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# E v o l D i r

February 1, 2010

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

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## Foreword

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

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

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



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### Barcelona EvolutionaryEngineering Jul18-23

2010 IEEE Congress on Evolutionary Computation  
(CEC) Special Session on Evolutionary Robotics

Barcelona, Spain. July 18-23, 2010

**\*CALL FOR PAPERS\***

**\*Organisers:\***

Patricia A. Vargas (Heriot-Watt University - Edinburgh) Steffen Wischmann (EPFL - Lausanne) Dario Floreano (EPFL - Lausanne) Phil Husbands (University of Sussex - Brighton)

Website: <http://lis.epfl.ch/specialsessions/CEC10/>

**\*Scope:\***

Evolutionary Robotics (ER) aims to apply evolutionary computation techniques, inspired by darwinian selection, to automatically design the control and/or hardware of both real and simulated autonomous robots. Having an intrinsic interdisciplinary character, ER is being employed towards the development of many fields of research, among which we can highlight neuroscience,

cognitive science, evolutionary biology and robotics. Hence the objective of this special session is to assemble a set of high-quality original contributions that reflect and advance the state-of-the-art in the area of Evolutionary Robotics, with an emphasis on the cross-fertilization between ER and the aforementioned research areas, ranging from theoretical analysis to real-life applications.

Topics of interest include (but are not restricted to):

- Evolution of robots which display minimal cognitive behaviour, learning, memory, spatial cognition, adaptation or homeostasis.
- Evolution of neural controllers for robots, aimed at giving an insight to neuroscientists or advancing control structures.
- Evolution of communication, cooperation and competition, using robots as a research platform.
- Co-evolution and the evolution of collective behaviour.
- Evolution of morphology in close interaction with the environment, giving rise to self-reconfigurable, self-designing, self-healing and self-reproducing robots.
- Evolution of robot systems aimed at real-world applications as in aerial robotics, space exploration, industry, search and rescue, robot companions, entertainment and games.
- Evolution of controllers on board real robots or the real-time evolution of robot hardware.
- Novel or improved algorithms for the evolution or robot systems.
- The use of evolution

for the artistic exploration of robot design.

\*Important Dates:\*

Paper Submission: January 31, 2010 Notification of Acceptance: March 15, 2010 Camera-Ready Submission: May 2, 2010

\*Paper Submission:\*

Submissions should follow the guidance given on the IEEE CEC 2010 conference website: <http://www.wcci2010.org>. When submitting, please select as the main research topic the Special Session on “Evolutionary Robotics” (S089). All submissions will be peer-reviewed with the same criteria used for other contributed papers. All accepted papers will be included and published in the conference proceedings.

\*Post Conference Publication:\*

Depending on the quality of the submissions, authors will be asked to contribute to a journal special issue on the topic of “Evolutionary Robotics”.

steffen.wischmann@unil.ch steffen.wischmann@unil.ch

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### Braga Portugal DNABarcoding Jun2-4

Dear Colleagues

You are cordially invited to participate in the 2nd Conference of the European Consortium for the Barcode of Life (ECBOL2): 2010 International Year of Biodiversity, to be held from 2 to 4 of June 2010 at the University of Minho, Braga, Portugal.

Please visit the ECBOL2 website <http://ecbol2.bio.uminho.pt/> < <http://ecbol2.bio.uminho.pt/> > for more information, and send a message with your name, institution and subject “pre-registration ECBOL2” to [ecbol2@bio.uminho.pt](mailto:ecbol2@bio.uminho.pt) <<mailto:ecbol2@bio.uminho.pt>> to be included in the mailing list and receive email updates of ECBOL2.

We sincerely hope that you will join us in making ECBOL2 a success. We look forward to welcome you in Braga.

Sincerely,

Filipe Costa

Chair ECBOL2 Centre of Molecular and Environmental Biology (CBMA) Department of Biology, University of Minho Braga, Portugal

Monica Landi, Ph.D. CBMA (Centre of Molecular and Environmental Biology) Department of Biology, University of Minho Campus de Gualtar 4710-057 Braga Phone:+351-253 604310 Fax:+351-253 678980 Email: [mlandi@bio.uminho.pt](mailto:mlandi@bio.uminho.pt)

Mónica Landi <[mlandi@bio.uminho.pt](mailto:mlandi@bio.uminho.pt)>

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### Cardiff ParasiteEvolution Mar30-Apr1

‘Parasites in Time and Space’ is the theme of this year’s British Society for Parasitology (BSP) Spring Meeting to be held at Cardiff University, 30 March ; 1st April 2010. In addition, to the two parallel sessions on Ecology and Evolution of Host-Parasite Interactions, there will be a further two parallel sessions on Malaria and Trypanosomes/Leishmania. Invited speakers include Roy Anderson, Mike Begon, Mike Boots, Francis Jiggins, Hamish McCallum, Arne Skorping and Richard Tinsley.

Registration is now open and early registration closes on January 29. Abstracts (for oral or poster presentations) should be submitted by Jan 16. PhD students can apply to the society for travel grants to attend the conference.

To register and submit your abstract online please visit: <http://www.bsp.uk.net/events.php?id=6> For further information contact, Jo Cable School of Biosciences Cardiff University CF10 3AX, UK [CableJ@cardiff.ac.uk](mailto:CableJ@cardiff.ac.uk)  
Joanne Cable <[CableJ@cardiff.ac.uk](mailto:CableJ@cardiff.ac.uk)>

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### Copenhagen SocialInsectEvolution Aug8-14

XVI International Congress of the IUSSI

The organizing committee takes great pleasure in inviting you to participate in the XVI International Congress of the International Union for the Study of Social Insects (IUSSI), to be held in Copenhagen, Denmark from 8 to 14 August 2010.

Over the years social insect research has made very significant contributions to the biological sciences in gen-

eral and to evolutionary biology in particular, because insect societies allow researchers to address questions of general significance. In many ways, social insects have become “model systems” and the distinction between them and other biological models has become blurred. Advanced social behaviours have been discovered in other groups of organisms and the known genomes of other, non-social insects have turned out to be crucial for understanding the many parallel developments towards the evolution of social life. In practice the Union’s profile has therefore been broadened to the study of social Interactions and their evolution. Social insects are prime model systems but no longer exclusive ones.

Registration and submission of abstracts is open!

- Early discount registration closes 1 March 2010 -  
Deadline for receipt of abstracts is 1 May 2010

Plenary speakers

\* Gene Robinson University of Illinois at Urbana-Champaign, USA \* Andrew Bourke University of East Anglia, UK \* Iain Couzin Princeton University, USA \* Kevin Foster Harvard University, USA \* Deborah Gordon Stanford University, USA \* Christina Grozinger Pennsylvania State University, USA \* Hanna Kokko University of Helsinki, Finland \* Kenji Matsuura Okayama University, Japan

Full details about the Congress can be found here: <http://www.iussi.org/iussi2010/> We are looking forward to welcoming you to wonderful Copenhagen!

Patrizia d’Ettorre, Congress Secretary

On behalf of the IUSSE2010 organizing committee  
IUSSE2010@bio.ku.dk

Patrizia D Ettorre <pdettorre@bio.ku.dk>

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### Edmonton ButterflyEvoDevo Jun29-Jul2

A Symposium on the Evo-Devo of Butterfly Patterning will take place during the 6th International Conference on the Biology of Butterflies, being held in Edmonton, CA from June 29 to July 2. I would like to invite those wishing to present at this symposium to visit the conference web site at <http://www.biology.ualberta.ca/-biobutterfly2010/> and submit an abstract to be considered for a oral presentation. Poster presentations are also welcome.

Looking forward to an exciting meeting!

Antonia Monteiro (symposium organizer)

Antónia Monteiro <antonia.monteiro@yale.edu>

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### GeorgiaTech SoutheasternEEC Mar26-28

Dear Friends and Colleagues,

I am writing to you on behalf of the Behavior, Evolution and Ecology Research Society at Georgia Tech. In conjunction with the School of Biology we are hosting the 7th annual Southeastern Ecology and Evolution Conference the weekend of March 26 - 28, 2010 on the Georgia Tech campus. We have a website which will provide all necessary information and links to registration, hotel accommodations, conference schedule and more at <http://www.seec.biology.gatech.edu> SEEC was started at Georgia Tech by alumnus Alan Wilson as a mirror to similar regional conferences in the northeast (NEEC) and midwest (MEEC). The meeting is aimed primarily at graduate students but also welcomes technicians, post-docs, and undergraduate researchers as well. The goal of this conference is to provide a relaxed atmosphere in which young scientists can present their research, share ideas and develop collaborations for the future.

We would like to cordially invite you to join us in Atlanta this spring, and please feel free to pass this invitation along and/or post it on your list servs. Please find our announcement flyer attached to this email.

Thank you and we hope to see you all in March!

Nicholas Parnell President Behavior, Evolution and Ecology Research Society School of Biology Georgia Tech

– Nicholas Parnell Ph.D. candidate Dept. of Biology Ecology, Evolution and Behavior Program Georgia Institute of Technology Atlanta, GA

Nicholas Parnell <nparnell@gatech.edu>

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### Hilo Hawaii ConservationGenomics Jul26-28

The American Genetics Association (publisher of the Journal of Heredity) will hold its annual meeting in Hilo, Hawaii from 26-28 July, 2010. AGA meetings focus on a single topic and last for 2.5 days. This year's topic is Conservation Genomics, and will include talks by a series of genomicists and conservation biologists, including those who are already shaping this emerging discipline. Our goal is to provide a focused forum for discussion, brainstorming, and development of collaborative efforts that leverage emerging genomic resources for applications in conservation biology. To learn more, visit the AGA website:

<http://www.theaga.org/meetings.php> We'll have additional announcements as we fill in our speaker list. We aim to make the meeting fun, inexpensive, and accessible for all who would like to participate. Please put this on your calendar, and stay tuned for registration details.

Any questions, contact

Brad Shaffer ([hbshaffer@ucdavis.edu](mailto:hbshaffer@ucdavis.edu)), President of the AGA, or

Anjanette Baker ([agajoh@oregonstate.edu](mailto:agajoh@oregonstate.edu)), Managing Editor, Journal of Heredity

H. Bradley Shaffer Department of Evolution and Ecology University of California One Shields Ave. Davis, CA 95616

phone 530-752-2939 fax 530-752-1449 Website <http://www2.eve.ucdavis.edu/shafferlab> Note: I will be on sabbatical at Harvard through March 2010. While there, my phone number is 617-384-8437

[hbshaffer@ucdavis.edu](mailto:hbshaffer@ucdavis.edu) [hbshaffer@ucdavis.edu](mailto:hbshaffer@ucdavis.edu)

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## IowaStateU MEEC2010 Mar26-28 2

Hello Evolutionary Biologists,

I am pleased to announce that The Midwest Ecology and Evolution Conference (MEEC) will be held Friday, March 26 to Sunday, March 28 2010, on the campus of Iowa State University, in Ames, Iowa. MEEC is a conference organized by and geared toward undergraduate and graduate students to present research and make connections. The heart of this event is composed of oral and poster presentations contributed by participating undergraduate and graduate students. The conference will also include an opening mixer, a banquet Saturday evening, and keynote addresses from three leading re-

searchers in ecology and evolution, including Dr. Jeff Feder from the University of Notre Dame, Dr. Alan K. Knapp from Colorado State University, and Dr. Ellen Damschen from Washington University.

For more information, please visit MEEC 2010 online at <http://www.midwesteec.org/> Facebook : <http://www.facebook.com/group.php?gid=205770509839> Abstract Submission

<http://www.midwesteec.org/guide.html> \*The deadline for Abstract Submission is February 15, 2010\*

In keeping with MEEC tradition, posters and oral presentations are limited to students X undergraduate and graduate. Faculty and post-docs are encouraged to attend in support of the students. Students interested in submitting poster/paper abstracts or in putting together a special session should visit <http://www.midwesteec.org/guide.html> . Hope to see you in March,

Tim

– Tim Mitchell Office: 353 Bessey Hall Mail: Dept. of Ecology, Evolution, and Organismal Biology 253 Bessey Hall Ames, IA 50011

Timothy Mitchell <[timmitch@iastate.edu](mailto:timmitch@iastate.edu)>

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## KansasCity ArthropodGenomics Jun10-13 RegistrationOpen

Arthropod Genomics: New Approaches and Outcomes 4th ANNUAL ARTHROPOD GENOMICS SYMPOSIUM June 10 - 13, 2010, in Kansas City, USA [www.k-state.edu/agc/symp2010](http://www.k-state.edu/agc/symp2010) Download brochure: <http://www.k-state.edu/agc/symp2010/Brochure-2010.pdf> REGISTRATION IS NOW OPEN to attend the 4th Annual Arthropod Genomics Symposium, "Arthropod Genomics: New Approaches and Outcomes," June 10 to 13, 2010, in Kansas City. Early registration deadline: Friday, March 26, 2010.

KEYNOTE SPEAKER Nora J. Besansky University of Notre Dame Population genomics of adaptation and speciation in malaria's vector

FEATURED SPEAKERS Michael Akam University of Cambridge, United Kingdom The genome of the Geophilomorph centipede, *Strigamia maritima*

Scott J. Emrich University of Notre Dame Opportunities and challenges of non-model transcriptome se-

quencing: From corn to wild butterflies and moths

Matthew Hudson University of Illinois at Urbana-Champaign Exploring the evolution of social behavior using genome sequencing and analysis

Anthony A. James University of California Message in a battle, using whole genome expression analyses to fight vector-borne diseases

Michael R. Kanost Kansas State University Functional genomics of cuticle sclerotization in *Tribolium castaneum*

Fabrice Legeai INRA, Rennes, France Prediction and analyses of non coding RNA sequences in the pea aphid genome

Barry R. Pittendrigh University of Illinois at Urbana-Champaign The Body Louse genome project

Patrick D. Schloss University of Michigan Bugs within bugs: Understanding the influence of the microbiome on arthropod health

Christian Schlötterer Vetmeduni Vienna, Austria Next generation sequencing in population genetics: From experimental evolution to gene expression

Zhijian Jake Tu Virginia Tech *Anopheles stephensi* genome assembly and transcriptome analysis

John (Jack) H. Werren University of Rochester Functional and evolutionary insights from the genomes of three parasitoid *Nasonia* species

Evgeny M. Zdobnov University of Geneva, Switzerland Genomics in the light of evolution

**FUNDING AGENCY PRESENTATIONS** Representatives from national funding agencies will make short presentations about funding philosophies and opportunities within their programs. Following each presentation, the floor will be open for questions and discussion. Speakers include: Alan Christensen, NSF Adriana Costero, NIAID, NIH Mary F. Purcell-Miramontes, USDA, NIFA

**PRE-SYMPOSIUM WORKSHOP:** Thursday afternoon, June 10, 4:00-6:00 pm Navigating NCBI's resources for insect genomics. Terence Murphy, NCBI/NIH, will provide training on utilizing NCBI's resources for insect genomics. Topics will include accessing data in the RefSeq and Entrez Gene databases, BLink, BLAST, NCBI's Map Viewer, and other resources. Issues regarding the submission of data to NCBI and options for linking outside resources to NCBI's databases will also be discussed. There is no cost to attend this optional workshop, but registration is requested.

