research. Experience with plants, herbivores and/or pathogens

Preferential requirements to post doc no. 1 Experience with ecological experiments Experience with molecular marker analysis Skills in statistical analysis of experiments Background in ecological and evolutionary theory

Preferential requirements to post doc no. 2 Experience in metabolite and expression analysis Experience in conducting plant-pathogen experiments Skills in bioinformatics Skills in statistical analysis

Terms of employment The post will be filled according to the Agreement between the Danish Ministry of Finance and the Danish Confederation of Professional Associations. The post is covered by the Protocol on Job Structure.

Questions For further information about the posts, please contact: Regarding Post doc 1: Thure Hauser, Department of Agriculture and Ecology, (+45) 3533 2818 , tpha@life.ku.dk; Regarding Post doc 2: Søren

Bak, Department of Plant Biology and Biotechnology, (+45) 3533 3346 , bak@life.ku.dk.

Application The application (please indicate whether you are applying for post doc position no.1 or post doc position no 2) must be submitted in 2 (sorted) hard copies; therefore it's not possible to receive the application by e-mail. The application must include a reply e-mail address. Each application must include the following appendices marked with the stated appendix numbers: Appendix 1: curriculum vitae with documentation of education. Appendix 2: a complete list of publications and list of submitted appendices. Appendix 3: a maximum of 10 relevant scientific works which the applicant wishes to be included in the assessment. Appendix 4: documentation of research and teaching qualifications.

The application must be accompanied by: A CD-ROM in Word XP/2003 legible format with appendices 1 and 2.

In addition to the material the applicant wishes to be included in the assessment, the Assessment Committee may include further material in their assessment of the applicant. In such circumstances, it is the responsibility of the applicant, on request, to send the material to the Committee.

Following processing of the application, any application material sent will be destroyed.

Receipt of the application will not be acknowledged, but the applicant will be kept continuously informed of the progress of the application.

The applicant will be assessed according to the Ministry of Science Technology and Innovation Executive Order no 284 of 25. April 2008.

The application, marked 621-230 should be sent to The Faculty of Life Sciences, Department of Agriculture and Ecology, The Executive Secretariat, Højbakkegård Allé 30, 2630 Taastrup, DK-1870 Frederiksberg C, Denmark, where it must be received no later than 1 April 2009, at 12.00 noon. Applications received after the closing date for applications will not be considered.

Thure P. Hauser, Ph.D., Associate Professor Department of Agriculture and Ecology Faculty of Life Sciences

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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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## UExeter FungalCellEvolution

Fungal Cell Evolution

Postdoctoral Research position

Salary circa £(E/26-F/31)

Fixed Term for 3 years

The School of Biosciences, Exeter wishes to recruit a Postdoctoral Researcher to support the work of Tom Richards on a grant funded by the Biotechnology and Biological Sciences Research Council (BBSRC) and will be available for 3 years from 1 June 2009 (or as soon as possible thereafter). The successful applicant will be required to join a laboratory focusing on molecular evolution of fungi and protozoa. The project involves using large-scale 454 genome sequence surveys of 'chytrid' fungi in order to understand ancient fungal cell evolution and the protist/fungi transition. You will be expected to contribute to projects on motor protein evolution, cell evolution, and eukaryotic phylogeny. Experience with comparative genomics is essential and experience with one or more of the following is desirable: phylogenetics, genome assembly and annotation, molecular biology, cell biology, microbial cell culture, and bioinformatics.

The post will include duties ranging from sequence analysis, comparative genomics, phylogenetics and DNA cloning. The successful applicant will be able to present information on research progress and outcomes, communicate complex information orally, in writing and electronically and prepare proposals and applications to external bodies.

Applicants will possess a relevant PhD and be able to demonstrate sufficient knowledge in the discipline and of research methods and techniques to work within established research programmes. Applicants will be able to design their own experiments and prepare data for publication.

Salary will be circa £(E/26-F/31) pa on the Associate Research Fellow scale, depending on knowledge, skills and experience.

For further information please contact Tom Richards, email [t.a.richards@ex.ac.uk](mailto:t.a.richards@ex.ac.uk) or telephone (01392) 263756. To apply, (send CV and covering letter with the contact details of three referees), to Tom Richards ([T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)).

The closing date for completed applications is (15/04/2009).

[T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)

[T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)

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## UExeter FungalCellEvolution corrected

Fungal Cell Evolution - correction in closing date and salary details confirmed

University of Exeter

School of Biosciences

Postdoctoral Research position (Ref: N1988)

Salary in the range £26,391 to £31,513 pa, according to qualifications and experience

Fixed Term for 3 years

The School of Biosciences, Exeter wishes to recruit a Postdoctoral Researcher to support the work of Tom Richards on a grant funded by the Biotechnology and Biological Sciences Research Council (BBSRC) for 3 years from 1 June 2009 (or as soon as possible thereafter). The successful applicant will be required to join a laboratory focusing on molecular evolution of fungi and protozoa. The project involves using large-scale 454 genome sequence surveys of 'chytrid' fungi in order to understand ancient fungal cell evolution and the protist/fungi transition. You will be expected to contribute to projects on motor protein evolution, cell evolution, and eukaryotic phylogeny. Experience with comparative genomics is essential and experience with one or more of the following is desirable: phylogenetics, genome assembly and annotation, molecular biology, cell biology, microbial cell culture, and bioinformatics.

The post will include duties ranging from sequence analysis, comparative genomics, phylogenetics and DNA cloning. The successful applicant will be able to present information on research progress and outcomes, communicate complex information orally, in writing and electronically and prepare proposals and applications to external bodies.

Applicants will possess a relevant PhD and be able to demonstrate sufficient knowledge in the discipline and of research methods and techniques to work within established research programmes. Applicants will be able to design their own experiments and prepare data for publication.

Salary will be £26,391 - £31,513 pa, depending on knowledge, skills and experience.

For further information please contact Tom Richards, e-mail [t.a.richards@ex.ac.uk](mailto:t.a.richards@ex.ac.uk) or telephone (01392) 263756. To apply, please send your CV and covering letter with the contact details of three referees to Tom Richards ([T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)), School of Biosciences, Geoffrey Pope Building, Stocker Road, Exeter, EX4 4QD quoting the job reference N1988.

The closing date for completed applications is 6 March 2009.

[T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)

[T.A.Richards@exeter.ac.uk](mailto:T.A.Richards@exeter.ac.uk)

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## UFlorida EvolutionVirulence

Applications are invited for an NIH funded postdoctoral research position with Marta L. Wayne in the Department of Biology (formerly Zoology) at the University of Florida.

The project will focus on testing tenets of evolution of virulence theory via experimental evolution with sigma virus, a negative-strand RNA virus endemic in natural *Drosophila melanogaster* populations. This position is primarily empirical, but there is opportunity for related theory collaboration with Drs. Ben Bolker and Bob Holt.

Candidates must have a Ph.D. in Genetics, Molecular or Evolutionary Biology or related field. The ideal candidate will be a creative self starter, and have excellent writing skills. Basic molecular skills, including experience working with RNA and QPCR, are a plus. We are a lab motivated by the question of what maintains genetic variation in natural populations. Expected start date is 15 May but there is some flexibility.

To apply, please submit application by email including (1) a CV, (2) a 1-page statement of your research interests and career goals; (3) names and contact information of three referees. Review of applications will begin immediately and will continue until the position is filled.

Marta L. Wayne, PhD Director, UF Genetics & Genomics Graduate Program Associate Professor P.O. Box 118525 Department of Biology University of Florida Gainesville, FL 32611-8525 <http://www.zoo.ufl.edu/mlwayne> email: [mlwayne@ufl.edu](mailto:mlwayne@ufl.edu)

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## UFribourg EvolutionPlantInvasions

1 PhD & 1 Post-Doc Position in Evolutionary Ecology of Plant Invasions, University of Fribourg, Switzerland

### Rationale

The proposed project will be the first one that considers the importance of polyploidy and herbivores for invasions simultaneously. Our leading hypothesis is that herbivore pressure and assemblage will, at least partially, explain the predominance of specific cytotypes both in the native and introduced range. The *Centaurea stoebe* L. (syn. *C. maculosa* Lam.) (Asteraceae) system provides an excellent model system to study these interactions, and we take advantage of the large knowledge already available on this plant and its herbivores. Native to Europe where it occurs as a diploid (2x) and a tetraploid (4x) cytotype, the species is highly invasive in North America, where nearly exclusively only 4x plants have been found. Several specialist insect herbivores have been introduced to North America for its biological control, with only partial success so far.

We seek two highly motivated researchers to help clarifying underlying mechanisms of this most successful plant invasion as a complement to various presently ongoing studies that we carry out in collaboration with both national (through NCCR Plant Survival) and international partners. We plan to (i) explore the relationship between type and amount of herbivory and the occurrence of the two cytotypes of *C. stoebe* in its native range by a European-wide survey combined with a replant/transplant experiment, (ii) carry out a series of experiments to analyze interactions between two selected specialist herbivores and the *C. stoebe* cytotypes, and (iii) investigate more generally into the role of generalist herbivores for plant invasions (in collaboration with Urs Schaffner, CABI Europe-Switzerland and our US counterparts).

### Requirements

- PhD position: Master Thesis in Biology, preferentially in ecology and evolution

- Post-Doc position: doctoral degree in plant ecology and evolution

For both positions, knowledge of, and experience in one or several of the following areas of research is desirable:

experimental (field) ecology and evolutionary biology, invasion biology, plant-herbivore interactions, experimental design and statistical analysis; furthermore, fluency in English and driver's license will be required.