**ORGANISM MEETINGS** - Friday afternoon/evening, June 11, 5:15-? p.m. Meet with scientists who are also working with your organism of interest during small group gatherings. Group leaders will be identified to coordinate topics and lead discussions. Additional information will be posted to the conference website as details are finalized.

**POSTER SESSIONS:** There will be two poster sessions. Six platform presentations will be chosen from submitted poster abstracts. Abstract Submission Deadline: Wednesday, May 19, 2010.

**SYMPOSIUM PROGRAM:** The symposium sessions will begin Thursday evening, June 10, and continue on Friday and Saturday, with additional events 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 Saturday morning. Activities will conclude by noon on Sunday, June 13.

**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 Friday, March 26, 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 Kansas City Marriott on the beautiful Country Club Plaza. Participants are invited to dine Saturday night at an optional banquet at the BRIO Tuscan Grille.

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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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**Leuven Belgium DaphniaGenomics  
Mar26-30**



When: 26th through 30th of March, 2010 Where: Leuven, Belgium

Deadline for registration and abstract submission is 15th of January! <http://bio.kuleuven.be/DGCmeeting2010.html> !!!!!note the updated list of our keynote speakers!!!!

Visit our website for the latest updates on the conference.

Dear colleagues and friends,

We are pleased to invite you to the DGC Meeting 2010.

The Daphnia Genomics Consortium (DGC) is an international network of scientists with a common goal to foster the freshwater crustacean Daphnia as a premier model system for genomics in ecology, evolution and the environmental sciences.

This meeting aims to bring together the members of the consortium at large, to facilitate the exchange of information on recent developments and results obtained from the ongoing investigations into the genome biology of Daphnia. Additionally, we welcome researchers working with Daphnia who are not yet DGC participants and researchers working with other model or non-model organisms in the field of ecological genomics.

The DGC meeting will have a significant impact on the future development of the research groups involved in the consortium. By this time, we will have finalized our initial investigations of the draft *D. pulex* genome sequence, and we will begin the work of exploring data obtained from the *D. magna* genome sequencing project. This upcoming meeting continues the tradition of also promoting collaborations between researchers working within related disciplines, including limnology, ecotoxicology, quantitative and population genetics, systematics, molecular biology and evolution, developmental biology, genomics and bioinformatics.

The meeting will have plenary lectures from keynote speakers in several research fields related to Daphnia and other model organisms.

Our keynote speakers are: John Colbourne (Indiana University ) Donald Gilbert (Indiana University) Joseph Shaw (Indiana University) Dieter Ebert (Universität Basel) Amanda Callaghan (University of Reading) Michael Pfrender (University of Notre Dame) Christian Laforsch (Ludwig-Maximilians Universität München) Jean-Christophe Simon (Inra France) Denis Tagu (Inra France) Abraham Tucker (Indiana University) Kelley Thomas ( University of New Hampshire) John Manak (The University of Iowa) Ralph Pirow (University of Münster)

The symposia of our meeting will touch on several re-

search topics:

\* Ecology and Evolutionary Genomics \* Toxicology and Environmental Genomics of Natural and Human Stressors \* Genotype by Environment Interactions \* Comparative Genomics and Development \* Gene Expression and Gene Function

Plan to also learn about the latest open source bioinformatic and high-throughput research tools, including databases, expression and genotyping microarrays, mapping panels for trait locus mapping, molecular genetic protocols and services.

The venue is at the five century-old Katholieke Universiteit Leuven, in Belgium. Leuven is a beautiful medieval town that combines a rich historical patrimonium with a cheerful, flourishing city culture and a creative atmosphere for lively exchanges and debates.

We look forward to welcoming you in Leuven.

The local organization committee (Luc De Meester, Luisa Orsini, Ellen Decaestecker, Kevin Pauwels, Mieke Jansen, Joost Vanoverbeke) and the co-organizers Dries Knapen, Ronny Blust and Wim De Coen (University of Antwerp), Karel De Schamphelaere and Colin Janssen (University of Gent), Michael Pfrender (University of Notre Dame) and John Colbourne (Indiana University).

on behalf of the committee Luisa Orsini

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Dr Luisa Orsini Laboratory of Aquatic Ecology and Evolutionary Biology, Katholieke Universiteit Leuven, Ch. Deberiotstraat 32, 3000 Leuven, Belgium

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<luisa.orsini@bio.kuleuven.be>

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## Marseilles 14th Evolutionary Biol Sep21-24

Dear all,

We are please to inform you that the deadline of the 14th Evolutionary Biology Meeting at Marseilles 21-24 September will be on 30th January.

The following subjects will be discussed:

- Evolutionary biology concepts and modelisations for biological annotation; - Biodiversity and Systematics; -

Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogeny; - Environment and biological evolution; - Origin of Life and exobiology; - Non-adaptative versus adaptative evolution; - The « minor » phyla: their usefulness in evolutionary biology knowledge.

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

Happy new year!

Axelle Pontarotti

Egee@univ-provence.fr

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### Marseilles EvolutionaryBiology Sep21-24

We are pleased to inform you that the 14th Evolutionary Biology Meeting will take place in Marseilles, France, September 21-24, 2010.

This is a general announcement but we contact you personally in order to have you taking part to the meeting because you wrote an article: “Does Gene Translocation Accelerate the Evolution of Laterally Transferred Genes?” and the Association for the Study of Biology Evolution has found very interesting and we would like you to share your knowledge in an international meeting.

Unfortunately, we are not in a financial position to invite you, but we did our best to charge the participants as little as possible. The purpose is not to make money but that research in Evolutionary Biology makes progress by sharing thoughts and works.

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

It would be great if you could participate this year to the Evolutionary Biology Meeting in order to present your work and results.

Please, do not hesitate to visit our website to find more information <http://sites.univ-provence.fr/>

evol-cgr (Programmes of former years, abstracts, information on location and registration are included)

We look forward to hearing from you.

Yours sincerely,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

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### Montpellier DispersalEvolution Jun13-18

Dear all,

The deadline for the submission of oral contributions to the symposium on dispersal evolution is coming soon (January 15, 2010).

The FSD2010 meeting will take place from the 13th to the 18th of June 2010 at the Congress Center, Corum in Montpellier, France (<http://www.fsd2010.org>). This is the 5th International Symposium / Workshop on seed dispersal after those held in Mexico (1985-1990), Brazil (2000) and Australia (2005). It is therefore a major scientific event regarding the role and the importance of seed dispersal by animals or other modes of abiotic dissemination on biodiversity and ecosystem functioning. The aim of this scientific event is to facilitate interactions and discussions between ecologists around the world interested in seed dispersal at large.

We propose a symposium entitled “Evolution of dispersal”. Dispersal is a ubiquitous trait in living organisms. In plants, adaptations to dispersal are highly diversified, from passive dispersal of seeds to active seed dispersal involving highly complex chemical or visual signals designed to attract dispersing agents. Despite the great diversity of adaptations, only a few selection pressures favor the evolution of dispersal. The cost of dispersal structures or the increased mortality risk that organisms face during the dispersal phase select against dispersal. In contrast, competition between relatives or temporal variability of the environment generally favors dispersal. Since the recent development of tools in population biology (molecular markers, methods for analyzing demographic data, etc), it is now possible to better characterize the features of dispersal and to infer the drivers of its evolution. Variations in selective pressures arising from global changes, such as habitat fragmentation or the spread of a new species in a new geographic area provide exciting opportunities for studying



the evolution of dispersal in a context where ecological and evolutionary drivers are more easily identified. Our symposium aims at presenting the state of the art in this topic in order to discuss emergent research themes based on both theoretical and experimental studies.

Further information is available at <http://www.fsd2010.org> and by contacting the organizers:

Pierre-Olivier Cheptou (CNRS-CEFE) : pierre-olivier.cheptou@cefe.cnrs.fr  
Hélène Fréville (MNHN, CNRS-CEFE): helene.freville@cefe.cnrs.fr  
Isabelle Olivieri (ISEM) : Isabelle.Olivieri@univ-montp2.fr

The organizers, Pierre-Olivier Cheptou, Hélène Fréville, Isabelle Olivieri

Helene FREVILLE <Helene.FREVILLE@cefe.cnrs.fr>

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## Moscow Molecular Phylogenetics May18-21

Dear colleagues,

Moscow State University and the Institute for Information Transmission Problems of the Russian Academy of Sciences announce the 2nd Moscow International Conference 'MOLECULAR PHYLOGENETICS MolPhy-2', which will take place at the Faculty of Biology of Moscow State University during 18 - 21 May 2010.

The conference mission is to provide a stimulating platform for the exchange of ideas and experiences, cross-disciplinary interactions, and long-term national and international collaborations. Discussions will concern the modern state of phylogenetics and systematics, the interfaces between molecular and phenosystematics, molecular phylogenetics of different organisms and development of natural classification systems, evolutionary genomics, applications of phylogenetics, development of state-of-the-art methods, algorithms and their implementations for analyses of genetic blueprints.

The conference will be attended by leading researchers in the field from around Russian Federation and abroad, with renowned scientists giving plenary lectures on hot subjects. Young specialists are especially encouraged to participate. Selected contributions will be accepted for extended publications in the conference proceedings.

The conference is organized and supported by the Faculty of Biology and Research & Training Center - Evolutionary Genomics and Bioinformatics- (Moscow State University), Belozersky Institute for Physico-

chemical Biology (Moscow State University), Institute for Information Transmission Problems (Russian Academy of Sciences), Central Botanical Garden (Russian Academy of Sciences), Russian Academy of Natural Sciences, Moscow Society of Naturalists, Russian Foundation for Basic Research, HealthGene Corp., and Applied Biosystems (Life Technologies).

Important conference deadlines are:

22 February 2010: deadline for abstract submissions requested for an extended publication in the conference proceedings. Registration deadline for their authors.

15 March 2010: registration deadline (if you are a EU resident you can register until March 31).

31 March 2010: final submission deadline for abstracts and extended papers.

Further information is available on the conference website at [www.en.molphy.ru](http://www.en.molphy.ru). You are welcome to reach the organizers by telephone +7-(495)-939-1440, fax +7-(495)-939-3181 or email [committee@molphy.ru](mailto:committee@molphy.ru) with any inquiries.

[rusin@iitp.ru](mailto:rusin@iitp.ru)

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## Okinawa Evolutionary Genomics May24-Jun4

Workshop/Summer School. <http://www.irp.oist.jp/qecg2010/> May 24-June 4, 2010; Okinawa, Japan.

Application Deadline: February 15, 2010. OIST (<http://www.oist.jp>) covers accommodation and travel expenses for all participants.

Confirmed Lecturers:

\* Nadav Ahituv, UCSF: Functional characterization of evolutionarily- conserved non-coding sequences. \* Peter Arndt, MPI Berlin: Dynamical models describing nucleotide evolution. \* Gill Bejerano, Stanford \* Emmanouil Dermitzakis, Geneva \* Takashi Gojobori, National Institute of Genetics, Japan: Genomic evolution of the neural system. \* Ueli Grossniklaus, Zurich \* Jotun Hein, Oxford \* Nancy Moran, Arizona \* Erik van Nimwegen, Basel \* Howard Ochman, Arizona \* Anirvan Sengupta, Rutgers: Long-range interactions: enhancers and insulators. \* Gasper Tkacik, U. Penn: From statistical mechanics to information theory: tools for understanding biophysical systems. \* Byrappa Venkatesh, IMCB Singapore \* Ting Wu, Harvard Medical School:

Ultra-conservation from the standpoint of genome integrity: from copy-counting to meiotic gene silencing.

OIST Summer School and Workshop: Quantitative Evolutionary and Comparative Genomics 2010

The theme of the 2010 Summer School is the phenomenon of strong (or extreme) sequence conservation, which will be explored from a quantitative and multidisciplinary perspective, and connections forged with parts of biology outside of genomics.

We are looking for a set of participants with a broad range of backgrounds, experimentalist and theorist: for example, biology, chemistry, computer science, ecology, engineering, evolution, genomics, mathematics, medicine, or physics. The essential prerequisite is an enthusiasm to overcome traditional boundaries of your own field of specialization.

Sequence conservation forms the basis of comparative genomics, has already played a pivotal role in biology and medicine, and is likely to become increasingly important in the eras of abundant sequence data and the personalized genome. Ultra-conservation has led to a broad appreciation of the need for a reevaluation of how the action of selection is inferred from sequence comparison. It has raised basic questions about the character of “neutral drift,” calling for new quantitative developments that may be facilitated by the cultures of mathematics, physics, computer science, and engineering; however, this pursuit - and the interpretation of genome sequence in general - ought to be firmly grounded in its biological context.

With a multitude of whole-genome sequences now publicly available, ultra-conservation is trivial to exhibit, but so far difficult to explain. Therefore it represents an ideal topic for a combined Summer School and Workshop, where the phenomenon can be appreciated by participants of diverse backgrounds, who can then bring their own perspectives to bear on the problem.

Broad Topic Categories:

\* Ultra-conservation: Theory & Experiment. \* Ultra-conserved Elements (UCEs) within Populations. \* Comparative, Evolutionary and Population Genomics. \* Recombination and Genome Rearrangement. \* Neutral and Adaptive Evolution: Proteins, RNA, Regulatory Sequences, Genomes. \* Experimental Evolution.

The format of the summer school consists of a three-hour presentation in the morning, with coffee breaks, followed by an hour or two of discussion in the afternoon. The summer school is aimed primarily at introducing approximately forty students and post-docs with quantitative backgrounds - not necessarily in biol-

ogy - to the splitting edge of contemporary comparative and evolutionary genomics research. As such, tutorials will be offered to get participants with less-developed quantitative skills or sparse biological background up to speed insofar as possible; however, we hope that presentations will be intense and self-contained.

Okinawa is a subtropical divers' paradise of diverse ecology and distinctive beauty and cultural flavor.

OIST provides summer school students with accommodation at Seaside House and financial support for their travel. Students will be selected competitively based upon their completed Applications, submitted by February 15, 2010 to [qecg2010#oist.jp](mailto:qecg2010#oist.jp) (replacing the “#” by “@” of course).

[jm@oist.jp](mailto:jm@oist.jp) [jm@oist.jp](mailto:jm@oist.jp)

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## Perth Behaviour Evolution

ISBE 2010 in Perth (Western Australia): Call for abstracts

The organising Committee for the 13th International Behavioural Ecology Congress 2010 invites you to be part of ISBE 2010 by submitting abstracts and taking advantage of the opportunity to present at the Congress. Abstracts can be submitted via the online submission process which is available on the ISBE 2010 website: <http://www.isbepertth2010.com/-abstracts.html> . The deadline for receipt of abstracts is Monday 1 March 2010.

Abstracts must be no longer than 200 words and text only. Graphics, pictures or graphs should not be submitted. Once you have submitted your abstract online, you will receive an email confirming your submission. Authors of accepted abstracts are required to register to attend the Congress as a delegate.

Key Dates:

Call for Abstracts Closes: Monday 1 March 2010

Anticipated Notification of Acceptance: End April 2010

For more information about the conference please visit <http://www.isbepertth2010.com/> We are very much looking forward to welcoming you in Perth!

The ISBE organizing committee

Boris Baer CIBER: The Collaborative Initiative for Bee Research MCS Building M 310 The University of Western Australia Crawley WA 6009 Aus-

tralia phone: +61 8 6488 4495 fax: +61 8 6488 4401 E-mail: [bcbaer@cyllene.uwa.edu.au](mailto:bcbaer@cyllene.uwa.edu.au) Website: [www.ciber.science.uwa.edu.au](http://www.ciber.science.uwa.edu.au) Boris Baer <[bcbaer@bi.ku.dk](mailto:bcbaer@bi.ku.dk)>

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## Portland Evolution Jun25-29

The Department of Biology <<http://www.bio.pdx.edu/>> at Portland State University will be hosting "Evolution 2010," the joint annual meeting of the Society for the Study of Evolution <<http://www.evolutionsociety.org/>> (SSE), the Society of Systematic Biologists <<http://systbiol.org/>> (SSB), and the American Society of Naturalists <<http://www.amnat.org/>> (ASN), on June 25-29, 2010, at the Oregon Convention Center <<http://www.oregoncc.org/>>.

Below are some updates for the conference. Check the web site for more news and updates! <http://www.evolutionsociety.org/SSE2010/> >>> Registration and presentation title submission will open January 29, 2010

>>> The iEvoBio (Informatics for Phylogenetics, Evolution and Biodiversity) conference will be held jointly with Evolution 2010 (June 29 - 30). More information soon.

>>> On-site childcare will be available for Evolution 2010!

>>> Day-trippers: Day camps will be conducted by Science Educators from the Oregon Museum of Science and Industry (OMSI <<http://www.omsi.edu/>>) for older children (8 years +). Day trips will include: Mount St. Helens, the Columbia River Gorge, the Oregon Coast, and the Evergreen Air and Space Museum. More details soon!

### The Evolution Meetings

This meeting is the premier annual opportunity for sharing scientific research related to evolution. Symposia presentations, concurrent contributed papers, and poster sessions will be presented by the 1,400 expected participants. Product and service providers will contribute to the meeting through their exhibits. Related activities will include opening and poster receptions, a picnic, and a banquet.

### Schedule in Brief

The meeting schedule will follow that of recent years.

For your travel planning purposes, here is a brief summary:

\* \*June 25 (day):\* K-12 workshop, society council member meetings. Arrival on June 24 is indicated if you are a society officer or attending a workshop. \* \*June 25 (evening):\* Opening reception; Gould Award lecture (open to the general public). \* \*June 26-29 (day):\* Symposia and concurrent paper sessions, presidential addresses, etc. \* \*June 26 (evening):\* Society presidential address; Picnic at the Oregon Zoo <<http://www.oregonzoo.org/>> (free for all attendees). \* \*June 27 (evening):\* Society presidential address; Poster session and mixer. \* \*June 28 (evening):\* Society presidential address; Poster session and mixer. \* \*June 29 (day):\* Society council members exit meetings; iEvoBio Conference. \* \*June 29 (evening):\* Banquet (student and faculty tickets available for purchase). \* \*June 30 (day):\* Post-conference field trips; iEvoBio Conference.

### Portland, Oregon

Portland, self-described as the "Rose City," offers mild weather and breathtaking sights of the nearby snow-covered mountains during the month of June. It is a city where there are "more trees than cars," and an extensive system of natural parks and waterways. It is a pedestrian <<http://www.portlandonline.com/Transportation/index.cfm?c=39402>> and bicycle <<http://bikeportland.org/>> friendly town, and there is an extensive public transportation system that includes bus lines, MAX light rail <<http://trimet.org/index.shtml>>, a downtown transit mall <<http://trimet.org/portlandmall/index.htm>>, and the Portland Streetcar <<http://trimet.org/streetcar/index.htm>>. The MAX light rail <<http://trimet.org/max/>> has regular service to the Portland Airport <[http://www.portofportland.com/PDX\\_Home.aspx?ep=-94b712b2577f461baddde1d9e6e127df](http://www.portofportland.com/PDX_Home.aspx?ep=-94b712b2577f461baddde1d9e6e127df)>, and MAX or streetcar rides downtown are free within the Fareless Square <<http://trimet.org/fares/fareless.htm>> (including the Oregon Convention Center <<http://www.oregoncc.org/>> and Portland State University <<http://www.pdx.edu/>>). Ample opportunities exist within Portland and the region for recreation and sightseeing, including the Columbia River

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## Portland Evolution Jun25-29 UndergradDiversity

Undergraduate Diversity at the Evolution meetings 2010

We are pleased to announce a NSF-funded program for bringing talented and diverse undergraduates to the Evolution meetings this June 25-29 in Portland, Oregon. For the eighth year in a row we will fly a cohort of 25 undergraduates from throughout the US and Puerto Rico to present a poster at the meetings, receive mentoring from graduate students, postdocs and faculty, and participate in the Diversity Social as well as a career-oriented 'Undergraduate Futures in Evolutionary Biology' panel and discussion. The program covers the costs of travel, registration, food and accommodation at the meetings. The application deadline is 1 March, but admissions will be reviewed as they are received, and so the earlier you apply, the better. Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students. In past years we have received fewer applications than we can fund, so we encourage you to send in an application! An overview of the program and student eligibility can be found at:

<http://www.oeb.harvard.edu/faculty/edwards/-community/application.html> The online application process is being handled by NESCent and can be found at:

[http://www.nescent.org/eog/-signup\\_evolution2010diversity.php](http://www.nescent.org/eog/-signup_evolution2010diversity.php) Applications consist of a short statement of interest, a letter of recommendation and the title and abstract of the poster to be presented.

In addition, we will be soliciting names of graduate students, postdocs and faculty members who would like to serve as mentors during the meetings. Mentors take pairs of students and attend talks with them, introduce them to colleagues, network and generally make the meetings a welcoming place for them. Although costs are not covered for mentors it is an unusually rewarding experience. Contact Richard Kliman <rmkliman@cedarcrest.edu> if you are interested in serving as a mentor.

For inquires contact one of the organizers:

Scott Edwards <sedwards@oeb.harvard.edu> Richard Kliman <rmkliman@cedarcrest.edu> Jory Weintraub <jory@nescent.org>

sedwards@fas.harvard.edu

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## RoyalSociety London BiologicalDiversity Apr19-20

Dear Members

The following free two-day conference to be held at the Royal Society in April may be of interest to you.

Biological diversity in a changing world Monday 19 and Tuesday 20 April 2010

Organised by Professor Anne Magurran and Dr Maria Dornelas

We live in a world in which biological diversity is under threat as never before. Drawing insights from organisms ranging from microbes to mammals this meeting will show why a deeper understanding of temporal turnover in ecological communities is essential in coping with the changes that the natural world will experience over the next 50 years.

<http://www.royalsociety.org/biological-diversity> Registration This discussion meeting is intended for researchers in relevant fields and is free to attend, but pre-registration online at [royalsociety.org/biological-diversity](http://royalsociety.org/biological-diversity) is essential.

Venue The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG

Claire.rawlinson@royalsociety.org

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## StirlingU EvolutionaryGenetics Apr6-8

Dear all,

A reminder that registration for the 54th Ecological Genetics Group meeting is now open. The deadline for submitting abstracts and registration for speakers is MONDAY 8th FEBRUARY. Register now to avoid disappointment!

Details for registration and abstract submission can be found on the EGG 2010 website:

<http://www.sbes.stir.ac.uk/egg/registration.html>

There are still a few twin rooms available, allocated on the first-come first-served basis. Check our facebook page to find a room mate.

Guest speakers

Opening address: Professor Laurent Excoffier (University of Bern)

Estimation of past history and test of evolutionary scenarios under an Approximate Bayesian Computation framework

Closing address: Professor Richard Abbott (University of St Andrews)

Plant invasions, introgression and species delimitation: some exceptions to the rules

More information and news can be found on the conference website: <http://www.sbes.stir.ac.uk/egg> Kind regards,

Cecile

Cecile FE Bacles Ph.D. Lecturer in Ecological Genetics School of Biological and Environmental Sciences University of Stirling Stirling FK9 4LA Tel: +44 (0) 1786 46 ext 6897 Email: [c.f.bacles@stir.ac.uk](mailto:c.f.bacles@stir.ac.uk)

PhD opportunities -visit : <http://www.sbes.stir.ac.uk/people/bacles> Registration Now Open! Ecological Genetics Group 54th Meeting 6-8 April 2010 <http://www.sbes.stir.ac.uk/egg> [c.f.bacles@stir.ac.uk](mailto:c.f.bacles@stir.ac.uk) [c.f.bacles@stir.ac.uk](mailto:c.f.bacles@stir.ac.uk)

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## Trondheim ConservationBiol Mar15-18

Dear colleagues and friends,

Please register for the conference:

“Sustainable Conservation: Bridging the gap between disciplines”

Which will be held 15-18 March 2010 in Trondheim, Norway.

Deadline for registration is 20 January: <http://www.biodivconf.ccb2010.no/> The conference is organized by the Centre Conservation Biology at the Norwegian University for Science and Technology (NTNU) and is part of the 250th Anniversary of the Royal Norwegian Society of Sciences and Letters.

The goal of the conference is to:

- Present the scientific basis for a sustainable conservation of natural resources.

- Focus on the process of extinction and management actions that can increase the lifetime of populations at the local and regional level.

- Identify common principles for a sustainable management that also can ensure conservation.

Speakers:

Prof. Ilka Hanski, University of Helsinki, Finland  
 Prof. Georgina Mace, Imperial College, London, UK  
 Prof. Stuart Pimm, Duke University, USA  
 Prof. Hugh Possingham, The Ecology Centre, Univ. of Queensland, Australia  
 Prof. Steve R. Beissinger, University of Berkley, USA  
 Dr. Hal Caswell, Woods Hole Oceanographic Institution, USA  
 Prof. Kjell Danell, Swedish Univ. of Agricultural Sciences, Umeå, Sweden  
 Dr. John M. Drake, University of Georgia, USA  
 Prof. Stephen P. Ellner, Cornell University, USA  
 Prof. Steinar Engen, Norwegian University of Science and Technology  
 Prof. William F. Fagan, University of Maryland, USA  
 Prof. John M. Fryxell, University of Guelph, Canada  
 Distinguished Professor Stephen L. Hubbell, Univ. of California, Los Angeles, USA  
 Dr. Penter Kareiva, The Nature Conservancy, USA  
 Prof. Russell Lande, Imperial College, London, UK  
 Dr. Thomas Lovejoy, The Heinz Center  
 Dr. Jane Reid, University of Aberdeen, UK  
 Prof. William J. Sutherland, University of Cambridge, UK  
 Prof. David Tilman, University of Minnesota, USA  
 Dr. Henri Weimerskirch, CNRS - Centre nat. de la recherche scientifique, France

The conference will bring leading researchers from around the world to present and discuss the scientific basis for a sustainable conservation of natural resources. In particular, we will focus on the process of extinction and management actions that can increase the lifetime of populations both at the local and regional level. A central goal for the conference will be to identify common principles for a sustainable management that also can ensure conservation.

The conference will be composed of four plenary talks that will provide a general overview of some broader issues related to sustainable conservations and four sessions which include talks of invited speakers, contributed talks and posters.

The first session will provide some general overviews of why conserving biodiversity. We will examine scientific evidence for system effects on changes in the biodiversity at the genetic, population and species level.

The second session will consider the five major threats for the Earth's biodiversity: habitat degradation and



fragmentation, climate change, introduction of alien species, pollution and over-exploitation. Our aim will be to present key-studies that give quantitative examples on how these drivers affect biodiversity at the genetic, population and/or ecosystem level.

Session 3 will deal with development of effective tools for predicting changes in biodiversity. In this section we will focus on how models can be used to predict changes in species composition or population viability, and how parameterization of these models often will require interdisciplinary collaboration between biology, mathematical and social sciences. We will focus on carefully selected model studies, which can be used as examples for such integration among different disciplines.

In the last section we will review practical examples in which management of biodiversity is based on principles integrating cross-disciplinary collaboration, where we will emphasize studies in which conservation and sustainable use of biodiversity are based on a science-based integrated approach unifying different science disciplines.

The program will include a mixture of talks by invited speakers and contributed talks by participants. In addition, there will be a poster session.

Henrik Jensen, PhD Centre for Conservation Biology  
Department of Biology Norwegian University of Science and Technology N-7491 Trondheim NORWAY

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E-mail: [Henrik.Jensen@bio.ntnu.no](mailto:Henrik.Jensen@bio.ntnu.no) Web-work: [www.ntnu.no/employees/henrik.jensen](http://www.ntnu.no/employees/henrik.jensen) Web-private: [www.inlicio.com](http://www.inlicio.com)

Henrik Jensen <[Henrik.Jensen@bio.ntnu.no](mailto:Henrik.Jensen@bio.ntnu.no)>

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### UdosAcores Biodiversity Sep22-25

On behalf of the Organizing Committee, we invite you to: International Symposium "WHAT DO WE KNOW ABOUT THE MACARONESIAN FLORA, TEN YEARS INTO THE 21ST CENTURY?" University of the Azores, Ponta Delgada, Sao Miguel Island, Azores (Portugal) 22-25 Sept. 2010

Celebrating 2010, the International Year on Biodiversity, we are organising an international symposium about the Macaronesian flora. Macaronesian islands are considered as important biodiversity hotspots, in-

cluding a wealth of plant biodiversity. This meeting will give a broad overview of Macaronesian plant diversity, from marine algae to angiosperms, in areas encompassing systematics, phylogenetics, evolution, biogeography, ecology, conservation, ethnobotany and plant resources. We also welcome communications dealing with the botanical history of Macaronesia. The symposium will address the flora from a biological perspective, but also facing it as crucial resource for sustainable development.