#### Salary and conditions

The positions are funded by the Swiss National Science Foundation, and start April 1, 2009. Salaries: PhD c. 43'000 SFr/year for 3 years; Post-Doc dependent on age and status, gross salary in the first year about CHF 70'000, for 2-3 years.

#### Applications

Applicants should e-mail their CV and publication list, together with a short motivation letter and a summary of research experience and interests, and the names of two professional referees to [Heinz.mueller@unifr.ch](mailto:Heinz.mueller@unifr.ch). Please indicate your earliest possible, and your ideal start.

For further information, please contact:

Prof. Dr. Heinz Müller-Schärer, Département de Biologie, Unité d'Ecologie & Evolution, Université de Fribourg, Chemin du Musée 10; CH-1700 Fribourg, SWITZERLAND; tel: + (41) (0) 26-300 88 35/50 cf. my research website at <http://www.unifr.ch/biol-ecology/muellerschaerer/group/mueller/> for further information and recent publications on this subject.

Heinz Müller-Schärer <[heinz.mueller@unifr.ch](mailto:heinz.mueller@unifr.ch)>

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## UGuelph MolecularBiodiversity

Postdoctoral position in Molecular Biodiversity analysis through Next-Gen sequencing

Biodiversity Institute of Ontario, University of Guelph

A postdoctoral position is available to work in Mehrdad Hajibabaei's group at Biodiversity Institute of Ontario, on developing molecular biodiversity approaches based on custom microarrays and Next-Gen sequencing platforms. This position involves working in a dynamic team equipped with cutting edge technologies including an in house 454FLX platform (and access to other Next-Gen sequencing platforms) and excellent molecular and computational infrastructure. The position requires deep understanding as well as hands on experience in molecular evolutionary biology, molecular biodiversity and bioinformatics.

The position is available from May 01, 2009 and is ini-

tially offered for one year with the possibility of renewal. Please send a complete CV, including names and contact information of three references, and a brief description of research interests to Mehrdad Hajibabaei ([mhajibab@uoguelph.ca](mailto:mhajibab@uoguelph.ca)). Review of applications will start on March 15, 2009 and will continue until the position is filled.

Mehrdad Hajibabaei, PhD Assistant Professor Biodiversity Institute of Ontario Department of Integrative Biology University of Guelph Guelph, ON N1G 2W1 Canada

Phone: 519-824-4120 x52487 Fax: 519-824-5703 Email: [mhajibab@uoguelph.ca](mailto:mhajibab@uoguelph.ca) Web: [www.dnabarcoding.ca](http://www.dnabarcoding.ca) [www.ibarcode.org/hajibabaei](http://www.ibarcode.org/hajibabaei) [hajibabaei@gmail.com](mailto:hajibabaei@gmail.com)

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## UHawaiiHilo EvolutionaryGenetics

Bulletin Board Posting: 02/05/09 RCUH Website: 02/05/09

POSTDOCTORAL FELLOWSHIP (EVOLUTIONARY GENETICS) ID# 29054. Tropical Conservation Biology and Environmental Sciences. Regular, Full-Time, Limited Term (Up to 1 year with the possibility of extension), RCUH Non-Civil Service position with the Tropical Conservation Biology and Environmental Sciences (TCBES) Program, located in Hilo, Hawaii. Continuation of employment is dependent upon program/operational needs, satisfactory work performance, and availability of funds. MINIMUM MONTHLY SALARY: Salary commensurate with qualifications. DUTIES: Participate in Moore Foundation-supported research into Deoxyribonucleic Acid (DNA) Barcoding of endemic Hawaiian species to develop and evaluate the suitability of various molecular genetics techniques to elucidate population-level and species-level genetic variation in several groups of Native Hawaiian insects and plants. Sample insects and plants across the Hawaiian Islands. Perform large-scale DNA sequencing and genotyping. Perform population genetic, phylogenetic, and/or genomics analyses. Collect morphological data and catalog data in electronic form; maintain project website. PRIMARY QUALIFICATIONS: EDUCATION: PhD from an accredited college or university in a relevant field. EXPERIENCE: Experience with two (2) of the following: population, phylogenetic, and genomics analyses. ABIL/KNOW/SKILLS: Knowledge in molecular DNA techniques. Strong quantitative and statistical skills;

self-starter and creative problem solver; strong communication and interpersonal skills; must possess a valid drivers license and be able to drive a 4-wheel drive vehicle with manual transmission. **PHYSICAL/MEDICAL REQUIREMENTS:** Ability to hike across uneven terrain from low to high elevation and camp overnight, as needed. **SECONDARY QUALIFICATIONS:** Extensive experience in DNA sequencing and analysis, genotyping and population genetic analysis, phylogenetic analysis, genomics analysis, or mathematical modeling in population genetic and phylogenetic contexts. **INQUIRIES:** Donald Price 974-7365 (Hawaii). **APPLICATION REQUIREMENTS:** The preferred method of applying for a job is through our on-line application process. Please go to [www.rcuh.com](http://www.rcuh.com), click on Employment and navigate to Job Announcements/Apply for a Job. However, if you do not have access to the Internet, you may apply by submitting resume; cover letter including Recruitment ID#, referral source, narrative of your qualifications for position and salary history; names, phone numbers and addresses of three supervisory references and copy of degree(s)/transcripts/certificate(s) to qualify for position by fax (808) 956-5022 or mail to Director of Human Resources, Research Corporation of the University of Hawaii, 2530 Dole Street, Sakamaki Hall D-100, Honolulu, HI 96822 before the closing date. If you have questions on the application process and/or need assistance, please call (808)956-3100. **CLOSING DATE:** March 6, 2009. EEO/AA Employer.

Dr. Donald K. Price Director, Tropical Conservation Biology & Environmental Science Graduate Program University of Hawaii at Hilo 200 W. Kawili St, Hilo, HI 96720 donaldp@hawaii.edu tel: 808-974-7365 Fax: 808-974-7693

<http://www.epscor.hawaii.edu/> <http://www2.hawaii.edu/~donaldp/> <http://www2.hawaii.edu/~tcbes/> <http://www.hawaii.edu/uhhbiology/> Donald Price <donaldp@hawaii.edu>

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## ULausanne Evolutionary Conservation

Available:

Postdoc position (2 years, elongation up to 5 years in total possible)

Department of Ecology and Evolution, University of Lausanne, Switzerland.

Start: spring 2009 or later

Our group studies the selective forces that act on freshwater fish, i.e. the effects of human activities in interaction to natural and sexual selection. We are also exploring the link between cooperation theory and conservation issues. See <http://www.unil.ch/dee/-page21537.html> for further information.

We are seeking candidates with an interest in evolution, conservation genetics, sex determination, host-pathogen interaction, population management, and/or life history.

Please send your application by email (all material in one attached file please) to Claus Wedekind (claus.wedekind@unil.ch). Include your Curriculum vitae, a short description of your research interests and research experience, and names and email addresses of one or two references who could be contacted. Review of applications will begin March 20th, 2009, but applications will be accepted until the position is filled.

— Claus Wedekind Department of Ecology and Evolution, Biophore, University of Lausanne, 1015 Lausanne, Switzerland. Tel. +41 21 692 42 50, Fax +41 21 692 42 65 [http://www.unil.ch/dee/page21538\\_fr.html](http://www.unil.ch/dee/page21538_fr.html) Claus Wedekind <claus.wedekind@unil.ch>

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## UMinnesota Population Genomics

Post-doc positions at the University of Minnesota

Collaborators and I expect to have two NSF-funded post-doctoral positions to investigate population genomics and association mapping of symbiosis-traits in the model legume *Medicago truncatula*.

The research will involve evolutionary analyses of whole-genome resequencing data (~ 380 genomes) and association analyses to identify genes responsible for variation in plant-Sinorhizobium symbioses. The phenotypic data for the association analyses will come from large-scale greenhouse experiments designed to investigate genotype-genotype interactions in symbiosis.

One position will focus on population genomic analyses. For this position, knowledge and experience in evolutionary genetics, statistical genetics, handling large data sets, and program skills are highly desirable.

The other position will be primarily involved with conducting and analyzing data from large-scale greenhouse experiments designed to investigate genotype-genotype

interactions in symbiosis. Knowledge of evolutionary genetics and experience conducting and analyzing data from large experiments are highly desirable.

Both positions will involve working closely with Univ. of Minnesota collaborators Nevin Young and Mike Sadowsky.

Applicants should send a CV, a short statement of research interests, and the name of two references. Start dates are somewhat flexible. The positions will stay open until filled, but if interested please apply by April 1.

If you have questions or would like to know more about the research please contact me (ptiffin@umn.edu).

Peter Tiffin Dept. of Plant Biology University of Minnesota

ptiffin@umn.edu

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## UMontreal Bioinformatics

Post-doctoral position in bioinformatics (-omics analysis)

A post-doctoral position is available to analyse large-scale genomics, transcriptomics, proteomics, and RNA-functional data. The aim is to understand the evolution of RNA maturation machineries catalyzing RNA editing and trans-splicing.

More details on the research projects of the lab are available at <http://megasun.bch.umontreal.ca/-People/burger/research.html> Sector/Affiliation Robert-Cedergren Centre for Bioinformatics and Genomics, biochemistry department, Université de Montréal, Montréal, Canada.

Training background PhD in molecular biology, biochemistry, or bioinformatics. Training in computer science.

Expertise The candidate should have expertise in computer-based large-scale data analysis, including genome and cDNA assembly and annotation, comparative genome and proteome analysis, and software tool development under Unix/Linux. Experience in database development is desirable.

Starting date Immediately.