Confirmed keynote speakers: David Bramwell, José María Fernández-Palacios, Javier Francisco-Ortega, Ricardo Haroun, José Luis Martín, Robert J. Whittaker

Deadline for ABSTRACT SUBMISSION is May 31.

Please visit [www.floramac2010.com](http://www.floramac2010.com) for further information. –

Dr Hanno Schaefer Ecology and Evolutionary Biology  
Imperial College London

[hanno.schaefer@imperial.ac.uk](mailto:hanno.schaefer@imperial.ac.uk)  
[hanno.schaefer@imperial.ac.uk](mailto:hanno.schaefer@imperial.ac.uk)

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### UTours BehaviorEvolution Apr12-16

Dear All,

This year, the "Ecology & Behaviour" Meeting, organized by the SERL association, takes place in Tours, from Monday 12 to Friday 16 April 2010.

This is an international meeting with the main purpose of promoting postgraduate research and interactions between young researchers in Behavioural Ecology. The one specificity of this meeting, which is organized by the SERL PhD students association, is that it is free for all participants: you only have to pay for your trip to Tours.

This year, the "Ecology & Behaviour" Meeting consists of four days of conferences divided into six themes:

- Sexual Selection - Foraging Strategies/ Parasitism - Habitat selection/ Dispersion - Group / Individual interactions - Neuro-ethology / Ecophysiology - Evolutionary Biology / Conservation/ Applied Research

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



ticipants are expected to give a 15-minute talk. In order to register please submit the abstract of your talk (or poster) (250 words maximum) on the website: <http://serl2010.univ-tours.fr> (see the website for supplementary information). Registration are opened until 5nd March 2010.

Hope to see you in April,

SERL Association 2010.

[serl.univtours@gmail.com](mailto:serl.univtours@gmail.com)

Do not hesitate to visit our website (<http://serl2010.univ-tours.fr> < <http://serl2009.univ-lyon1.fr/> >) and to diffuse the news!

SERL 2010 <[serl.univtours@gmail.com](mailto:serl.univtours@gmail.com)>

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## WashingtonState EvolutionaryBiol Apr23-25

The biennial meeting of Pacific Northwest Evolutionary Biologists (EVO-WIBO) will be held this April 23-25 at Fort Worden State Park on Washington's Olympic Peninsula. Registration will open on January 20 and will close on March 15. For more information and to register online, surf on over to the meeting web site: <http://www.zoology.ubc.ca/evo-wibo/> . Cheers,

Scott

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

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## WashingtonState EvolutionaryBiol Apr23-25 2

Registration for the biennial meeting of Evolutionary Biology in the Pacific Northwest (EVO-WIBO)

is now open through the meeting web site <http://www.zoology.ubc.ca/evo-wibo/>. This year's meeting will be held April 23-35 at Fort Worden State Park in Port Townsend, Washington. The deadline for registration is March 15. Additional information on the meeting and venue is available on the meeting web site.

This year, The American Society of Naturalists has made it possible to provide a reduced registration fee (\$115) for student members of the society. Students can become members by visiting The American Naturalist subscription page at <https://subfill.uchicago.edu/JournalPUBS/threeyear1.aspx> . Scott Nuismer Associate Professor Department of Biological Sciences University of Idaho Moscow, Idaho 83844 Phone: 208 885 4096

[http://www.webpages.uidaho.edu/~snuismer/Nuismer\\_Lab/](http://www.webpages.uidaho.edu/~snuismer/Nuismer_Lab/)

Scott Nuismer <[snuismer@uidaho.edu](mailto:snuismer@uidaho.edu)>

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## Wierzba Poland EMPSEB May23-28 RegistrationOpen

Second Announcement of 16th European Meeting of PhD Students in Evolutionary Biology

Dear All,

We are pleased to invite you to 16th European Meeting of PhD Students in Evolutionary Biology, EMPSEB, which is going to be held from 23 to 28 May 2010 in Wierzba, Poland.

Registration is open now and will close 15th February.

More information can be found at [www.empseb2010.pl](http://www.empseb2010.pl) . You can contact us at: [empseb2010@uw.edu.pl](mailto:empseb2010@uw.edu.pl).

We are looking forward to welcoming you in Poland!

EMPSEB 2010 organising committee: Barbara Pietrzak, Anna Bednarska, Łukasz Dziewit, Ma<sup>3</sup>gorzata Grzesiuk, Anna Karnkowska, Magdalena Szuplewska (University of Warsaw) and Agata Jakubowska, Agnieszka Marek (Jagiellonian Univeristy)

[empseb2010@uw.edu.pl](mailto:empseb2010@uw.edu.pl)

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### Barcelona Spider SystematicsEvolution

PhD fellowship in Spider systematics and evolution at University of Barcelona

A four-year Phd fellowship is available through the FPI program of the Spanish Ministry of Science and Innovation, funded as part of the research project 'The ecosystem watchers: Mygalomorph spiders as bioindicators for monitoring ecological changes and evolutionary potential of terrestrial ecosystems'

Mygalomorph spiders are exceptionally well-suited for monitoring conservation status of terrestrial ecosystems in the Mediterranean basin. They exhibit high habitat fidelity, limited potential for dispersal and restricted distributional ranges, and are abundantly present in most Mediterranean habitats. Biologists, however, have long overlooked mygalomorph spiders due to their secretive habits and challenging taxonomy.

The promising use of these spiders as bioindicators is therefore not fully developed. We propose to overcome these limitations by integrating genomic tools with ecological modelling techniques. We anticipate that results of our research will be relevant for conservation, management, and sustainable use of natural landscapes in the Mediterranean basin.

The post will be based at the Biodiversity Research Institute of the University of Barcelona. For additional information about the research group and the project visit [www.marnedo.net](http://www.marnedo.net) We look for a highly motivated student with an interest in evolutionary biology and experience in molecular biology tools, taxonomy or GIS techniques. Candidates must have excellent oral and written communication skills, and demonstrate evidence of past research achievement. The anticipated start date is fall 2010.

Potential candidates should contact Miquel A. Arnedo ([marnedo@ub.edu](mailto:marnedo@ub.edu)) and include their curriculum vitae and a statement of research interests.

For details, conditions and instructions on how to apply, please visit <http://web.micinn.es/planidi/fpi/> (in Spanish). The expected publication date of the call is

mid January 2010 (check the website), and the deadline for applications will be 15 days after its publication.

–  
Miquel A. Arnedo

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

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

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## Braunschweig Germany MarineBacteriaPhylogenomics

A position for a PhD student in bioinformatics is available in the Department of Microbiology at the German Collection of Microorganisms and Cell Cultures (DSMZ) in Braunschweig, Germany. The project is entitled 'Phylogenomics And Functional Genomics of The Roseobacter Clade' and part of the recently established Transregional Collaborative Research Centre – Special Research Field 'Roseobacter' funded by the German Research Foundation (DFG).

The Roseobacter clade is one of the most abundant and successful groups of non-obligately phototrophic prokaryotes in the marine environment. The major goal of the Special Research Field is the understanding of evolutionary, genetic and physiological principles which constitute the secret of success for these bacteria. Consequently, marine microbial ecologists, bacterial physiologists, biochemists, natural product chemists, geneticists and computer scientists from Braunschweig and Oldenburg join forces to investigate the Roseobacter clade from the ecosystem level down to systems biology of model organisms with respect to important metabolic processes.

The candidate's tasks include the implementation of a software pipeline for the phylogenomic analysis of completely sequenced genomes and its application to members of the Roseobacter clade. Particular emphasis will be laid on devising and assessing programs for species delimitation and phylogenetic reconstruction directly based on whole genomes.

This PhD project is also tightly integrated with the DSMZ's current research related to the Genomic Encyclopedia of Archaea and Bacteria (GEBA); see <http://www.nature.com/nature/journal/v462/n7276/full/nature08656.html>.

The successful candidate will hold a master or diploma degree in informatics or bioinformatics and will be experienced with programming in compiled languages such as Java or C++ and scripting languages such as Ruby or Python. Preferred students will also have experience in at least some of the following fields: database programming, web programming (e.g., Ruby on Rails, PHP), linux administration, phylogenetic inference and genomics.

The DSMZ – Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (German Collection of Microorganisms and Cell Cultures; <http://www.dsmz.de/>) is the most comprehensive Biological Resource Centre in Europe. With more than 18.000 microorganisms, 1.200 plant viruses, 600 human and animal cell lines, 770 plant cell cultures and more than 7.100 cultures deposited for the purposes of patenting, we have demonstrated our obligation to serve science for decades. The DSMZ is an independent, non-profit organisation.

For further details regarding the position please contact Dr. Hans-Peter Klenk (e-mail: [hans-peter.klenk@dsmz.de](mailto:hans-peter.klenk@dsmz.de); phone: +49-(0)531-2616-227) or Dr. Markus Goeker (e-mail: [markus.goeker@dsmz.de](mailto:markus.goeker@dsmz.de); phone: +49-(0)531-2616-272).

Applications should be addressed until 15/03/2010 to:

Carl von Ossietzky Universitaet Oldenburg

ICBM

Prof. Dr. Meinhard Simon

26111 Oldenburg, Germany

(phone: 0441/798-5361; e-mail: [m.simon@icbm.de](mailto:m.simon@icbm.de))

[markus.goeker@dsmz.de](mailto:markus.goeker@dsmz.de)

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## DalhousieU 2 PhylogeneticMethods

The Blouin lab at Dalhousie University (<http://peta.cs.dal.ca/blouinlab>) is seeking two Ph.D. candidates to conduct research on new projects in the area of Evolutionary Bioinformatics. The successful candidates will either have a background in Computer Sci-

ence, Mathematics or the biological sciences. Potential candidates in from Math/CS should have a theoretical inclination or an interest in either combinatorial optimization or graph theory. Potential candidates from the Biological science should have an interest in either protein science or molecular evolution. Although the thrust of the two research projects will be adjusted based on background and interests of the applicants, all candidates must be interested in conducting research in the field of evolutionary science, and either possess strong coding skills or the willingness to acquire such skills.

The Blouin lab is member of the Centre for Genomics and Evolutionary Bioinformatics ([www.CGEB.dal.ca](http://www.CGEB.dal.ca)), which offers a stimulating environment and a large number of peers for trainees at all levels.

The applicants can apply to the most suitable program from the Ph.D. Computer Science, the Ph.D. Science (Biochemistry) or the interdisciplinary Ph.D. program. Interested candidates should send their C.V. and the contact information for 2 or more individuals capable to provide an informal reference.

Contact information: [cblouin@cs.dal.ca](mailto:cblouin@cs.dal.ca)

– Christian Blouin, Assoc. Prof. Faculty of Computer Science AND Department of Biochemistry and Molecular Biology Dalhousie University Halifax, NS, Canada

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

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## InstZoology London EvolutionaryBiol SocialEvolution

PhD Position: Evolutionary Biology - Social Evolution

We seek a PhD student for a 3 year studentship, starting October 2010 at Institute of Zoology, Zoological Society of London. [http:// www.zsl.org/science/](http://www.zsl.org/science/). This project addresses how sociality evolves, by testing key hypotheses on the origins of queen and worker castes in eusocial insects. Explaining worker behaviour (altruism) in the eusocial insects was one of biggest problems facing Darwin in developing his theory of natural selection. Over the last few decades, our understanding of caste evolution has been greatly advanced by kin-selection theory, which explains altruism in terms of the genetic fitness benefits workers gain from helping raise relatives. Recently, the role of kin-selection in social evolution has been questioned, and alternative, mechanistic explanations for the evolution of queen and

worker castes have been proposed. One such model (the diapause hypothesis) posits that queen and worker castes originated as two distinct developmental pathways, that arose from the bivoline life- history traits of their solitary ancestor. This suggests that obligatory hibernation (diapause) imposes a nutrient-dependent switch during larval development, and that this is sufficient for the evolution of queen and worker developmental pathways. In this way, altruism could evolve in the absence of kin-selection. This studentship tests the diapause hypothesis for the origins of caste by disentangling the proximate and ultimate role of diapause in caste determination in a primitively eusocial wasp, *Polistes canadensis*. *P. canadensis*, is a paper wasp found in tropical America, where females reproduce all year round. The student will look for evidence of diapause and pre-imaginal caste differentiation using a combination of behavioural manipulation experiments, gene expression analyses and demographic traits. The student will therefore receive a broad basis of training in evolutionary biology, behavioural ecology, molecular biology and genomics, whilst addressing fundamental questions in evolutionary biology.

The Institute of Zoology (IoZ) is the research division of the Zoological Society of London. It is a government-funded research institute specialising in scientific issues relevant to the conservation of animal species and their habitats. The student will be based jointly at the Institute of Zoology, (supervised by Dr Seirian Sumner (principle) and Dr Nichola Raihani), and the Dept of Biology at University of Sussex (supervised by Prof. Jeremy Field). The student will therefore benefit from becoming a full member of these active research groups that specialise in studying the evolution of sociality and behavioural ecology. The project involves several months of fieldwork in Panama, gene expression analyses using cutting edge molecular techniques, and lab-based manipulation experiments. Candidates should have a minimum of a good first degree (at least 2.1) in Biology or related subject. Fieldwork and molecular experience is desirable, but not essential. Interested candidates should email Dr Sumner ([Seirian.Sumner@ioz.ac.uk](mailto:Seirian.Sumner@ioz.ac.uk)) for further information prior to applying. Applications should be sent to Dr Sumner by 25th January 2010. Please include a CV and covering letter explaining your research interests and why you would be a suitable candidate. Interviews will be held in mid February.

Eligibility Funding would cover tuition fees and stipend for UK students. EU students that have not been living in the UK for 3 years or more, will only be eligible for tuition fees. International students will not be eligible for this funding however they are still welcome to ap-

ply for this project but would have to find alternative funding.

Dr Seirian Sumner Research Fellow Institute of Zoology Zoological Society of London Regent's Park London, NW1 4RY

Tel: +44 (0) 207 449 6617 Fax: +44 (0) 207 586 2870 Home: +44 (0) 1491 652 882

Web: [www.zsl.org/seiriansummer](http://www.zsl.org/seiriansummer) ZOOLOGICAL SOCIETY OF LONDON LIVING CONSERVATION Registered Charity no. 208728

Seirian Sumner <[seirian.sumner@googlemail.com](mailto:seirian.sumner@googlemail.com)>

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## Leuven InsectEvolution

PhD studentship: Population differentiation along a latitudinal gradient

GENERAL THEME: Evolutionary ecology of population differentiation along a latitudinal gradient in damselflies. The PhD project will be part of a larger research program where we address following questions in the damselfly *Ischnura elegans*: (1) how do larvae and adults differentiate phenotypically along a latitudinal gradient; (2) how is this related to genetic differentiation and (3) how does this affect ecological interactions with conspecifics (sexual selection) and natural enemies (predators and parasites).

PRACTICAL WORK will be a combination of (1) monitoring natural field populations, (2) common garden experiments in the laboratory, and (3) genetic analyses. We have excellent research facilities with an outdoor research area, several temperature-controlled rooms, incubators, and a well-equipped laboratory for quantification of behavioural and physiological traits and for studying genetic variation. The candidate will analyze and publish existing datasets and is expected to also collect new data.

PROFILE: master degree in Biology or related field and with a strong interest in both field and laboratory work. Preference will go to candidates with experience in scoring behavioural and physiological traits and in analyzing genetic variation, or at least a strong motivation to learn relevant techniques. It is expected that the candidate applies for national funding opportunities. A car driving license is required.

OFFER: A full time job initially for a period of one year, but extendable to a total of three years pend-

ing good evaluation. Leuven (<http://www.leuven.be>) is a pretty historical university city with a very high and pleasant standard of living. The historic university, founded in 1425 (<http://www.kuleuven.be/english>), has a top research and teaching standard. Within our research group we have ample expertise working with damselflies ([http://bio.kuleuven.be/de/dea/people\\_detail.php?pass\\_id=u0034380](http://bio.kuleuven.be/de/dea/people_detail.php?pass_id=u0034380)).

INTERESTED? Please send your CV, a letter of motivation including relevant experience, and contact details of two referents to Dr. Robby Stoks ([robby.stoks@bio.kuleuven.be](mailto:robby.stoks@bio.kuleuven.be)), University of Leuven, Laboratory of Aquatic Ecology and Evolutionary Biology, Deberiotstraat 32, B-3000 Leuven, Belgium

Applications will be reviewed starting February 1 until the position is filled. The start date is spring 2010, preferentially as soon as possible.

[robby.stoks@bio.kuleuven.be](mailto:robby.stoks@bio.kuleuven.be)

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## Luebeck Ploen Germany HostMicrobeEvolution

PhD Position in Genetics of Host - Microbiota Interactions and Chronic Inflammatory Diseases, Luebeck/Ploen, Germany

A PhD position is available in the labs of Prof. Saleh Ibrahim at the University of Luebeck and Prof. John Baines at the Max-Planck-Institute for Evolutionary Biology in Ploen ([www.evolbio.mpg.de/english/index.html](http://www.evolbio.mpg.de/english/index.html)) as part of the German Research Foundation (DFG) Cluster of Excellence "Inflammation at Interfaces" ([www.inflammation-at-interfaces.de/en.startseite.phtml](http://www.inflammation-at-interfaces.de/en.startseite.phtml)).

The successful candidate will be enrolled in the "Genes, Environment and Inflammation" research training program of the Cluster and participate in a large-scale collaborative effort to study the genetic basis of host - microbiota interactions and susceptibility to chronic inflammatory diseases in the house mouse system. The main task will be to apply metagenomics techniques (including 454 GS-FLX sequencing) to characterize the microbial communities of the gut and skin in inbred mouse strains that differ in susceptibility to chronic inflammatory diseases including colitis, arthritis, lupus and epidermolysis bullosa acquisitor. An advanced, 4-way intercross between resistant and susceptible mouse strains is available and will be used to map loci con-



tributing to disease susceptibility and/or host - microbiota interactions. Candidate genes will be studied in the context of host - microbiota coevolution and the evolutionary origin of disease-associated variation.

Job requirements include a Master's Degree or equivalent in Biology, Bioinformatics or a related field and a strong interest and experience in one or more of the following: bioinformatics, immunogenetics, evolution, population genetics or microbiology. The position is available immediately and will remain open until a suitable candidate is found.

The work will be performed in close cooperation between the laboratories at the University of Luebeck and the MPI for Evolutionary Biology in Ploen (50 km, 40 min via public transport) and take advantage of the mouse and genomics facilities of both locations. The everyday working language in both groups is English. Basic knowledge of German would be helpful, but not required.

Applications should be submitted as a single pdf document containing: (1) a one page cover letter summarizing research interests and experience, (2) full CV and (3) contact information of at least 2 references.

Applications and informal inquiries should be sent via Email to:

Prof. Dr. John Baines AG Evolutionary Genomics Institute for Experimental Medicine Christian-Albrechts-University of Kiel & Max-Planck-Institute for Evolutionary Biology August-Thienemann-Str. 2 24306 Ploen Germany Tel: +49-4522-763-367 Email: baines@evolbio.mpg.de

#### References

Yu X, Gimsa U, Wester-Rosenl f L, Kanitz E, Otten W, Kunz M, Ibrahim SM. Dissecting the effects of mtDNA variations on complex traits using mouse conplastic strains. *Genome Res* 2009;19:159-165

Johnsen JM, Teschke M, Pavlidis P, McGee BM, Tautz D, Ginsburg D, Baines JF. Selection on cis-regulatory variation at B4galnt2 and its influence on von Willebrand factor in house mice. *Mol Biol Evol* 2009;26:567-578

Yu X, Bauer K, Koczan D, Thiesen HJ, Ibrahim SM. Combining global genome and transcriptome approaches to identify the candidate genes of small-effect quantitative trait loci in collagen-induced arthritis. *Arthritis Res Ther* 2007;9:R3

Yu X, Bauer K, Wernhoff P, Koczan D, M ller S, Thiesen HJ, Ibrahim SM. Fine mapping of collagen-induced arthritis quantitative trait loci in an advanced intercross line. *J Immunol* 2006;177:7042-7049

baines@evolbio.mpg.de baines@evolbio.mpg.de

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## NatUIreland CodPopulations

PhD Studentship in Molecular Biology and Aquaculture

A PhD studentship is available within the Martin Ryan Institute (MRI), National University of Ireland, Galway, Ireland (<http://mri.nuigalway.ie/>); as part of the Sea Change Initiative-funded EIRCOD project, with the support of the Marine Institute and the Marine Research Sub-programme of the National Development Plan 2007-2013.

This position will focus on the application of genetic markers, such as microsatellites and SNPs, to the study of both wild populations and farmed (captive) stocks of Atlantic cod (*Gadus morhua*). The main aims will be to investigate population structure of cod in waters around Ireland and to support the ongoing EIRCOD broodstock and breeding programme. The increasing number of genetic markers in combination with the availability of captive stocks in a controlled environment also offers the potential to study mutational models and variation of candidate genes, as well as their association to quantitative traits of commercial value.

Skills required:

This position is suitable to graduate students holding at least a BSc (Hons) or equivalent in biological sciences or related fields. Familiarity in molecular research and population genetics are an asset, but preference will be given to applications with previous experience in molecular techniques, including microsatellite genotyping, DNA sequencing and relevant data analyses. The successful candidate should be able to undertake research independently as well as part of a team, showing good organizational skills, creativity, initiative and ability to cooperate. Some field sampling is expected (e.g. sampling fish in cages at sea and commercial landings at ports), although most of the lab work will be based at MRI Carna laboratories, which are located in Carna, Connemara, in proximity to the captive stocks.

The PhD studentship is available immediately and it will be funded for 4 years with a student fellowship of 25,000 euro p.a., which is tax-free and includes College fees (currently c.5,400 euro p.a.).

Further information about this position can be obtained by sending an e-mail enquiry to



(luca.mirimin@nuigalway.ie). Applicants should submit i) a research statement of 250 - 400 words in which they describe their understanding of the project and their interest in the subject area and ii) a CV to include the names and contact details of two academic referees. These must be submitted to Dr Luca Mirimin (luca.mirimin@nuigalway.ie) OR

Dr Richard D FitzGerald, Project Co-ordinator EIRC-COD (richard.fitzgerald@nuigalway.ie)

The closing date for receipt of applications is 5.00 pm on 22nd Jan 2010

This PhD is funded by the EIRC-COD project (Grant-Aid Agreement No. PBA/AF/07/004) carried

out under the Sea Change strategy with the support of the Marine Institute and the

Marine Research Sub-programme of the National Development Plan 2007-2013,

co-financed by the European Regional Development Fund.

Dr. Luca Mirimin Research Fellow MRI Carna National University of Ireland, Galway Connemara Carna Co. Galway

Tel: +353 95 32201 Fax: +353 95 32229 e-mail: luca.mirimin@nuigalway.ie

“Mirimin, Luca” <luca.mirimin@nuigalway.ie>

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## NIOZ Netherlands Benthic Marine Biodiversity

NIOZ, the Royal Netherlands Institute for Sea Research, is the Dutch national oceanographic institute, and it is one of the most important oceanographic institutes in the world. NIOZ is uniquely located on the beautiful island of Texel on the Wadden Sea coast. It employs over 250 staff: research scientists, lab assistants, technicians, ship crews, and auxiliary staff. NIOZ is one of the nine institutes that are part of the Netherlands Organisation for Scientific Research (NWO).

The department of Marine Ecology, which studies the structure and functioning of marine foodwebs, has a vacancy for a PhD student

“Ecological effects of predation by intertidal shorebirds on marine benthic communities”

In the current biodiversity decline, predators are often the first to disappear. Predators are thought to play a positive role in biodiversity maintenance as they prevent certain prey species in achieving dominance, relaxing resource competition among prey, hence promoting prey growth rates, prey coexistence and diversity. Losses of species at the highest trophic levels in communities may therefore cause extinctions and shifts in size structure at lower trophic levels. However, this role of predators is still often underappreciated, largely because many ecosystems have already lost their top-predators and/or human-induced disturbances now blur the positive predation effects. Furthermore, the role of migrant predators structuring communities along their migratory route has mostly been neglected.

For this reason, this project explores the effects of predation in one of the most pristine and undisturbed intertidal ecosystems in the world, the Banc d'Arguin (Mauritania, West Africa). Here we will study the structuring role of molluscivore shorebirds, notably the red knot (*Calidris canutus*), on the intertidal benthic community. The decline of wintering population of knots at Banc d'Arguin (due to habitat-destruction elsewhere along the flyway) coincides with an increase in the knot's main prey species and a decline in overall mollusc diversity. Taking an experimental approach, we will explore whether these are causal relationships. For example, by excluding knots from small-scale study plots, the PhD-student will focus on how prey competition and species coexistence are affected by predation. Modelling tools will be employed in order to explore the consequences at the ecosystem level.

### REQUIREMENTS

We are looking for an enthusiastic young biologist interested in scaling-up from behavior to community ecology, both empirically but also theoretically. The candidate should be able to cope with the primitive and sometimes harsh field conditions when working in Mauritania. Affinity with birds is not a requirement, and neither is a command of French, but both will be seen as assets. The assignment should lead to the completion of a PhD-dissertation at the University of Groningen through Prof. T. Piersma.

We offer a full-time PhD position for 4 years, a pension scheme, a health insurance allowance, a yearly 8% vacation allowance, year-end bonus and flexible employment conditions. Conditions are based on the Collective Employment Agreement of the NWO Research Institutes.

Further information on the project and the position can be obtained from Dr Jan van Gils (Jan.van.Gils@nioz.nl or otherwise from Jolanda Ev-

ers, Human Resources (Email: [Jolanda.evers@nioz.nl](mailto:Jolanda.evers@nioz.nl), phone +31-222-369371). General information about NIOZ can be found at: <http://www.nioz.nl> Application:

Applicants should send a cover letter with motivation for this project, CV, a statement of research interest and the name and email address of two referees, to the Human Resources Department attended to Ms. Jolanda Evers, Royal Netherlands Institute for Sea Research (NIOZ), P.O. Box 59, 1790 AB Den Burg, Texel, The Netherlands or preferably by e-mail to: [jobs@nioz.nl](mailto:jobs@nioz.nl)<<mailto:jobs@nioz.nl>>

Closing Date: 8 March 2010 or until a qualified candidate is identified.

[Jan.van.Gils@nioz.nl](mailto:Jan.van.Gils@nioz.nl) [Jan.van.Gils@nioz.nl](mailto:Jan.van.Gils@nioz.nl)

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## OhioStateU InvasiveInsectPopGenet

Invasive species permeate both the natural and managed landscapes. These exotic species often have profound negative impacts on native biodiversity by influencing abiotic conditions, or increasing competition for food or other resources. Increasingly, invaders also interact with one another in ways that exacerbate their impacts on ecological communities and environments. The success of an invasive species depends not only on the biology of the invader itself, but the ecological community and environment that is being invaded. Often these lead to invasion meltdowns, where the introduction of one species facilitates the invasion of additional species. The soybean aphid plays a key role in a recent ecological invasion meltdown involving its invasive primary host plant, buckthorn, and its key predator, the multi-colored Asian lady beetle. This USDA-funded position will specifically focus on soybean aphid population and landscape genetics, with emphasis on the role of buckthorn during secondary and primary host colonization. The project will combine field work (including soybean aphid collecting at various sites across the Midwestern US), as well as molecular data generation (microsatellites and single nucleotide polymorphisms). Ph.D. students are preferred, but Master's students are strongly urged to apply. The ideal start time would be summer of 2010, but start date is flexible. For more information, please contact Dr. Andy Michel ([michel.70@osu.edu](mailto:michel.70@osu.edu)).

[michel.70@osu.edu](mailto:michel.70@osu.edu) [michel.70@osu.edu](mailto:michel.70@osu.edu)

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## SanFranciscoStateU Zooplankton

Evolutionary genetics of estuarine zooplankton

Part of a new NSF-funded opportunity for two graduate research assistantships in zooplankton evolution and genetics, at the Romberg Tiburon Center for Environmental Studies, located on San Francisco Bay (<http://rtc.sfsu.edu/>)

Collaborative research between labs of Wim Kimmerer ([http://rtc.sfsu.edu/in\\_kimmerer.htm](http://rtc.sfsu.edu/in_kimmerer.htm)) and Sarah Cohen ([http://rtc.sfsu.edu/in\\_cohen.htm](http://rtc.sfsu.edu/in_cohen.htm)). Funding for graduate students pursuing a Master's degree in the Biology Department of San Francisco State University begins Fall 2010.