Application Interested candidates are encouraged to send their CV, PhD thesis, relevant publications (latter two in electronic form only), and addresses for potential

reference letters to

Gertraud Burger, PhD Robert-Cedergren Centre for Bioinformatics and Genomics Département de Biochimie Université de Montréal, Pavillon Roger Gaudry 2900 Blvd Eduard-Montpetit Montréal, Québec, H3T 1J4, CANADA Email: jobs@bch.umontreal.ca (Subject: "PDF-bioinfo")

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## UNottingham SnailChirality

We are looking for an enthusiastic postdoc, graduating PhD student, or highly competent RA to work on a three year BBSRC post to "unwind snail chirality". The most essential skill is that the person should be an excellent molecular biologist. It would also be a benefit if they have experience with RNA and/or mapping, but neither are strictly necessary.

One bonus is that technological improvements mean that the project is now easier than originally envisaged. A second bonus is that snails are officially hot!!! (Grande & Patel 2008 Nature doi:10.1038/nature07603)

Work will take place within newly refurbished laboratories in the School of Biology, and in conjunction with colleagues in the Evolutionary Biology and Developmental Genetics research groups. We are a friendly research group on a green and spacious campus, with suitable housing within walking distance. As the person will gain experience in a wide range of techniques, including extensive use of new sequencing technologies via our collaborator Mark Blaxter (in beautiful Edinburgh), the post should be excellent training for a future career in research.

[This is a readvertisement because the original candidate was forced to pull out at the last minute for personal reasons. Previous candidates may wish to informally contact me if they are considering applying again].

Thanks, Angus angus.davison@nott.ac.uk

The official blurb follows... —

School of Biology - Institute of Genetics

Research Associate/Fellow

Unwinding snail chirality

Applications are invited for the above post to work on a project funded by the BBSRC to "unwind snail chi-



ality". A deep-seated theoretical problem has stoked a burning interest in understanding the symmetry-breaking event during development - how is one side of an organism consistently distinguished from the other, given that the side that is called 'right' is essentially arbitrary? Although most prior research has concentrated on models such as the mouse, chick and frog, the coiling or chiral variation of the pond snail *Lymnaea* may be crucial in coming to understand asymmetry. This is especially so, since it has very recently been discovered that a key asymmetry gene has a conserved function in both molluscs and vertebrates, implying a common origin (Grande & Patel 2008 *Nature Advance Online* doi:10.1038/nature07603).

The objective of this project is to take advantage of the latest advances in DNA sequencing technology to characterise the maternally-inherited determinant of chirality in snails. A parallel postdoctoral researcher in Professor Mark Blaxter's laboratory at the University of Edinburgh will lead the bioinformatic analyses, and there may also be collaboration with David Lambert's laboratory in Rochester, New York. As the person appointed will gain experience in a wide range of techniques, including extensive use of new sequencing technologies, the post should be excellent training for a future career in research. Work will take place within newly refurbished laboratories in the School of Biology, and in conjunction with colleagues in the Evolutionary Biology and Developmental Genetics research groups.

Candidates should ideally, although not necessarily, possess a PhD in molecular genetics or equivalent qualification in a related discipline. Experience of working with RNA and/or genetic mapping will be an advantage, but is not essential.

Salary will be within the range £24,152 - £35,469 per annum, depending on qualifications and experience (salary can progress to £38,757 per annum, subject to performance) - (£26,391, maximum without PhD). This post, funded by the BBSRC, is available to start as soon as possible and will be offered on a fixed-term contract for a period of three years.

Informal enquiries may be addressed to Dr A Davison, tel: 0115 823 0322, Email: [Angus.Davison@Nottingham.ac.uk](mailto:Angus.Davison@Nottingham.ac.uk) or Dr A Aboobaker, Email: [Aziz.Aboobaker@Nottingham.ac.uk](mailto:Aziz.Aboobaker@Nottingham.ac.uk). Additional information on Dr Davison's research is available at: <http://www.nottingham.ac.uk/biology/contacts/davison/research.php>. For more details and/or to apply on-line please access: <http://jobs.nottingham.ac.uk/MED432>. Please quote ref. MED/432.

This is a re-advertisement and previous candidates

may wish to informally contact Dr Davison before re-applying.

Concurrent advert to be published as follows:

Jobs.ac.uk - Friday 6 February Nature Online - Thursday 5 February Closing date: 23 February 2009

- Dr. Angus Davison

Institute of Genetics School of Biology The University of Nottingham Nottingham NG7 2RD

[angus.davison@nott.ac.uk](mailto:angus.davison@nott.ac.uk) [www.molluscs.org](http://www.molluscs.org) tel 0115 823 0322 (int. 30322) fax 0115 823 0338

[Angus.Davison@nottingham.ac.uk](mailto:Angus.Davison@nottingham.ac.uk)

Angus.Davison@nottingham.ac.uk

[Angus.Davison@nottingham.ac.uk](mailto:Angus.Davison@nottingham.ac.uk)

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## UOslo 2 Biosystematics

2 POSITIONS AS POSTDOCTORAL FELLOWSHIPS in biosystematics/evolutionary biology available at National Centre for Biosystematics (NCB), Natural History Museum, University of Oslo (UiO). The National Centre for Biosystematics (NCB) (<http://www.nhm.uio.no/ncb/>) is a strategic, interdisciplinary research centre at the Natural History Museum (NHM), performing research in modern systematics and biodiversity at a high international level. The NCB integrates research groups working on plants, fungi and animals, which to a large extent utilize similar molecular genetic tools in their research. The NHM has a modern DNA laboratory with all necessary facilities and has access to a pyrosequencing instrument at the UiO. The postdocs will work in an interdisciplinary and stimulating research environment together with other postdocs, Ph.D. students, and guest researchers. The postdocs will work on the following project, funded by the Research Council of Norway: BarFrost V Reconstruction of past ecosystems by barcoding DNA preserved in permafrost. The objective of the project is to reconstruct past ecosystems from molecular analyses of permafrost soils and to assess ecological implications of the results by 1) developing new DNA markers for several groups of organisms to be used for species identification based on degraded DNA, 2) constructing taxonomic reference databases of the most common arctic species based on sequencing of these DNA markers in field and recent museum collections, 3) identify species by pyrosequencing environmental ancient DNA from dated permafrost cores, and 4) to assess to which extent these

new reconstructions can be used to address species turnover dynamics, niche stability, and backward testing of predictive species distribution models. The project includes vascular plants, bryophytes, fungi, invertebrates, and vertebrates. It is connected to a large, ongoing EC-funded project, ECOCHANGE (<http://www.ecochange-project.eu>), where one of the main activities concerns similar analyses of vascular plants. The postdocs will stay for periods in other ECOCHANGE laboratories to develop expertise in ancient DNA analysis, pyrosequencing, and bioinformatics. Applicants must hold a PhD degree (or equivalent) in biology and have a solid practical and theoretic background in molecular genetic methods. Good knowledge of at least one of the groups of organisms involved is preferable, as well as some previous training in bioinformatics. Emphasis will be given to the applicants academic competence and personal abilities to carry out the project. The postdocs will also participate in supervision of PhD and Master students. Candidates whose thesis is accepted for public defense are also able to apply. The postdocs will initially be hired for 2 years, with a possible extension for up to 1 year. The procedures for employments are in general regulated by the rules for employment in post doctor positions/scientific positions at the University of Oslo, <http://www.uio.no/-admhb/reglhb/personal/tilsettingvitenskapelig/-ansettelsesvilkar/guidelinespostdoctor.xml> Female applicants are encouraged to apply. UiO has an agreement for all employees, aiming to secure rights to research results a.o.

For further information please contact Professor Christian Brochmann, phone +47 22851611, e-mail [christian.brochmann@nhm.uio.no](mailto:christian.brochmann@nhm.uio.no) or Associate Professor Arild Johnsen, phone 22851860, e-mail [arild.johnsen@nhm.uio.no](mailto:arild.johnsen@nhm.uio.no). Pay grade: 57-64 (NOK 435 700 V 496 300 per year) (Norwegian LTR scale, depending on qualifications) Application Deadline: 9 March 2009 Ref. No.: 2009/1252 To apply please provide three copies of CV and certificates of education, three sets of scientific publications, names and addresses of two reference persons, and a covering letter outlining relevant work experience, to the following address: Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, NO-0318 Oslo, Norway An extended applicant form must be completed and submitted together with the application. This form is available at: <http://www.admin.uio.no/opa/ledigestillinger/english/sokerskjema.GBR.rtf>. or contact the personell officer at +47 22851819 Application papers will not be returned.

eva <[evabellemain@gmail.com](mailto:evabellemain@gmail.com)>

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## UOxford PlantEvolution

Postdoc: Plant evolutionary ecology

Applications are invited for a full-time postdoctoral position for three years. It is funded by the Natural Environment Research Council, with ideally a start date on 1 April 2009, or as soon as possible thereafter. The grant is held by Dr John Pannell with Dr Rob Freckleton (University of Sheffield) as co-investigator. The work will be conducted in Dr Pannell's lab in Plant Sciences, Oxford; substantial interaction with Dr Freckleton is anticipated, particularly in the later stages of the project.

The objective of the project will be to build conceptual and empirical bridges between plant population dynamics and selection on plant sex allocation. The project combines manipulative experiments on annual plants with demographic and modelling in evolutionary ecology. Applicants will be expected to have expertise and experience with statistical hypothesis testing. There will be scope within the project for the appointed postdoc to pursue a range of questions related to those of the project aims, in collaboration with Pannell and Freckleton.