Dr. Sarah Cohen Associate Professor in Biology Romberg Tiburon Center for Environmental Studies San Francisco State University [sarahcoh@sfsu.edu](mailto:sarahcoh@sfsu.edu) 415-338-3750 (office)

Sarah Cohen <[sarahcoh@sfsu.edu](mailto:sarahcoh@sfsu.edu)>

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## StockholmU PlantCoevolution

PhD position/scholarship in Plant Ecology Regional variability and coevolutionary responses: purple loosestrife (*Lythrum salicaria*) and its associated food web

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

Project description: The purpose is to examine how difference in food web structure among sites from Uppland to Norrbotten has affected the interaction between purple loosestrife and its two main herbivores. A key issue to explore in this project will be plant odours and how the regional variation in volatiles affect both the plant-herbivore interaction as well as the interaction between the herbivores and their natural enemies. The PhD-project will mainly examine the interaction from the herbivore perspective and will study the role of plant chemistry, herbivore behaviour and population dynamics for the strength of species interaction and for the evolution of species traits. The work will involve both field and laboratory work, behavioural studies and chemical analyses. The chemical work will be

done in collaboration with chemical ecologists at KTH and other parts of the work will be done together with ecologists from SLU and Uppsala University.

Further information: Professor Peter Hambäck, Dept. of Botany, Stockholm University, 106 91 Stockholm. Ph +46 (0)8 161288 e-mail: [peter.hamback@botan.su.se](mailto:peter.hamback@botan.su.se), home page: [www.botan.su.se](http://www.botan.su.se) The application should include a letter of intent, a certified curriculum vitae that includes information on previous education, two copies of the masters thesis (or 'examensarbete'), other documents supporting your competence and suitability for the position, and address and phone number to two reference persons. The application can be written in English or Swedish.

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

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

A PhD education is 4 years (48 months). During the first two years the student receives a scholarship (Sw: "utbildningsbidrag") and during the last two years the student has a PhD position (Sw: "doktorandanställning"). Up to 20% of teaching may be included in the position.

The application should be labeled with the reference number 2/2010, and should be received at the following address no later than February 25, 2010:

Registrator Mirska von Kraskowski, Department of Botany, Stockholm University, SE-10691 Stockholm, Sweden

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

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

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## StockholmU SystematicZoology

Ref nr 2/10UJ? PhD position in zoology, systematic zoology and evolutionary research Department of Zoology, Stockholm University and Swedish Museum of Natural History, Department of Invertebrate Zoology

Closing date: 15 February 2010 Project description: Project title: Phylogeny, taxonomy and character evolution in Acoela. Acoela are marine worms usually about 1 mm in length. Molecular phylogenetic studies have demonstrated that Acoela are the oldest extant bilaterian clade. Consequently, acoels have recently received a lot of attention from biologists studying bilaterian evolution. There are about 380 known species of acoels world-wide, and 56 of these are recorded in Swedish waters. Currently there is no comprehensive phylogenetic hypothesis for Acoela, and the legacy classification that is in use is problematic. The aims of the project are to reconstruct phylogeny, character evolution and species delimitation within two problematic acoel families. One of the aims is to establish a phylogenetic classification for the studied groups. Acoel anatomy is simple, but also highly variable. Phylogenetic hypotheses generated within the project will be used to study correlations between morphological and molecular evolution within the group. The project will include molecular phylogenetic lab work and analysis of data using phylogenetic methods and bioinformatics. Acoels have no planktonic larvae or other dispersal stages. Their dispersal abilities are therefore likely to be poor. Nevertheless, there are many morphological species that are considered cosmopolitan. Species delimitation in morphological species will be studied using molecular genetics. The project will partly rely on previously collected material, but a significant collection effort is necessary requiring travel to marine field stations. Identification of Acoela requires study of live material under a light microscope.

The working language will be English and Swedish.

Qualifications: To be qualified for research studies in systematic zoology the applicant needs to have passed at least 120 hp of biology studies, including an approved independent project in systematic zoology of at least 30hp at the advanced level. Applicants who have acquired the corresponding competence at another Swedish or foreign university are also qualified.

Criteria for selection: Among qualified applicants, se-

lection is made according to ability to profit from the studies. The criteria to be used are the applicant's documented knowledge in subjects of relevance for the research area, ability to master language (including both spoken and written English), analytical ability, creativity, initiative, independence, and ability to cooperate. The basis for judgement of how well the applicant fulfils these criteria is: the relevance of earlier studies for the research area, grades on courses at the university level, the quality of the independent project, references, relevant practical experience, interviews and the applicant's letter of intent. Previous experience of molecular phylogenetics, bioinformatics and documented studies in invertebrate zoology and marine biology are considered particularly relevant.

To be included in the application: Maximum one A4-page of personal presentation and your reasons for applying (letter of intent). Curriculum vitae. Copy of independent project report (previous thesis work) and publications. Documentation of other activities of relevance. Copy of degree certificates, or LADOK-excerpt.

Terms of employment: The research education comprises 48 months at full time. The position is financed by a fellowship ("utbildningsbidrag") for the first two years, and then continues with PhD-employment until the end of the PhD-program.

Information: Ulf Jondelius, Swedish Museum of Natural History, Invertebrate Zoology Department. Telephone: 08 5195 4150. E-mail:ulf.jondelius@nrm.se  
 Union representatives: Bo Ekengren, SACO, Lisbeth Häggberg, ST and Gunnar Stenberg, SEKO.

You are welcome with your application with the specified ref.nr no later than February 15, 2010 to:

Stockholms universitet Prefekten Zoologiska institutionen 106 91 Stockholm Sweden

jondelius@gmail.com

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## Tanzania Evolutionary Networks

Dear EvolDir Members,

Please share the below PhD Studentship advertisement with any interested parties.

Thank you, Anne Smith

PhD Studentship in Ecology

Evolutionary interaction networks: Application to on-

going field work in Tanzania

Evolutionary systems consist of a complex web of interactions: among species, and between species and their environment. Understanding these interactions is important for predicting how factors - such as biological or chemical control agents, grazing pressure, or climate change - may affect ecosystem function. However, unravelling such complex networks of interactions stretches the boundaries of current research; new methods are needed to handle the complexity of real ecosystems.

This studentship explores the use of a methodology new to ecological analysis, Bayesian networks, for revealing ecological interaction networks. You will develop Bayesian network algorithms for handling ecological data and incorporating spatial information. Methods developed will be applied to real ecological data, including data collected in an ongoing field project in Tanzania. There is opportunity for a field season in Tanzania, where you would perform targeted manipulation experiments based on your models (e.g., targeted removal and addition of species within caged areas).

This project will be based in Dr Anne Smith's lab at St Andrews and be in collaboration with Dr Colin Beale (York University, currently based in Tanzania) and Dr Dirk Husmeier (Biomathematics & Statistics Scotland). In this studentship, you will gain both computational and field skills.

For more details, please contact [anne.smith@st-andrews.ac.uk](mailto:anne.smith@st-andrews.ac.uk) and/or visit: <http://biology.st-andrews.ac.uk/vannesmithlab/> Funding by NERC: UK residents (stipend and fees) or EU citizens (fees only)

A PDF of the above advertisement is downloadable from: <http://biology.st-andrews.ac.uk/vannesmithlab/NERC2010.pdf> - Dr V Anne Smith School of Biology Sir Harold Mitchell Building University of St Andrews St Andrews, Fife KY16 9TH United Kingdom +44 (0)1334-463368 [anne.smith@st-andrews.ac.uk](mailto:anne.smith@st-andrews.ac.uk) [biology.st-andrews.ac.uk/vannesmithlab/](http://biology.st-andrews.ac.uk/vannesmithlab/) [biology.st-andrews.ac.uk/vannesmithlab/](http://biology.st-andrews.ac.uk/vannesmithlab/)

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## TexasAMU FishPopulationGenetics

Biology MS Assistantships

We are seeking two highly motivated graduate stu-



dents to participate in research on the population genetics and conservation of fish species native to eastern California. The species of concern include tui chub (*Siphateles bicolor*), speckled dace (*Rhinichthys osculus*), sucker (*Catostomus fumeiventris*), and pupfish (*Cyprinodon amargosae*). Students will have opportunities to interact and coordinate their research with collaborators at the U. S. Fish & Wildlife Service, the U. S. National Park Service, and California Department of Fish & Game.

Students will present their findings in international/national professional conferences and prepare manuscripts for submission to peer-reviewed journals. We welcome students who are diligent and interested in fish evolution, ecology and conservation. Experience in population genetics, ichthyology, geographic information systems (GIS), freshwater ecology, and/or fish breeding/ husbandry would be helpful.

Texas A&M University - Corpus Christi is a vibrant and growing university of approximately 9,500 students located on Ward Island between Oso and Corpus Christi bays. The appointments would be in the Department of Life Sciences which offers MS degrees in Biology and Marine Biology, and a PhD in Marine Biology. For more information visit the university at [www.tamucc.edu](http://www.tamucc.edu). We will provide support (salary & tuition) via research and teaching assistantships starting in June, 2010. Interested students should contact Dr. Frank Pezold by email ([Frank.pezold@tamucc.edu](mailto:Frank.pezold@tamucc.edu)) for more information by March 1, 2010 and include a curriculum vitae.

Yongjiu Chen, Ph. D. College of Science & Technology Texas A&M University Corpus Christi, TX 78412 Email: [Yongjiu.chen@tamucc.edu](mailto:Yongjiu.chen@tamucc.edu) Phone: 361-825-2081

“Chen, Yongjiu” <[Yongjiu.Chen@tamucc.edu](mailto:Yongjiu.Chen@tamucc.edu)>

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## TexasAMU ForestEvolutionaryGenetics

### LEADERSHIP FELLOWSHIPS IN FOREST RESOURCES MANAGEMENT AND GLOBAL CHANGE

The Department of Ecosystem Science and Management at Texas A&M University (<http://essm.tamu.edu/national-needs.aspx>) is launching a Ph.D. fellows program aimed at producing scien-

tific leaders with expertise in forest and woodland ecosystems in the context of a rapidly changing global environment. These fellowships, which will be partially funded by the USDA National Needs Program, provide a \$30,000/yr stipend, a \$10,500/yr cost-of-education allowance, and a \$1,500/yr travel allowance for a three-year period. The total award value over a period of three years is \$126,000.

Opportunities exist in a wide array of specialties, including ecology, ecosystem restoration, spatial sciences, ecohydrology and watershed management, ecological, evolutionary and conservation genetics, and human dimensions.

The Department is seeking exceptional individuals who can excel in a challenging, interdisciplinary academic environment. Applicants should aspire to become scientific leaders whose research solves socio-ecological problems related to global change in forest and woodland ecosystems. Successful candidates will be co-advised as members of an integrative research program, and interdisciplinary research interests are highly encouraged.

Applicants must have completed (or be close to completing) an M.S. degree in the life sciences, environmental sciences, or environmental engineering field. They must also be U.S. citizens. Review of applications will start March 1, 2010. Application details may be found at <http://essm.tamu.edu/-academics/graduate-programs/application-process>. Contact [k-krutovsky@tamucc.edu](mailto:k-krutovsky@tamucc.edu) or [j-gan@tamucc.edu](mailto:j-gan@tamucc.edu) for details.

The state of Texas encompasses 10 diverse ecoregions that include forest and savannas. Forested lands in Texas cover some 60 million acres more than in any other state of the lower 48 United States. Texas A&M University is rated the number 5 university nationwide by Washington Monthly, on the basis of recruiting, research, and service. It is rated the number 17 among 6000 universities worldwide by Webometrics. Bryan College Station, home of Texas A&M University, offers a safe, culturally diverse community and affordable living. It is located within a short drive of three major Texas cities Houston, Austin, and Dallas as well as numerous beaches along the Gulf of Mexico.

Konstantin (Kostya) V. Krutovsky, PhD Associate Professor Department of Ecosystem Science & Management Texas A&M University #319 Horticulture and Forest Science Building (HFSB) 2138 TAMU College Station, TX 77843-2138 Phone: (979) 458-1417 (office) (979) 458-0471 (lab) Fax: (979) 845-6049 or 458-0159 E-mail: [k-krutovsky@tamucc.edu](mailto:k-krutovsky@tamucc.edu) <http://essm.tamu.edu/people-info/faculty/krutovsky-konstantin.aspx> Kostya

Krutovsky <k-krutovsky@neo.tamu.edu>

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## TexasAMU MosquitoEvolutionaryGenetics

A PhD student position is available for conducting NIH-funded research in the Slotman lab in the Department of Entomology at Texas A&M University. The Slotman lab is interested in the evolutionary genetics of malaria mosquitoes, with an emphasis on the *Anopheles gambiae* complex. The major malaria vector in this complex, *An. gambiae* s.s, strongly prefers blood feeding on humans and it is strongly attracted to the smell of human sweat. This anthropophily or preference for humans is one the main reasons *An. gambiae* is such an efficient malaria vector.

The PhD candidate will investigate the genetic basis of the strong preference of *An. gambiae* for human hosts, using QTL mapping, evolutionary genetics, and gene expression approaches. The ultimate goal of the project is to identify olfaction genes responsible for the attraction of *An. gambiae* to humans. The results of this research would contribute greatly to our understanding of the biology of this important vector, and would promote the development of novel malaria control methods. For example, we expect that anthropophily genes will be promising targets for designing repellents/attractants, or for transgenic mosquito efforts.

The preferred candidate should have a strong interest in medical entomology, and some background in (evolutionary) genetics is preferred. The successful candidate will be expected to conduct mosquito crosses and behavioral assays at Wageningen University in The Netherlands at the start of the PhD program. Preferred start date; early summer 2010, but not later than Sept 2010.

For further information please contact :

Michel Slotman

maslotman@ag.tamu.edu

Office: (979) 845 7556

Or: to be considered for this position please send a CV

a copy of your GRE scores

university transcripts

contact information for three references

a cover letter explaining your interest in the topic

MASlotman@ag.tamu.edu MASlotman@ag.tamu.edu

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## Trentino Italy FruitGenomics

International PhD Programme in Genomics and Molecular Physiology of Fruits (GMPF) in San Michele all'Adige, Trentino, Italy

The GMPF international PhD programme consists of 13 highly competitive research institutions spread all over the world. The aim of the programme is to establish an international network of PhD students working on genomics, bioinformatics, functional genomics, proteomics, metabolomics, genetics, genetic improvement and molecular physiology of fruit trees.

The GMPF programme offers 14 PhD Fellowships starting in spring 2010. Talented and motivated candidates who have, or are expecting to obtain by end of July 2010 a Master or equivalent degree in Life Sciences and Bioinformatics, are invited to submit their application by 31st January 2010.