Further particulars may be downloaded from <http://www.plants.ox.ac.uk> and are also available from the Administrator. Informal enquiries may be addressed to Dr John Pannell at [john.pannell@plants.ox.ac.uk](mailto:john.pannell@plants.ox.ac.uk)

Applications including curriculum vitae, name and contact details of two referees and clearly quoting post reference no AP09003 to be sent to the Administrator at the Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB or by email [recruit@plants.ox.ac.uk](mailto:recruit@plants.ox.ac.uk) The closing date for applications is noon on 5 March 2009.

John Pannell <[john.pannell@plants.ox.ac.uk](mailto:john.pannell@plants.ox.ac.uk)>

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## USapienzadiRoma AncientAnimalDNA

Hallo,

Post-Doc position for the work on ancient animal DNA (in particular Bos, Equid, Ovis and Capridae), within a three year project on “Ancient diets and reconstructions of systems of animal husbandry in the Middle and Upper Euphrates (Turkey) from the VII to the II millennia B.C.” is offered at the Tuscia University, Viterbo, Italy. Candidate must have less than 33 years of age at the 27th February 2009 and be resident in Italy. Those interested please write to francesca.balossi@uniroma1.it

Yours Sincerely,

Francesca Balossi

Francesca Balossi Restelli Preistoria e Protostoria del Vicino e Medio Oriente Università Sapienza di Roma Via Palestro 63 00185 Roma tel. +39 064454603 (int.20) francesca.balossi@uniroma1.it

francesca balossi <francesca.balossi@uniroma1.it>

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## UWarwick ExperimentalEvolution

Postdoctoral position, Experimental evolution in Chlamydomonas, University of Warwick, UK.

We have recently been awarded Leverhulme Trust funding for an exciting new project to study the experimental evolution of resistance to herbicides in the unicellular chlorophyte, *Chlamydomonas reinhardtii*. As part of this 3-year project we are looking to recruit a postdoctoral researcher.

There is increasing recognition that human activities are accelerating rates of global environmental change. There is a concern that these changes are driving increased rates of evolutionary change in the global biota. The emerging and vibrant discipline of experimental evolution offers the possibility to study such ‘evolution in action’ to address fundamental and applied questions in ecology and evolution. Our research uses *Chlamydomonas* as a model photosynthetic organism to study the dynamics of evolution of resistance to herbicides. This work addresses fundamental questions relating to the evolution of tolerance/resistance to a novel stress as well as practical issues surrounding the management of a significant constraint to global food production.

We are looking for enthusiastic and committed applicants with a strong academic record in disciplines related to ecology and evolution. Experience of techniques in microbial experimental evolution would be an advantage. The project will start in September 2009

and will be supervised by Dr Paul Neve (Warwick HRI, University of Warwick) and Dr Nick Colegrave (Institute of Evolutionary Biology, University of Edinburgh). The positions will be based at University of Warwick, though it is expected that successful applicants could spend some time in Edinburgh.

Indicative areas of research are: impacts of herbicide dose on fitness landscapes and rates of evolution, population size and mutation supply rate, fitness costs associated with evolution of herbicide resistance and the potential for reversion of resistance and/or compensatory evolution, the impacts of sex on the evolution of resistance.

For further details please contact Paul Neve: Email: p.neve@warwick.ac.uk Tel: +44 24 7657 5843.

Dr Paul Neve Warwick HRI University of Warwick Wellesbourne Warwickshire CV35 9EF

Tel: +44 2476 575843 Fax: +44 2476 574500

“Neve, Paul” <P.Neve@warwick.ac.uk>

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## UWuerzburg EvolutionOfMovement

\*PostDoc Evolution of Movement & Dispersal. Application deadline: March 20th, 2009.\*

We are looking for a theoretical ecologist/modeler to fill (as soon as possible) a full three year PostDoc position to work on evolutionary ecology of movement and dispersal. The successful candidate will join the Theoretical Ecology group at the Field Station Fabrikschleichach 60km east of Wuerzburg (Germany) and work in an EU funded project addressing questions concerning the evolution and ecological consequences of movement rules (and the dispersal deriving from them) in heterogeneous landscapes. We are striving for an approach to first, identify individual movement rules, second to integrate the consequences of such rules for population level processes and third, to understand the influence of these population level consequences for the evolution of movement rules. The project is carried out together with field ecologists and theoreticians in France and the UK. From the successful candidate we expect the ability and an interest to work on conceptual and theoretical issues in evolutionary ecology. We will certainly appreciate experience in simulation programming and/or development of numerical programs. A background in dispersal ecology or other areas of spatial ecology will be helpful. We are seeking a team oriented candidate

with high intrinsic motivation to solve theoretical problems. Some engagement in teaching and administration is expected.

Request for further information and applications (including the names of two potential referees) should be sent to Thomas Hovestadt, Field Station Fabrikschleichach, University of Wuerzburg, Germany Email: [hovestadt@biozentrum.uni-wuerzburg.de](mailto:hovestadt@biozentrum.uni-wuerzburg.de)

– PD Dr. Thomas Hovestadt Field Station Fabrikschleichach University of Wuerzburg Glashuettenstrasse 5 OT Fabrikschleichach 96181 Rauhenebrach

Email [hovestadt@biozentrum.uni-wuerzburg.de](mailto:hovestadt@biozentrum.uni-wuerzburg.de) Phone: 0049 931 3182065 (Secretary) 3183083 (direct) Fax: 3183089

Thomas Hovestadt <[hovestadt@biozentrum.uni-wuerzburg.de](mailto:hovestadt@biozentrum.uni-wuerzburg.de)>

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## WashingtonU ComplexTraitEvolutionI

POSTDOCTORAL RESEARCH ASSOCIATE

GENETICS OF COMPLEX TRAITS

MOUSE GENE MAPPING of BONE MORPHOLOGY

and BIOMECHANICS

Washington University School of Medicine

A position is available for a postdoctoral research associate to work on the genetics of complex traits in a biomedical and evolutionary context, specifically bone morphology and biomechanics in relation to obesity and leptin levels. We are especially interested in the context dependence of gene effects and the role of epistasis and genotype by environment interaction in the genetic architecture of complex traits. We are currently fine-mapping QTLs affecting bone morphology and biomechanics to a sub-cM level in an advance intercross of LG/J and SM/J mice. Morphological measurements of long bones and vertebra will be collected from microCT scans and bones tested for their strength in response to controlled forces. Mapping analysis will identify small sets of positional candidate genes that will be evaluated using bioinformatics, epistatic relationships, and sequence and expression polymorphisms. Transgenic and complementation tests will be performed for select positional candidate genes.

It is desirable that candidates have some familiarity with bone biology and statistical analysis of gene mapping data. The position is available immediately. Interested candidates should submit a letter of application and their vitae to:

James M. Cheverud

Department of Anatomy & Neurobiology

Washington University School of Medicine

660 S. Euclid Ave.

St. Louis, MO, 63110, USA

E-Mail:

HYPERLINK

“mailto:Cheverud@pcg.wustl.edu” [Cheverud@pcg.wustl.edu](mailto:Cheverud@pcg.wustl.edu)

Phone: 314-362-4188

FAX: 314-362-3446

AA/EOE M/F/D/V

Jim Cheverud <[cheverud@pcg.wustl.edu](mailto:cheverud@pcg.wustl.edu)>

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## WashingtonU ComplexTraitEvolutionII

POSTDOCTORAL RESEARCH ASSOCIATE

GENETICS OF COMPLEX TRAITS

MOUSE GENE MAPPING and QTL IDENTIFICATION

Washington University School of Medicine

A position is available for a postdoctoral research associate to work on the genetics of complex traits in a biomedical and evolutionary context, focused on obesity, diabetes, and diet-specific gene effects in mice. We are especially interested in the context dependence of gene effects and the role of epistasis and genotype by environment interaction in the genetic architecture of complex traits. We are currently fine-mapping QTLs affecting obesity, diabetes, and other metabolic syndrome traits to a sub-cM level in an advanced intercross of LG/J and SM/J mice. This mapping replicates results from earlier generations. Positional candidate genes will be evaluated using bioinformatics, patterns of epistatic interaction, and sequence and expression polymorphisms. Transgenic and complementation tests will be performed for select positional candidate genes.

It is desirable that candidates have a familiarity with the molecular methods used in gene mapping studies,

including development of genetic markers, primer design, sequence analysis, and gene expression studies using qPCR. The position is available immediately. Interested candidates should submit a letter of application and their vitae to:

James M. Cheverud Department of Anatomy & Neurobiology Washington University School of Medicine 660 S. Euclid Ave. St. Louis, MO, 63110, USA

E-Mail: [Cheverud@pcg.wustl.edu](mailto:Cheverud@pcg.wustl.edu) HYPERLINK  
 "mailto:Cheverud@pcg.wustl.edu"Cheverud@pcg.wustl.edu  
 Phone: 314-362-4188 FAX: 314-362-3446 AA/EOE  
 M/F/D/V

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**YaleU**  
**GeneRegulatoryNetworkEvolution**

Postdoctoral position available in gene regulatory network research is available in Dr. Gunter Wagner's lab at Yale University's Dept of Ecology and Evolutionary

Biology and Yale's Institute for Systems Biology. This work will investigate the evolution of regulatory networks related to evolution of pregnancy in mammals. The work will involve high-throughput assays to map transcription factor binding sites on a genomic scale, i.e. ChIP/Sequ.

We are seeking motivated and ambitious candidates with a PhD in Biology, Biochemistry, or related areas. Demonstrated experience with ChIP-Chip or ChIP-Seq assays is required. Successful applicants will have experience in molecular/cellular biology and biochemistry. Familiarity with immunoprecipitation assays, transcription/expression assays, DNA binding assays and/or RT-PCR is also desirable.

The position is fully funded and provides competitive salary and benefits.

To apply send or email cover letter, CV, names and contact information (email, address, and telephone number) of three references to:

Gunter Wagner, Ph.D. Alison Richard Professor Yale University <[wagner.postdocsearch@yale.edu](mailto:wagner.postdocsearch@yale.edu)>

"Wagner, Gunter" <[gunter.wagner@yale.edu](mailto:gunter.wagner@yale.edu)>

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**Bialowieza Poland Adaptation  
 Jun28-Jul2**

ESF workshop on evolutionary and physiological adaptation to climate induced environmental changes:

Dear all,

We would like to invite young scientists to submit abstracts for oral and poster presentations for a workshop on evolutionary and physiological adaptation to climate induced environmental changes.

The European Science Foundation finances the workshop through the networking programs ConGen and ThermAdapt. In the workshop, we will merge knowledge from population genetics and molecular and evolutionary physiology in a multidisciplinary fashion and discuss possible approaches to get a deeper understanding of mechanisms behind adaptation to thermal changes.

We have invited approximately twenty leading researchers within the field to give talks and have space for additional 30-35 short presentations and/or poster presentations. Priority will be given to young scientists (PhD or post docs) from EU countries, particularly from those countries that support one or both of the ESF programmes (see [www.esf.org/thermadapt](http://www.esf.org/thermadapt) and [www.esf.org/congen](http://www.esf.org/congen) for a list of countries).

The workshop will be held in Bialowieza (Poland) from 28 June (date of arrival) to 2 July 2009 in the EU Centre of Excellence (MRI PAS) Mammal Research Institute (Polish Academy of Science). Accommodation and food are covered by the ESF. Furthermore, after application some young researchers may get covered their travel expenses or parts thereof.

Further information about the workshop including application procedures, a list of invited speakers and information about accommodation and transportation from Warsaw to Bialowieza (and return) can be found at the homepage: <http://asg.agrsci.dk/workshop/bialowieza> < <http://asg.agrsci.dk/workshop/bialowieza> > . The deadline for applications is March 15.

If necessary, Torsten Nygaard Kristensen ([torsten.nygaard@agrsci.dk](mailto:torsten.nygaard@agrsci.dk)) can also be contacted for further information.

Aarhus University, Denmark Department of Biological Sciences/ Department of Genetics and Biotechnology Telephone: +4589423135/+4589991076

Torsten Nygaard <[Torsten.Nygaard@agrsci.dk](mailto:Torsten.Nygaard@agrsci.dk)>

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## EAWAG Switzerland Aquatic Evolution Jul5-18

This is an announcement of:

PhD Summer School 2009 at Eawag in Kastanienbaum, Switzerland: "Interactions between ecological and evolutionary processes in aquatic systems"

July 5-18, 2009

The course will confront selected PhD students with the challenge of integrating ecosystems ecology and evolutionary biology, arguably the least well-integrated pair of disciplines in ecology. Some have described this challenge as the last missing synthesis in ecology. We will take a multidisciplinary look at lake ecology, ask how nutrient fluxes shape microbial and algal activity and diversity, how these in turn exert ecological and evolutionary pressure on organisms at higher trophic levels, and lastly, how adaptive evolution at higher trophic levels exerts ecological pressures at lower levels that possibly change ecosystem dynamics. The 2009 course will be built around different aspects of ecological stoichiometry. The course will consist of theoretical and conceptual lectures and practical research modules including laboratory and fieldwork that seek to demonstrate experimental approaches. Lectures will be given by our invited lecturers James Elser, Nelson Hairston, Eric Triplett, Andrew Hendry and Eawag scientists. Concepts taught include e.g. feedback between biogeochemical conditions and microbial ecology, microbial structure and activity, food webs, adaptive evolutionary dynamics of predator-prey relations, ecosystem effects of evolution at ecological time scales.

The Summer School course will be held at Eawag Kastanienbaum, near Lucerne, in Switzerland. Eawag is the Swiss Federal Institute of Aquatic Science and Technology, and the Kastanienbaum Centre for Ecology, Evolution and Biogeochemistry (CEEB) is situated at the shores of Lake Lucerne. It offers seminar rooms, laboratories, and on-site housing for students.

For further information and application, please visit our website: [http://www.eawag.ch/programs/-phd\\_ss\\_2009/index\\_EN](http://www.eawag.ch/programs/-phd_ss_2009/index_EN) Hitoshi Araki

Eawag, Swiss Federal Institute of Aquatic Science and Technology Center for Ecology, Evolution and Biogeochemistry Department of Fish Ecology and Evolution Seestrasse 79, CH-6047 Kastanienbaum, Switzerland

hitoshi.araki@eawag.ch

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## Groningen Speciation Ar21-23

Workshop “Theory of Speciation” Groningen 21-23 April 2009 Marie Curie ITN Speciation

PhD students and postdoctoral scientists interested in speciation research are invited to attend the workshop “Theory of Speciation” organised by the Marie Curie SPECIATION Initial Training Network (see [www.speciation.group.shef.ac.uk/itn/](http://www.speciation.group.shef.ac.uk/itn/)). The aim of this workshop is to introduce young researchers to the range of modelling approaches used in speciation research and to the principal results of recent theoretical work in this area. The workshop consists of lectures given by leading scientists in speciation theory (including Nick Barton, Mark Kirkpatrick and Sander van Doorn) and practicals where the participants learn to understand and analyze the building blocks of speciation models.

The workshop will focus on three themes:

- Population genetics of speciation - Adaptive dynamics of speciation - Sexual selection and speciation

Each day will be dedicated to one of these themes. In the morning, the instructors will give two or three review lectures, while the afternoons will be devoted to practicals and paper discussions.

Detailed information about the workshop programme, registration and accommodation in Groningen will be available soon on the SPECIATION ITN website [www.speciation.group.shef.ac.uk/itn/](http://www.speciation.group.shef.ac.uk/itn/). The workshop will be held in Groningen (The Netherlands) on 21-23 April 2009. The number of attendants is restricted. The ITN has funds to cover the expenses (including travel costs) of a limited number of participants from outside the network but there are additional (self-funded) places available. Registration fee is 100 Euros. This includes dinners but participants will have to arrange their own accommodation and other meals. Students attending the workshop may get a certificate and earn 1 ECTS credit.

If you would like to attend the workshop, please send a short motivation letter and brief CV to Prof. Dr. Leo Beukeboom (e-mail [l.w.beukeboom@rug.nl](mailto:l.w.beukeboom@rug.nl)) or to Prof. Dr. Franjo Weissing ([f.j.weissing@rug.nl](mailto:f.j.weissing@rug.nl)). Application deadline is 8 March 2009.

[S.Paolucci@rug.nl](mailto:S.Paolucci@rug.nl) [S.Paolucci@rug.nl](mailto:S.Paolucci@rug.nl)

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## Guarda Switzerland Evolution Jun20-27

Course: Workshop in evolutionary biology for master students and first or second year PhD students.

It is my pleasure to announce this years Guarda workshop in Evolutionary Biology. The main aim of this 1 week course is to develop the skills to produce an independent research project in evolutionary biology. The course is for students with a keen interest in evolutionary biology.

The course takes place in the June 2009 (20.-27.June) in the Swiss mountain village Guarda. Faculty includes Richard Lenski, Peter and Rosemary Grant, Sebastian Bonhoeffer, Walter Salzburger and Dieter Ebert (organizer).

The course is intended for master (Diploma) students and early PhD students. For the course 3 ECTS credit points are awarded.

The web page with all the details can be found under:

<http://www.evolution.unibas.ch/teaching/guarda/-index.htm> Please communicate this information to interested students.

dieter ebert

<[dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch)>

<http://www.evolution.unibas.ch/> Universität Basel, Zoologisches Institut, Vesalgasse 1 4051 Basel, Switzerland Tel. +41-(0)61-267 03 60

[dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch) [dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch)

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## Honolulu StatGenetics Jul13-17

The University of Alabama at Birmingham’s Section on Statistical Genetics is pleased to announce the 2nd Annual NSF-funded Short Course on Statistical Genetics & Statistical Genomics in Honolulu HI on Mon 7/13/2009 - Fri 7/17/2009. Focusing on the analysis of complex traits characterized by quantitative variation, this five-day course will offer an interactive program to enhance researchers’ ability to understand & use statistical genetic methods, as well as implement & interpret

sophisticated genetic analyses.

Topics: Microarray, Image, GWAS, Pathway & Haplotype Analysis; TDT/PDT/FBAT; Structural Association Mapping; Multiple QTL Analysis & R/qtlbim; Bayesian model selection; Measuring fitness & detecting selection; Copy Number Variations; Proteomics; Integrative Biology

Speakers: David Allison, Ph.D.; Hemant Tiwari, Ph.D.; L. Kelly Vaughan, Ph.D. Atul Butte, M.D., Ph.D.; Warren J Ewens, Ph.D.; Soledad Fernandez, Ph.D.; Rebecca Jenny Jornsten, Ph.D.; Carl Langefeld, Ph.D.; Kimberly F. Sellers, Ph.D.; Guilherme J. M. Rosa, Ph.D.; Bruce Walsh, Ph.D.; Brian Yandell, Ph.D.

For more details & registration please see <http://www.soph.uab.edu/ssg/nsfstatgen/nsfsecondannual>. Funded by the National Science Foundation.