The candidates can postulate for one to three specific projects. Each project is developed as collaboration between the research centre of the Fondazione Edmund Mach and one of the other 12 institutions members of the GMPF programme:

Fondazione Edmund Mach, Trento (I) • Hebrew University of Jerusalem (IL) • IRTA, Barcelona (S) • INRA, Montpellier (F) • Julius-Kühn-Institut, Dresden (D) • Plant and Food Research Institute, Palmerston North (NZ) • Plant Research International, Wageningen (NL) • University of Bologna (I) • University of Ghent, VBI (B) • University of Milano (I) • University of Trento (I) • University of Udine (I) • Washington State University (USA)

For more information about the GMPF international PhD programme, PhD projects, host laboratories, and application procedure visit: [www.fmach.it/gmpf-phd](http://www.fmach.it/gmpf-phd) or contact:

Elisa Piaia, PhD GMPF International PhD Programme  
Fondazione Edmund Mach Innovation and Research  
Centre Via E. Mach 1 38010 San Michele a/A (TN)  
Italy Email: [elisa.piaia@iasma.it](mailto:elisa.piaia@iasma.it) Phone: +39 0461  
615559 Fax: +39 0461 6509546

[elisa.piaia@iasma.it](mailto:elisa.piaia@iasma.it)



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## TrentU badger conservation

Graduate Student Position (to start between in May or Sept 2010) - Trent University (Ontario, Canada)

Conservation Biology/Genetics of an Endangered North American Badger Population

A graduate student position will be available to investigate demographic trends, ecological parameters, and genetic attributes relevant to the conservation of an endangered badger subspecies in Ontario, *Taxidea taxus jeffersoni*. Specifically, we are seeking to further our understanding of this species in Ontario through analysis of biological samples obtained from badger burrows, with the aim of refining population estimates of badgers and identifying the structure of their diet. We are also interested in understanding how the distribution of specific molecular traits can provide insight into the potential of this species to locally adapt and persist in a rapidly changing landscape in Ontario. This work is part of an ongoing collaboration between Trent University (Dr. Kyle) and the Ministry of Natural Resources in Ontario (Dr. Nocera), and the student would be co-supervised by both individuals. The student would be expected to perform both field and laboratory (molecular and stable isotope) studies.

Most lab research will take place within the new DNA Building at Trent University that houses the Natural Resources DNA Profiling and Forensics Centre and the Wildlife Research and Development Section of the Ontario Ministry of Natural Resources. This venue provides an exciting collaborative research environment with field and lab-based researchers and unsurpassed infrastructure for wildlife genetic and wildlife disease research. Refer to the websites below for further information.

<http://web.nrdpfc.ca> <http://www.wildliferesearch.mnr.gov.on.ca/spectrasites/-internet/wrds/wrds.cfm> <http://www.trentu.ca/-dnabuilding> <http://www.ontariobadgers.com> <http://people.trentu.ca/joenocera> Candidates are expected to commence their studies between May - September 2010.

Interested individuals should provide a recent CV with referee contact information, copies of any publications, approximate GPA, and a brief description of their interest in the position. A review of applications will begin

on February 1, 2010 and continue until the position is filled.

Contact: Dr. C. J. Kyle Research Chair in Wildlife Genetics and Forensics Natural Resources DNA Profiling and Forensics Centre Trent University, 2140 East Bank Drive Peterborough, ON, K9J 7B8

[chris.kyle@nrdpfc.ca](mailto:chris.kyle@nrdpfc.ca)

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## TrentU Spider Evolutionary Physiology

M.Sc. position in spider evolutionary physiology.

Applications are invited from potential graduate students interested in studying the relationship between reproductive success and exercise endurance and energy expenditure in male spiders. The student will be co-supervised by Matthias Foellmer and Gary Burness, at Trent University. The project will be conducted in collaboration with Maydianne Andrade and Jeff Stoltz from U Toronto at Scarborough, and a substantial part of the lab work will likely be done in Toronto. Therefore, a willingness and ability to live temporarily in Toronto (perhaps on the Scarborough campus) is a prerequisite. Students with a background or interest in animal physiology, behavioural ecology and evolution are encouraged to apply. Please send CV with names and contact information of two references and cover letter to either Matthias Foellmer or Gary Burness (via email). Applications will be accepted until a suitable candidate is found. Projected start date: May 2010. For more information please contact: Gary Burness ([garyburness@trentu.ca](mailto:garyburness@trentu.ca)) or Matthias Foellmer ([matthiasfoellmer@trentu.ca](mailto:matthiasfoellmer@trentu.ca)), Department of Biology, Trent University, Peterborough, Ontario

Many thanks for your efforts!

Matthias

Matthias Foellmer Assistant Professor Department of Biology, Adelphi University 1 South Ave., Garden City, New York, 11530, USA w: <http://panther.adelphi.edu/~fo17044/MWFoellmermain.html> ( <http://panther.adelphi.edu/~fo17044/-MWFoellmer%20main.html> ) P: (516) 877-4206

Matthias Foellmer <[FOELLMER@adelphi.edu](mailto:FOELLMER@adelphi.edu)>

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## UAntwerp BirdParasite

Call for applicants on bird-parasite research

In the framework of its research on host-parasite interactions between birds and Ixodid ticks, the Evolutionary Ecology Group of the University of Antwerp is looking for candidates who want to apply for either a PhD scholarship (4 years) or a visiting postdoc fellowship (6 to 12 months). Applications will be submitted to and evaluated by the Belgian Fund for Scientific Research.

We welcome applications on the following topics, or a combination of them: (1) ecology of ectoparasite transmission in a guild of cavity-nesting birds, using field studies and/or cage experiments; (2) life-cycle and host preference of nidicolous cavity-dwelling ticks (3) population structure and host differentiation in ticks using molecular markers; (4) molecular identification of hosts in blood meals; (5) individual-based modelling of tick transmission and evolution of host specialization in relation to resource use by hosts.

PhD scholarships can be awarded for 4 years, starting 1st October 2010, with application deadline 1 February 2010. Candidates should have an MSc degree from an EU university and have excellent student grades (ranking among the top 10% of their graduation cohort). Publications also increase the chance of being selected. Specific expertise is not required.

Visiting postdoctoral fellowships can be awarded to non-Belgian postdocs for a maximum of 12 months. Candidates are selected based on publication record and expertise. Applications can be submitted at any time with a minimum of three months before the starting date.

If you are interested or need further information, contact Prof. Erik Matthysen at [erik.matthysen@ua.ac.be](mailto:erik.matthysen@ua.ac.be) <<mailto:erik.matthysen@ua.ac.be>>

Prof. Dr. Erik Matthysen Evolutionary Ecology Group  
Department of Biology, University of Antwerp

Groenenborgerlaan 171, 2020 Antwerpen +32 3 265 3464

[erik.matthysen@ua.ac.be](mailto:erik.matthysen@ua.ac.be) [erik.matthysen@ua.ac.be](mailto:erik.matthysen@ua.ac.be)

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## UCollegeCork BioinformaticsComputationalBiol

PhD Studentship in Bioinformatics/Computational Biology

Title: Understanding Microsatellite Mutation and Evolution - A Bioinformatics Analysis of 1000 Human Genomes

Supervisor: Dr. Avril Coghlan, University College Cork, Ireland.

Application Deadline: 16 March 2010 or as soon as a qualified candidate is found

Funding Details: Science Foundation Ireland - EU students only

Contact: Avril Coghlan, email  
[avril.coghlan@googlemail.com](mailto:avril.coghlan@googlemail.com)

Project Description: A 3-year Science Foundation Ireland PhD studentship is available to start in April 2010 to work on an internationally collaborative project between Dr Avril Coghlan in University College Cork, Ireland and Dr Richard Durbin at the Wellcome Trust Sanger Institute, Cambridge, U.K. The successful candidate will be based at University College Cork but will visit the Sanger Institute for meetings with collaborators.

The project involves the development of a novel bioinformatics approach for inferring the genotypes of individuals at microsatellite (simple repeat) loci, using data from new DNA sequencing technologies. The novel bioinformatics method will be applied to data from the 1000 Genomes Project, an international project which aims to sequence the whole genomes of 1000 humans from around the world. By inferring genotypes at microsatellite loci in 1000 human individuals, this PhD project aims to investigate important unanswered questions about microsatellite processes and evolution.

The ideal candidate will have an honours B.Sc. or M.Sc. in bioinformatics, computational biology, or a related subject. Candidates with a background in genetics or a related biological subject with strong mathematical skills, or with a background in mathematics or computer science with a strong interest in biology, are also encouraged to apply.

To apply for this position please send a cover letter,

copy of B.Sc. transcript and your CV to Dr. Avril Coghlan by email to [a.coghlan@ucc.ie](mailto:a.coghlan@ucc.ie)

The closing date for applications is March 16th 2010 or as soon as a qualified candidate is found.

Salary/Stipend: The PhD student will have his/her fees paid, and will receive a tax-free stipend of 18500 euro in year 1, 19500 euro in year 2 and 20500 euro in year 3.

Avril Coghlan University College Cork Ireland

[A.Coghlan@ucc.ie](mailto:A.Coghlan@ucc.ie)

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## UCollegeDublin FreshwaterFishEvolution

UCD School of Biology & Environmental Science

PhD position in freshwater fisheries ecology & evolution:

A three-year funded position is available to work in the research laboratories of Dr Mary Kelly-Quinn and Dr Stefano Mariani to study the trophic ecology and life-history of pike (*Esox lucius*) populations in Irish lakes and rivers and to investigate the colonisation history of this species in Ireland, using a range of molecular genetic approaches. The project will be carried out in collaboration with Irelands Central Fisheries Board, it will entail sampling in several Irish ecosystems, interacting with the angling community, as well as conducting sophisticated laboratory work, including the application of DNA technologies and spectroscopy for stable isotope analysis.

The successful candidate will possess an honours primary degree (at least 2.1) or equivalent, in the field of ecology, evolution, environmental science and/or conservation biology. Previous research experience in both aquatic biology and molecular genetics will be desirable. Master-level education would of course be a bonus. A commitment to scientific inquiry and excellent communication skills, both written and oral, are paramount.

The position is based at the School of Biology & Environmental Science (<http://www.ucd.ie/bioenvsci/index.html>), University College Dublin, Irelands largest University (ranked 89th in the 2009 Times Higher Education Supplement worlds universities table). Both the campus and the city offer vibrant cultural environments and a myriad of opportunities for scientific and cultural growth.

Please send your CV, along with a covering letter describing your skills and experiences and why you are interested in this project. Include also names and contacts of at least two referees. Applications should be sent by email to: [mary.kelly-quinn@ucd.ie](mailto:mary.kelly-quinn@ucd.ie) and [stefano.mariani@ucd.ie](mailto:stefano.mariani@ucd.ie) Closing date for applications is Friday 26th of February. Start date of the project is April 1st.

Please note that university fees are covered for EU nationals. Non-EU applicants would have to cover the additional costs.

stefano mariani <[stefano.mariani@ucd.ie](mailto:stefano.mariani@ucd.ie)>

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## UCollegeLondon SexualSelection

NERC funded PhD Studentship

Identifying genes involved in sexual selection

Supervisors: Professor Andrew Pomiankowski & Dr Kevin Fowler

The Galton Laboratory

Research Department of Genetics, Evolution and Environment

University College London

The goal of this project is to improve our understanding of the genetic basis of female sexual preferences. This will be undertaken using the African stalk-eyed fly *Diasemopsis meigenii*. We already have a good understanding of how to accurately measure individual mate preference in this species. Our aim is to uncover the number of genes involved, their effect sizes and linkage patterns. It will also be interesting to map the genes for the male ornamental trait (eyespan), and uncover the nature of any genetic covariance with female preference. The student will also map genes for male fertility and ejaculate properties (sperm and accessory gland proteins) as these are thought to be important in determining the benefits of mate choice. The genetic analyses will be carried out using QTL (quantitative trait locus) mapping on a SNP map of the *Diasemopsis meigenii* genome. The student will work closely with a postdoctoral fellow and research technician employed on our NERC grant addressing these topics, and with other members of the stalk-eyed fly group with diverse interests in reproductive biology and sexual selection.

Applications should be sent with a covering letter, CV, and the names and contact details of two referees to

Professor Pomiankowski by email: [ucbhpom@ucl.ac.uk](mailto:ucbhpom@ucl.ac.uk). Applications should be sent as soon as possible, and by Feb 19th at the latest. Start date Sept/Oct 2010. Full studentships (providing stipend and tuition fees) are available to applicants who satisfy NERC's eligibility requirements:

<http://www.nerc.ac.uk/funding/available/postgrad/-eligibility.asp>

For further information:

<http://www.ucl.ac.uk/biology/academic-staff/pom/-pomiankowski.htm>      <http://www.ucl.ac.uk/stalkie/>

[ucbhpom@ucl.ac.uk](mailto:ucbhpom@ucl.ac.uk)    [ucbhpom@ucl.ac.uk](mailto:ucbhpom@ucl.ac.uk)

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## UEdinburgh HostParasiteCoevolution

PhD positions studying host-parasite coevolution at the University of Edinburgh, UK

Up to 4 PhD studentships are available at the Institute of Evolutionary Biology (<http://web.bio.ed.ac.uk/research/institutes/evolution/>) to study coevolution. The projects are especially suitable for UK residents, though any strong candidates are encouraged to apply.

Contact Tom Little ([tom.little@ed.ac.uk](mailto:tom.little@ed.ac.uk)) or Amy Pedersen ([amy.pedersen@ed.ac.uk](mailto:amy.pedersen@ed.ac.uk)), depending on the project (described below)

See also <http://ciie.bio.ed.ac.uk/iie/node/261> <http://www.biology.ed.ac.uk/research/groups/tlittle/>

Project Descriptions:

Evolution and coevolution of *Daphnia* and their parasites

Host-parasite coevolutionary interactions may impact population densities, genetic diversity and breeding systems. There is however, limited knowledge of just how dynamics work in natural systems and in the wild. We investigate a genetic variation in the crustacean *Daphnia*, focusing on key traits that influence parasite-mediated selection: maternal effects, immune responses (both cellular and molecular) and immunosenescence. We have also recently initiated large-scale genomic/transcriptomic work.

Applications are invited from students with a suitable degree in biological sciences for a studentship to investigate *Daphnia* immunity and coevolution. There is also

ample scope to widen the research towards other aspects of the ecology, evolution or molecular evolution of *Daphnia* and their parasites

The dynamics of cross species transmission in multi-host systems

The dynamics of infectious disease have often been studied in single host species infected by a single parasite species, and yet the majority of parasites can infect more than one host species. These multi-host pathogens are associated with emerging infectious diseases (EIDs), which pose great risks to human health and biodiversity. The likelihood of disease emergence from a reservoir species will depend on dynamic processes determined by both between- and within-species transmission rates. The long-term consequences of cross species transmission are hard to predict and range from transient, non self-sustaining "spillover" events (Hantavirus) to persistent self-sustaining epidemics (HIV). Ecological and evolutionary forces acting on both hosts and pathogens will influence these long-term consequences. However, the factors that constrain or facilitate such emergences are poorly understood.