With thanks,

Richard F. Sarver Program Manager II UAB SOPH Department of Biostatistics Section on Statistical Genetics 1665 Univ Blvd, RPHB 414 Birmingham AL 35294-0022 205.975.9169 T 205.975.2541 F rsarver@uab.edu <http://www.ssg.uab.edu>

Richard Sarver <RSarver@ms.soph.uab.edu>

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## LakeTahoe InvasiveSpecies Mar19-22

Special Workshop: Synthesizing Ecology and Evolution for the Study of Invasive Species

Organizers: Carol Lee, Kristina Schierenbeck, Robert Holt

We have organized a workshop to promote the integration of ecological and evolutionary perspectives and approaches toward the study of invasive species. Our aim is to create a venue in which discussion among participants would lead to novel synthetic research and papers that reflect the novel syntheses. For example, the integration of population genetics and population dynamics could yield insights into the lag period of invasions, evolutionary responses to novel environments, and range expansions, oscillations, and extinctions. Also, integrating empirical data on ecological factors, such as predation or competition, with genetic factors, such as quantitative genetic variance or the genomic architecture of critical traits, could enhance our understanding on factors that limit invasions and improve the ef-

ficacy of predictive models, including those that might aid in biological control. Invasive species provide an ideal testing ground for many basic evolutionary theories, and we hope that this workshop will help expand this potential.

This event will be held March 19-22, 2009 at North Lake Tahoe, California, USA. The workshop will consist of talks by invited speakers (listed below), group discussions, and posters sessions. Conference attendance will be limited to 100.

The workshop will take place during prime ski season at the scenic Granlibakken Conference Center & Lodge, which is nestled between trees, mountains, and Squaw and Alpine Ski Resorts. The Reno-Tahoe International Airport provides ready access to Lake Tahoe.

The all-inclusive meeting package of \$799.00 (single-occupancy) or \$608.00 (double occupancy) includes conference registration fees, three nights lodging (Thursday, Friday, and Saturday), dinner on Thursday, three meals on Friday and Saturday, and breakfast and lunch on Sunday. Day passes to the conference (conference attendance + lunch) are available at \$120 per day or \$252 for the entire conference.

We recommend that you plan on arriving a few days early or a stay a few days later if you plan to take advantage of the local skiing, showshoeing, ice-skating, and hiking opportunities. On site amenities include ski lessons and on-site cross country ski trails.

The registration deadline is February 15. You may register at <http://www.granlibakken.com>. Click on "Make a Reservation" button to the left, select "Conference Participant." The user name and password are: usda09. Workshop participants are eligible for a discount lodging fee of \$145 per night for a Standard Room for days before or after the conference (call to make sure you receive this discount).

Poster titles may be submitted to Kristina Schierenbeck ([ka.schierenbeck@ars.usda.gov](mailto:ka.schierenbeck@ars.usda.gov)).

List of Invited Speakers and Titles:

Richard Gomulkiewicz, Robert Holt & Scott Nuismer Genetic complexity, adaptation, and invasion in harsh environments

Alex Perkins Effects of evolutionarily labile interspecific interactions on spatial spread dynamics

Judith Miller The fate of neutral mutations arising during invasions

Andrew Kanarek & Colleen Webb Allee effects and invasion success through coupled evolutionary and ecological dynamics



Carol Eunmi Lee, Yuseob Kim & Davorka Gulisija Testing for genetic signatures of selection during independent invasions into novel environments

Marc Kramer Application of climate models to understand and model environmental processes

Neil Tsutsui, Andy Suarez & David Holway Insights into invasion success from comparing the biology of ant invaders in their native and introduced ranges

Kevin Rice The role of trans-generational plasticity (i.e. maternal effects) in biological invasions

George Gilchrist & Raymond Huey Developmental plasticity evolves during biological invasions

Heinz Müller-Schärer Adaptive evolutionary change in an invasive plant: Tracking its evidence

Elizabeth Leger & Erin Espeland Evolution of native plants in response to invaders

George Roderick & Maria Navajas Evidence for evolutionary change in classical biological control and what this says about invasions

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

<https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html> Carol Eunmi Lee <carollee@wisc.edu>

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## LakeTahoe InvasiveSpecies Mar19-22 ExtendedRegistration

Extended Registration Deadline: March 1, 2009

Special Workshop: Synthesizing Ecology and Evolution for the Study of Invasive Species

Organizers: Carol Lee, Kristina Schierenbeck, Robert Holt Conference Website: <https://mywebspace.wisc.edu/carollee/web/Lee/Invasion-BiologyWorkshop.html>

We have organized this workshop to promote integration of ecological and evolutionary perspectives and approaches toward the study of invasive species. Our aim is to create a venue in which discussion among participants would lead to novel synthetic research and papers that reflect the novel syntheses. For example, the integration of population genetics and population dynamics could yield insights into the lag period of invasions, evolutionary responses to novel environments, and range

expansions, oscillations, and extinctions. Also, integrating empirical data on ecological factors, such as predation or competition, with genetic factors, such as quantitative genetic variance or the genomic architecture of critical traits, could enhance our understanding on factors that limit invasions and improve the efficacy of predictive models, including those that might aid in biological control. Invasive species provide an ideal testing ground for many basic evolutionary theories, and we hope that this workshop will help expand this potential.

This event will be held March 19-22, 2009 at Granlibakken Lodge, North Lake Tahoe, California, USA. The workshop will consist of talks by invited speakers (listed below), group discussions, and posters sessions. Papers resulting from the workshop will be submitted to the journal *Evolutionary Applications* for a special issue.

The registration deadline is March 1. You may register at <http://www.granlibakken.com>. Click on "Make a Reservation" button to the left, select "Conference Participant." The user name and password are: usda09. The all-inclusive meeting package of \$799.00 (single-occupancy) or \$608.00 (double occupancy) includes conference registration fees, lodging, and meals. Day passes (conference attendance + lunch) are available at \$120 per day or \$252 for the entire conference. Workshop participants are eligible for a discount lodging fee of \$120 per night for a Standard Room for days before or after the conference (call Granlibakken to make sure you receive this discount). Workshop participants will also receive special discounts at Homewood Mountain Ski Resort. Poster titles may be submitted to Kristina Schierenbeck (ka.schierenbeck@ars.usda.gov).

Invited Speakers and Titles:

Richard Gomulkiewicz, Robert Holt & Scott Nuismer Genetic complexity, adaptation, and invasion in harsh environments

Alex Perkins Effects of evolutionarily labile interspecific interactions on spatial spread dynamics

Judith Miller The fate of neutral mutations arising during invasions

Andrew Kanarek & Colleen Webb Allee effects and invasion success through coupled evolutionary and ecological dynamics

Carol Eunmi Lee, Yuseob Kim & Davorka Gulisija Testing for genetic signatures of selection during independent invasions into novel environments

Marc Kramer Application of climate models to under-

stand and model environmental processes

Neil Tsutsui, Andy Suarez & David Holway Insights into invasion success from comparing the biology of ant invaders in their native and introduced ranges

Kevin Rice, Cynthia Brown, Andrew Dyer, Erin Espeland, John McKay & Harald Meimberg The role of trans-generational plasticity (i.e. maternal effects) in biological invasions

George Gilchrist & Raymond Huey Developmental plasticity evolves during biological invasions

Heinz Müller-Schärer Adaptive evolutionary change in an invasive plant: Tracking its evidence

Elizabeth Leger & Erin Espeland Evolution of native plants in response to invaders

George Roderick & Maria Navajas Evidence for evolutionary change in classical biological control and what this says about invasions

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

<https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html> carollee@wisc.edu

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## Montreal HumanPopGenetics May19-22

Montreal - May 19-22 2009

[www.MontrealSpringSchool.ca](http://www.MontrealSpringSchool.ca)

Description:

The main objective of the School is to provide training in rapidly developing disciplines that are becoming increasingly important in health sciences. It includes genetic epidemiology and human evolutionary genetics, population genomics and bioinformatics. The training will be based on real-data examples from the research of the instructors' laboratories. In one module we will also present genealogical resources specific to Quebec and introduce informatics methods for their use in population analysis and epidemiology. The School consists of four days of lectures and computer labs, starting with basic concepts and methods of analysis in biostatistics and population genetics before turning to genetic epidemiological applications.

Application Procedures:

If you wish to participate in the workshop, please visit our website for instructions and to download the application form. All applications should be submitted no later than Friday, February 27, 2009.

Because of a limited number of places, participants will be selected based on their academic/scientific background, research record, and their specific research interests and needs.

Registration fees: 250\$

Faculty:

Alexandre Alcais, Paris, France Philip Awadalla, Montreal, Canada

Luis B. Barreiro, Chicago, IL Louis Houde, Trois-Rivières, Canada

Lluis Quintana-Murci, Paris, France Marie-Hélène Roy-Gagnon, Montreal, Canada

Hélène Vézina, Chicoutimi, Canada Rob Sladek, Montreal, Canada (Invited speaker)

Scientific Committee:

Jamie Engert, Montreal, Canada France Gagnon, Toronto, Canada

Maja Krajinovic, Montreal, Canada Julian Little, Ottawa, Canada

Erwin Schurr, Montreal, Canada Terry-Lynn Young, St. John's, Canada

Organized by:

Damian Labuda, Philip Awadalla and Marie-Hélène Roy-Gagnon for the Réseau de Médecine Génétique Appliquée (RMGA) of the Fonds de la recherche en santé du Québec (FRSQ), CHU Sainte-Justine Research Centre, and Departments of Pediatrics, Biochemistry, Social and Preventive Medicine, and Robert Cedergren Centre for Bioinformatics and Genomics of the Université de Montréal.

To apply or for more information please contact:

Ms. Dominika Kozubska E-mail: [info@montrealspringschool.ca](mailto:info@montrealspringschool.ca) Phone: 514-345-4691

Or visit our website: [www.montrealspringschool.ca](http://www.montrealspringschool.ca)

Damian Labuda, Ph.D., D.Sc. Professor, Pediatrics Department, Montreal University Sainte-Justine Hospital Research Center, room B-607 b 3175 Cote Sainte-Catherine Montreal, PQ Canada H3T 1C5

tel: (514) 345-4931 ext.3586 [sec. 3282] fax: (514) 345-4731 [damian.labuda@umontreal.ca](mailto:damian.labuda@umontreal.ca) Damian Labuda <[damian.labuda@umontreal.ca](mailto:damian.labuda@umontreal.ca)>

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## NatIU Ireland MolEvolution summer

Undergraduate research experience at the Summer School of Molecular Evolutionary Research (the SoMER school) in Ireland.

The Department of Biology of the National University of Ireland, Mynooth is announcing its second summer School of Molecular Evolutionary Research (the SoMER school). Our aim is to provide research training and expertise to enthusiastic undergraduate students with a special interest in molecular evolution, and more generally evolutionary biology.

Every student will be integrated into an active research group at the Department of Biology of the NUI Maynooth, and will be assigned an individual research project. A key focus of the school is that every student should experience every one of the steps involved in evolutionary research. The students will thus participate in field work where they will sample biological specimens, they will extract and sequence DNA from the samples they collected, and they will use bioinformatics/computational techniques to analyse the data they generated.

Other activities will include one day workshops carried out by members of the Department of Biology and invited external speakers (see our website for details).

The SoMER school will run for ten weeks, starting the 8th of June 2009, and will accept 10 students. It is open to undergraduate students from every country and nationality. The only requirement is that you must have a strong interest in evolutionary biology, and an interest in pursuing a career in this research area. For every student, funding will be available in the form of a - 300 per week salary. Travel expenses will also be covered, up to - 300 for EU students, and up to - 800 for non-EU students. On-campus, discounted self-catering accommodation will be provided for the SoMER students.

The SoMER school will be based in the Department of Biology of the NUI Maynooth, which is very conveniently located in the Irish countryside, only 34 Km (21 Miles) from Dublin City International Airport, and 28 Km (17 Miles) from Dublin city centre. Maynooth is very well connected to Dublin through regular train and bus services.

Maynooth is a picturesque village, which has hosted

universities and colleges since 1795, and currently hosts two independent universities: The National University of Ireland, Maynooth, and a branch of the Pontifical University (St. Patrick's College). Maynooth's culturally rich history is reflected in the architectural beauty of the old campus, and if you are a non-Irish student it is fair to say that Maynooth is probably the ideal place to carry out a research experience, while experiencing life in Ireland.

Visit our website <http://bioinf.nuim.ie/ureka/> if you are interested and would like to apply.

Alternatively send us an e-mail: [ureka2009@gmail.com](mailto:ureka2009@gmail.com)

The deadline to apply to the SoMER school is the 6th of March.

\*\*\*\*\* Dr. Davide Pisani Bioinformatics & Molecular Evolution Unit The National University of Ireland, Maynooth Maynooth, Co. Kildare, Ireland [Davide.Pisani@nuim.ie](mailto:Davide.Pisani@nuim.ie)

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## RennesFrance EvolutionaryBiol Jun8-12

“Evolutionary biology 2009: phylogenetics, speciation, co-evolution, development, genomes, life histories, plasticity... What is new?” In the context of the bicentenary of Darwin's birth and the 150th anniversary of the publication 'On the origin of Species', we organize an advanced course in Evolutionary Biology, including 4 days of conferences, open to PhDs and researchers, followed by one practical day in phylogenetics analysis, open to PhDs only for French and other European PhD students in Evolutionary Biology. The course will give an overview of the research methods in evolutionary biology and will provide state of the art reviews on timely questions in evolutionary biology, by internationally leading scientists in the field. Posters could be proposed by the participants, to be discussed with the invited speakers in evening sessions. A price of the best poster will be organized. This event will take place on the main campus of the University of Rennes 1, Rennes, France, on June 8-12, 2009.

Detailed information and membership form will be very soon available on the following sites: [www.darwin2009.fr](http://www.darwin2009.fr) [www.vas.univ-rennes1.fr](http://www.vas.univ-rennes1.fr) Thank you in advance, on behalf of the organizing committee, Marie-Agnès Coutellec

Marie-Agnès Coutellec UMR INRA-Agrocampus Ouest  
985 ESE Equipe Ecotoxicologie et Qualité des Milieux  
Aquatiques 65 rue de Saint-Brieuc - CS 84215 35042  
Rennes cedex - FRANCE

tél.: +33(0)2 23 48 52 48 fax: +33(0)2 23 48 54 40

Marie-Agnes Coutellec <marie-agnes.coutellec@rennes.inra.fr>

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## Roscoff France Marine Evolutionary Genomics

Summer Course - Marine Genomics Europe Marine  
Evolutionary & Ecological Genomics May 25th à June  
5th, 2009 Station Biologique de Roscoff, France

Aims to give an introduction on genetic and genomic  
approaches to analyze biological diversity, evolution  
and adaptation at the species and population level in  
the ocean

Confirmed teachers

Sandie Baldauf, Univ of York, UK

Erik Bonivard, Univ. Paris 6, FR

Galice Hoarau, Univ of Groningen, NL

Wiebe Kooistra, SZN, IT

FrÃ©dÃ©ric Partensky, SB-Roscoff, FR?

Klaus Valentin, AWI-Bremerhaven, DE

FrÃ©dÃ©rique Viard, SB-Roscoff, FR

ClÃ©mentine Vitte, Univ. Paris 6, FR

Filip Volckaert, KULeuven, BE

Organizing committee

HÃ©lÃ©ne Huelvan, SB-Roscoff, FR

Jeanine Olsen, Univ of Groningen, NL

Anne Saisi, SB-Roscoff, FR

Arnaud Tanguy, SB-Roscoff, FR

FrÃ©dÃ©rique Viard, SB-Roscoff, FR

Filip Volckaert, KULeuven, BE

Target group

PhD students (at least in their second year) and post  
docs with a solid knowledge in phylo- and/or popula-

tion genetics. This course is open to MGE members as  
well as non-members.

Topics

The course will consist of lectures, tutorials and com-  
puter based exercises in the following subjects.

\* Phylogeny - sequence analyses, phylogenetic tech-  
niques (clustering, Bayesian statistics), molecular clock,  
case studies \* Population genetics à allele and genotype  
analyses, population genetic structure and gene flow,  
assignment tests, effective size and population dynam-  
ics, case studies \* Phylogeography - molecular evolu-  
tion through networks, phylogeographical techniques,  
coalescence, population dynamics, case studies \* Envi-  
ronmental, functional and comparative genomics - 1.  
Genome structure and architecture. 2. Markers in  
the genomics realm. 3. Methods for detecting struc-  
ture. 4. Introduction to functional genomics. 5. Meth-  
ods for detecting adaptive variation (including selective  
sweeps) within and among populations; linking hydro-  
graphical/environmental and demographic data to pop-  
ulation structure and local adaptation. 6 Quantitative  
genetics: evolution of traits. 7. EST libraries: why and  
how. 8. Introduction to comparative genomics (whole  
genome comparisons, concatenated phylogeny, genome  
organization, annotating genomic information, trans-  
posable elements in marine species) 9. Case studies  
\* Phylogenomics - 1. What is comparative genomics?  
2. Genomics and genetics of speciation/ what makes a  
species from a genome point of view? 3. Comparative  
marine genomics. 4. Case studies

Costs; course, accommodation and meals

\* The course fee is paid by the MGE Network for all  
academics (pre and post doc). Welcome reception, ex-  
cursion (incl lunch) and farewell dinner are included.

\* All participants pay their own travel, accommoda-  
tion and board (self catering is possible) \* Participants  
are offered to be accommodated at the SBR guesthouse  
which is situated directly at the institute. The cost for  
this is 13 per night in double room incl. breakfast. The  
guesthouse can also offer lunch and supper for a cost of  
5.50 per person and meal.

Application and contact

To apply please fill in the application form and send  
to Anne Saisi (saisi@sb-roscoff.fr) together with a 2-  
paged CV before April 10, 2009. This information +  
application form can also be found on the MGE web-  
site: [www.marine-genomics-europe.org](http://www.marine-genomics-europe.org) under Training  
& Education.

16 participants will be selected by the following criteria:

1. Relevance of the course for their PhD or post-doc

project

2. Background and experience of applicant

3. We will aim at mixing people from different research areas and therefore probably no more than one person per institute will be considered. We will also aim at an equal distribution of women and men.

The selected persons will receive a notification at the end of April that has to be confirmed within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Contact

Anne Saisi

European Project Manager

Station Biologique de Roscoff

BP 74, 29680 ROSCOFF CEDEX

France

Email: saisi@sb-roscoff.fr

Phone: (33)2 98 29 23 45

Fax: (33)2 98 29 23 80

Disclaimer: [http://www.kuleuven.be/-cwis/email\\_disclaimer.htm](http://www.kuleuven.be/-cwis/email_disclaimer.htm) Filip Volckaert  
<Filip.Volckaert@bio.kuleuven.be>

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## UAdelaide BioinformaticsMolEvol Apr14-17

Phylogenetics Workshop: Methods in Bioinformatics and Molecular Evolution, 14-17 April, 2009 Venue: The University of Adelaide, South Australia

The Australian Centre for Ancient DNA is running a phylogenetics workshop that will feature hands-on training from 4 international experts, in leading software packages for the analysis of genetic data. This workshop is targeted to early career researchers (2nd or 3rd year Postgraduate Candidates or Postdocs in the early stages of their career), and will be mostly practical and take place in a computer lab setting.

Presenters are: Dr Alexei Drummond, University of Auckland (bioinformatics and coalescent methods and covering the program BEAST); Professor Peter Lockhart, Massey University (molecular evolution, phylogenetics); Professor Mark Pagel, University of Reading (comparative phylogenetics and the mode and tempo of

gene evolution); and Christian Anderson, (Serial SimCoal and the newly released Bayesian Serial SimCoal, which is useful for both contemporary and ancient samples).

To register, please visit the official website >>>  
< <http://www.adelaide.edu.au/acad/biomaths/> >  
<http://www.adelaide.edu.au/acad/biomaths/>. Registration closes 2 March, 2009 Early registration is encouraged as there are only 20 places available.

Cheers, Maria

Maria Lekis Network Administrator ARC Environmental Futures Research Network School of Earth & Environmental Sciences The University of Adelaide Darling Building, Rm 209a North Terrace Campus, Adelaide SA 5005 AUSTRALIA Ph: +61 08 8303 3952 Fax: +61 08 8303 4364 Visit us at: < <http://www.adelaide.edu.au/efn> > <http://www.adelaide.edu.au/efn> or < <http://www.adelaide.edu.au/acad/> > <http://www.adelaide.edu.au/acad/> Maria Lekis  
<maria.lekis@adelaide.edu.au>

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## UCaliforniaDavis TreeGenomics Jun15-19

The Conifer Translational Genomics Network is offering a shortcourse entitled "Genomics in Tree Breeding and Forest Ecosystems" to be held on the UC Davis campus, June 15-19, 2009.

Additional details including an outline of the course content are available at the main workshop page: <http://www.pinegenome.org/ctgn/workshop.html> .

Interested persons are requested to submit application documents online by March 15, 2009.

Successful applicants will be notified by April 1, 2009 with additional instructions for completing the registration process.

Jill L. Wegrzyn Bioinformaticist Department of Plant Sciences University of California at Davis One Shields Avenue, MS 6 Davis, California 95616

<http://dendrome.ucdavis.edu> E-mail: jlwegrzyn@ucdavis.edu phone: 530-752-1663 fax: 530-754-9366

jillylee@gmail.com

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## UVirginia FieldBiology

SUMMER 2009 Field Biology Courses and REU Internships; Mountain Lake Biological Station; MLBS.org Mountain Lake Biological Station (University of Virginia) announces its summer field biology program: 1) Courses - Field-based undergraduate and graduate-level biology credit courses and workshops offered by nationally recruited faculty. 2) NSF REU-Sites Program - Undergraduate independent research internship program now in its 17th year. Work at MLBS focuses on field-based evolution, physiology, and behavior. Courses web page:

<http://mlbs.org/courses.html> REU web page: <http://mlbs.org/REU.html> Fliers to Distribute or Post:

[http://mlbs.org/download/MLBS\\_Poster.pdf](http://mlbs.org/download/MLBS_Poster.pdf) [http://mlbs.org/download/MLBS\\_Courses.pdf](http://mlbs.org/download/MLBS_Courses.pdf) [http://mlbs.org/download/MLBS\\_REU\\_Poster.pdf](http://mlbs.org/download/MLBS_REU_Poster.pdf) \*\*\*\*

Learn all about Mountain Lake opportunities at MLBS.org \*\*\*\* Thank you very much, Butch Brodie, Director Eric Nagy, Associate Director

Eric S. Nagy, Ph.D. Associate Director Mountain Lake Biological Station, Department of Biology University of Virginia / P.O. Box 400327 Charlottesville, VA 22904-4327 USA street address: 485 McCormick Road / 219 Gilmer Hall tel: +1-434-243-4989 (+1-540-626-5227 summer) fax: +1-434-982-5626 (+1-540-626-5229 summer) cel: +1-434-906-3122 eml: enagy@virginia.edu skype: flightofthesandor web:

virginia.edu/biology/faculty/nagy.htm MLBS web page: mlbs.org

enagy@virginia.edu

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## UWashington InstStatGenetics Jun15-Jul1

Summer Institute in Statistical Genetics registration now open.

Applications are now being accepted for registration and scholarships at <http://sisg.biostat.washington.edu> for the 14th annual Summer Institute in Statistical Ge-

netics, June 15-July 1, 2009. (Also for the European version in Liege, August 31-September 9, 2009).

SISG09 is a series of 20 short courses in modern statistical methods for genetic data. Topics include: Probability & Statistical Inference, Molecular Genetics, Computing for Statistical Genetics, Interpreting DNA Evidence, Regression & Analysis of Variance, Genetic Data Analysis, MCMC for Genetics, Molecular Phylogenetics, Quantitative Genetics, Population Genetics, Relationships & Relatedness, Comparative Genomics, QTL Mapping, Functional Genomics & Proteomics, Association mapping, Coalescent Theory, Genetic Epidemiology, Genetic Imprinting.

Parallel institutes will cover Public Health Genomics and Infectious Disease Modeling.

Institute participants are invited to attend a Symposium in Honor of Elizabeth Thompson on June 27.

Bruce S. Weir Professor and Chair, Department of Biostatistics University of Washington Seattle, WA 98195-7232 Phone (206) 221-7947. Fax (206) 543-3286.

Bruce Weir <bsweir@u.washington.edu>

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## UWashington StatGenetics Mar31-Jun13

In Spring quarter 2009 (March 31-June 13) University of Washington Online Learning is again offering the Stat550 (DL) course Statistical Genetics I; Discrete Mendelian traits see: <http://www.outreach.washington.edu/ol/courses/mat/stat550.asp> with instructor Elizabeth Thompson (eathomp@u.washington.edu) (<http://www.stat.washington.edu/thompson/>)

Interested participants should contact UW distance learning <http://www.outreach.washington.edu/ol/> for registration and administrative details, but are very welcome to contact Elizabeth Thompson (eathomp@u.washington.edu) for more information about course content or requirements.

Some information about the 2008 offering of this DL class is available at [http://www.stat.washington.edu/thompson/Stat550/Online\\_2008/](http://www.stat.washington.edu/thompson/Stat550/Online_2008/) The 2009 class is expected to follow a very similar schedule.

Thanks,

Bruce bsweir@u.washington.edu

Bruce Weir <bsweir@u.washington.edu>

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## Venice EvoDevo Sep14-17

Summer School on Evolutionary Developmental Biology Venice, September 14th-17th 2009

Organizers Alessandro Minelli, Michael Akam, Gerd B. Müller and Giuseppe Fusco

A summer school on Evolutionary Developmental Biology will be held at the Istituto Veneto di Scienze, Lettere ed Arti (Venice, Italy) from September 14th to September 17th 2009.

The school will be articulated into eight theoretical/practical units introducing the students to a diversity of resources and working tools in evo-devo, and to likely pitfalls in their use.

The School is sponsored by the Istituto Veneto di Scienze, Lettere ed Arti, the Konrad Lorenz Institute for Evolution and Cognition Research, Vienna, and the University Museum of Zoology, Cambridge.

The teaching panel includes M. Akam (Cambridge), M. Babu (Cambridge), G. Fusco (Padova), J. Jaeger (Barcelona), R. Jenner (London), J. Jernvall (Helsinki), A. Minelli, (Padova), G.B. Müller (Vienna), S.A. Newman (New York), I. Salazar-Ciudad (Barcelona), E. Schierenberg (Köln).

The school is hosted in Palazzo Franchetti, a splendid, recently restored building, located in the very centre of Venice and facing the Grand Canal.

Participants will be asked to pay a fee of 300 Euros, to contribute to their living expenses in Venice.

Deadline for applications: May 30th 2009.

For details, visit < <http://www.istitutoveneto.it/-EDB/> ><http://www.istitutoveneto.it/EDB/>

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## WoodsHole MolEvol Jul26-Aug7

Workshop on Molecular Evolution, Woods Hole

<http://workshop.molecularevolution.org/mbl/> 26 July - 7 August 2009, extended topics session 7 August - 14 August 2009

Application Deadline 2 March 2009

Michael P. Cummings, Director

The Workshop on Molecular Evolution has been the finest course in the subject since it was started in 1988. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. A distinguishing feature of the Workshop is a well-equipped computer laboratory with Apple Macintosh computers and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as AWTY, BEAST, Clustal W and Clustal X, FASTA, FigTree, GARLI, LAMARC, MAFFT, MrBayes, PAML, PAUP\*, and PHYLIP provide demonstrations and consultations. This two-week program is designed for established investigators, post-doctoral fellows, and advanced graduate students with prior experience in molecular evolution and comparative genomics. Lectures and computer laboratories total ~90 hours of scheduled instruction. An optional all-computer laboratory of 54+ hours of independent work with guidance and consultation of some faculty and teaching assistants is offered during the third week. Admission is limited and highly competitive, with admissions decisions determined by an international committee. Many participants find the extended topics session to be especially useful.

Topics to be covered include:

- Databases and sequence matching: database searching: protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches
- Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis; hypothesis testing
- Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters
- Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conser-

vation - Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution - Comparative genomics: genome content; genome structure; genome evolution - Molecular evolution integrated at lower levels: biochemistry; cell biology; physiology; relationship of genotype to phenotype

2009 Fees: \$2500 (room and board at no additional

charge), plus an additional \$900 for the extended topics session.

More information is available at <http://-workshop.molecularevolution.org/mbl/> Direct link to application information is - <http://gosnold.mbl.edu/-StudentApp/StudentApp.asp?CourseID=3DMOLE>  
mike@umiacs.umd.edu mike@umiacs.umd.edu

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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email [evoldir@evol.biology.McMaster.CA](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 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.