The aim of this project is to understand the ecological and evolutionary conditions that determine the dynamics of cross species transmission in multi-host systems. While most research on disease emergence occurs after the event, here the student will use a tractable laboratory system to (1) measure rates of cross species transmission, (2) determine the ecological and evolutionary factors that favour transmission, and (3) ultimately make predictions about when and where cross species transmission is likely to cause novel disease emergence. The research will focus on a model multi-insect multi-virus system, consisting of stored food moths and their associated baculoviruses.

While the research will be focused on this insect system, on-going projects in my group also include (1) experiments with wild rodent populations and their parasite communities and (2) comparative studies of disease emergence in primates and humans. Both research areas incorporate multi-host pathogens, allowing for broad cross-system investigations of the dynamics of cross species transmission. Given the recent surge of EIDs, understanding the dynamics of disease persistence in novel hosts has never been more important.

Evolution and coevolution in amoeba and their bacterial parasites

Host-parasite coevolutionary interactions may impact population densities, genetic diversity and breeding systems. Outside of a few carefully controlled laboratory systems, we have little appreciation of coevolutionary

dynamics. Are frequency-dependent cycles common, or does coevolution occur in random busts? Does environmental noise overwhelm genetic interactions? We have recently initiated evolutionary studies on a set of interactors that are highly amenable to study in the wild: *acanthamoeba* and amoeba-resisting bacteria. We hope to continue this work with a focused PhD.

Applications are invited from students with a suitable degree in biological sciences for a studentship to investigate amoeba-bacteria interactions and coevolution. There is also ample scope to widen the research towards almost any aspects of the ecology or evolution of these biological enemies.

Tom Little Wellcome Trust Senior Research Fellow in Basic Biomedical Sciences

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## UEdinburgh TreeEvolution

Evolution in the Scottish Highlands: have forest trees adapted to local environments ?

Individuals should send a CV and a personal statement of research interests and aims directly to: Dr. Richard Ennos [rennos@ed.ac.uk](mailto:rennos@ed.ac.uk) (see [www.findaphd.com](http://www.findaphd.com) Search: pine edinburgh)

Recent work has shown that populations of Scots Pine are phenotypically different. However, because the species migrated north to Scotland from continental Europe after the end of the last Ice Age, the variation we see may be no more than a reflection of the different origins of the earliest migrants. Disentangling the effects of population history and natural selection in this species is the key to understanding its genetic diversity, and to the long term protection of the last fragments of the ancient Caledonian Forest. Resolving the influence of these two forces is a key question in contemporary evolutionary research and is of keen interest in fields from bacterial to human biology. This project will combine the power of next-generation sequencing technology and classical genetics to examine the history and origins of the last remnants of the original Scots Pine forests in Scotland and test for adaptive responses to the wide environmental spectrum the tree

meets on these sites. By engaging directly with Forest Research, the successful candidate will help to define adaptive management strategies for the species to ensure resilience of the species to projected environmental change.

Specifically, the project will: 1. Use high-throughput sequencing to characterise variation across more of the Scots Pine mitochondrial genome than any previous study, and use this data to resolve the historical origins of the Scottish populations. 2. Use experimental approaches to probe adaptive differentiation among populations, by a combination of detailed phenotyping, stress-testing and quantitative genetics.

The project will be jointly supervised by Dr. Richard Ennos (University of Edinburgh), Dr. Stephen Cavers (Centre for Ecology and Hydrology, Edinburgh) and Dr. Joan Cottrell (Forest Research, Edinburgh).

[scav@ceh.ac.uk](mailto:scav@ceh.ac.uk) [scav@ceh.ac.uk](mailto:scav@ceh.ac.uk)

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## UHouston Evolution

### GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Biology and Biochemistry at the University of Houston (UH) welcomes applications for its graduate program in Evolutionary Biology and Ecology for Fall 2010. The following faculty in the area of Evolutionary Biology and Ecology are seeking graduate students for their labs:

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



2010, but students are encouraged to apply as soon as possible.

razevedo@uh.edu razevedo@uh.edu

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## UKiel FishStressEvolution

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

### \*JobDescription\*

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 *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.

### \*Qualification\*

We request a Msc or Diploma degree in (Marine) Biology, Evolution, Ecology, Genetics, Aquaculture or a related subject.

Basic knowledge in molecular genetic techniques is required, advanced knowledge in transcription profiling is desirable, as is experience in cultivating marine organisms or fish.

Candidates with a freshwater background are also encouraged to apply, provided they commit to entering the marine world.

This is a half time position is initially available for a period of 30 months. The salary depends on qualification up to the class 13 TV-L of the German tariffs for public employees (approximately 25 000 Euro gross).

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 10 February 2010 by e-mail using the keyword "fish gene expression" to the following addresses:

Prof. Reinhold Hanel ([reinhold.hanel@vti.bund.de](mailto:reinhold.hanel@vti.bund.de)) and Prof. Thorsten Reusch ([treusch@ifm-geomar.de](mailto:treusch@ifm-geomar.de))

Please give name and address of two references and enclose a letter of motivation.

Questions are answered by Prof. Reinhold Hanel ([reinhold.hanel@vti.bund.de](mailto:reinhold.hanel@vti.bund.de)) or Prof. Thorsten Reusch ([treusch@ifm-geomar.de](mailto:treusch@ifm-geomar.de))

[treusch@ifm-geomar.de](mailto:treusch@ifm-geomar.de) [treusch@ifm-geomar.de](mailto:treusch@ifm-geomar.de)

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## ULiverpool Experimental Evolution

NERC-funded PhD position to study "parasite life history evolution" using experimental evolution with microbes at the University of Liverpool, UK

Project: Genetic basis of parasite life-history evolution  
Supervisors: Steve Paterson and Mike Brockhurst.  
Start date October 2010.

Description: Parasites have the ability to rapidly adapt to their hosts, a process that is critical to understanding and controlling infectious disease. One important challenge from a practical perspective is to understand how parasite virulence (the damage they cause to hosts) and infectiousness (the ability to establish new infections) evolve in response to changes in host ecology. In this project we will examine the genes responsible to changes in key life-history traits, such as virulence and transmission, and how these genes evolve in response to changes in host density, quality, etc. We will use an experimental bacteria-phage system in which we can; observe evolution over the course of days rather than years, control the ecology of both host and parasite, and freeze populations to trace evolution back through time. This experimental evolution system will be combined with molecular and population genetic methods, which are a novel and exciting, approach that has re-



cently led to a publication in Nature from our group.

Training for both projects will be provided in: microbiology, molecular ecology, evolutionary genetics, statistics, bioinformatics, molecular biology, and sequencing. There is considerable flexibility within the project for the student to develop his/her own interests, with guidance and support from the supervisors.

Informal enquiries to: [brock@liv.ac.uk](mailto:brock@liv.ac.uk) or to [s.paterson@liv.ac.uk](mailto:s.paterson@liv.ac.uk)

Positions available to UK citizens and EU nationals that have been resident in the UK for at least 3-years, and have at least a 2:1 Honours degree (or EU equivalent). Application details and further details on department and staff are available at: <http://www.liv.ac.uk/biolsci> Enquiries about application procedure to: [biolres@liv.ac.uk](mailto:biolres@liv.ac.uk) For more information on the lab and our research: <http://sites.google.com/site/brockhurstlabliverpool/Home> References: Paterson S, Vogwill T, Buckling A, Benmayor R, Spiers AJ, Thomson NR, Quail M, Smith F, Walker D, Libberton B, Fenton A, Hall N, and Brockhurst MA (2010) Antagonistic coevolution accelerates molecular evolution. Nature in press

Brockhurst MA, Morgan AD, Fenton A and Buckling A (2007) Experimental coevolution with bacteria and phage: The *Pseudomonas fluorescens*-phi2 model system. *Infection, Genetics and Evolution* 7, 547-552

Paterson, S and Barber, R (2007) Experimental evolution of parasite life- history traits in *Strongyloides ratti* (Nematoda). *Proceedings of the Royal Society B, Biological Sciences* 274, 1467-1474

[Michael.Brockhurst@liverpool.ac.uk](mailto:Michael.Brockhurst@liverpool.ac.uk)  
[Michael.Brockhurst@liverpool.ac.uk](mailto:Michael.Brockhurst@liverpool.ac.uk)

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## ULondon UKent 2 CulturalEvolution

Two Linked PhD Studentships:

Human Cultural Transmission: From Psychology Lab To The Artefactual Record Queen Mary, University of London and University of Kent (UK)

Applications are invited for two linked Leverhulme Trust-funded, 3-year PhD studentships for the project Human Cultural Transmission: From Psychology Lab To The Artefactual Record.

The two scholarships cover all tuition fees at UK/EU

rates plus an annual tax-free stipend of approximately 15,000. The aim of this project is to use a combination of experimental and analytical methods to explain the cultural evolution of prehistoric artefacts. Experimental methods will be used to simulate the cultural transmission of computer-generated and physical-replica Acheulean handaxes along chains of participants in the lab. Specific studies will address the influence of perceptual and motor constraints on artefact transmission, the effect of social learning mechanism (e.g. imitation, teaching), and the role of intergroup boundaries. The resulting data will be analysed using a range of evolutionary-based methods (e.g. phylogenetic analyses, cultural evolution models, agent-based simulations) allowing quantitative comparison with actual prehistoric Acheulean datasets. One student, supervised by Dr Alex Mesoudi and based at Queen Mary, University of London, will specialise in computer-based experiments, psychological theory and mathematical/agent-based models. The other, supervised by Dr Stephen Lycett and based at the University of Kent, will specialise in physical (non-computerbased) experiments, archaeological theory and phylogenetic analyses. Regular meetings between both sets of students and supervisors will encourage inter-disciplinary interaction. Both students will acquire expertise and key skills across a range of disciplines, including biological anthropology, archaeology and psychology. Applications are invited from candidates with, or expecting to obtain, at least an upper-second class honours degree in an area relevant to the project (e.g. psychology, archaeology, anthropology, biology). Candidates with suitable MSc training are particularly welcome to apply. Applications will be considered separately for each studentship. Applicants may apply for both positions, but should apply separately and demonstrate in each case how they are suitably qualified.

The application deadline for both studentships is 1st March 2010. Interviews will be held in April for a 1st Sept 2010 start date. Funding covers fees and tuition for UK/EU students, although international students may be eligible depending on circumstances. Please direct informal enquiries to either Dr Alex Mesoudi ([a.mesoudi@qmul.ac.uk](mailto:a.mesoudi@qmul.ac.uk)) or Dr Stephen Lycett ([S.J.Lycett@kent.ac.uk](mailto:S.J.Lycett@kent.ac.uk)).

Studentship 1 (Queen Mary, University of London)  
 Supervisor: Dr Alex Mesoudi ([a.mesoudi@qmul.ac.uk](mailto:a.mesoudi@qmul.ac.uk);  
<http://sites.google.com/site/amesoudi2/>) Home  
 department: Biological and Experimental Psychology Group, School of Biological and Chemical Sciences, Queen Mary, University of London  
 Application Deadline: 1st March 2010 Start Date: 1st September 2010 Apply online via this link:

<http://www.sbcs.qmul.ac.uk/prospectivestudents/-research/studentships/> You will be required to upload degree transcripts, a CV, contact details of two referees, and a statement of purpose/cover letter (N.B. a research proposal is not required for this studentship).

Studentship 2 (University of Kent) Supervisor: Dr Stephen Lycett (S.J.Lycett@kent.ac.uk; <http://sites.google.com/site/sjlycett/>) Home department: Department of Anthropology, University of Kent, Canterbury Application Deadline: 1st March 2010 Start Date: 1st September 2010 How to apply: interested applicants should in the first instance contact Dr Lycett via email with a CV, contact details of two referees, and a statement of purpose/covering letter (N.B. a research proposal is not required for this studentship). To be considered eligible for this studentship, applicants are also required to submit a standard post-graduate application to the University of Kent via: <http://www.kent.ac.uk/studying/postgrad/-apply/apply.html> Send instant messages to your online friends <http://uk.messenger.yahoo.com> Alan McElligott <amcellig1@yahoo.ie>

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## UMadrid

### Evolutionary Behavioral Genetics

PhD position Complutense University Madrid // Evolutionary Behavioral Genetics

A PhD position will be available in the Vertebrate Biology and Conservation Group at the Complutense University Madrid as of autumn 2010. The 4-year position is financed by the Spanish Ministry of Science and Innovation (FPI programme) and is part of a research project entitled '\$B!H(BGenetic and environmental control of partial migration in the blackcap (*Sylvia atricapilla*)'. This project is studying the control of bird migration using a multidisciplinary approach integrating remote sensing techniques in the field, experimental work with birds in captivity and physiological and genetic analyses of behaviour under different controlled environmental conditions. The aim is to obtain a better understanding of the mechanisms underlying current changes in bird migration in response to climate change and to predict future evolutionary response. The PhD project will specifically study the diversity, function and evolution of genes linked to migratory behaviour, and will be conducted in collaboration with researchers at the department of Behavioural Ecology and Evolution-

ary Genetics at the Max Planck Institute of Ornithology (Seewiesen, Germany). We look for a highly motivated student with an interest in evolutionary biology and experience in molecular genetic work.

If you are interested in this position contact Francisco Pulido (f.pulido@bio.ucm.es) attaching your curriculum vitae and a statement of research interests. For more details on our group see our webpages ([http://www.ucm.es/info/zoo/bcv\\_eng/index.html](http://www.ucm.es/info/zoo/bcv_eng/index.html)).

The call for the 2010 FPI programme is about to be published (mid January 2010), and the deadline for applications will be 15 days after its publication. Details and conditions of this programme are found at [http://web.micinn.es/contenido.asp?menu1=-1&menu2=&menu3=&dir=03\\_Plan\\_IDI/00-LIAs/-00@LIARRHH/00-Formacion/00-FPI](http://web.micinn.es/contenido.asp?menu1=-1&menu2=&menu3=&dir=03_Plan_IDI/00-LIAs/-00@LIARRHH/00-Formacion/00-FPI)

Francisco Pulido

Vertebrate Biology and Conservation Department of Zoology, Faculty of Biology Universidad Complutense de Madrid E-28040 Madrid, Spain

Tel.: (0034) 91 394 49 49 Fax: (0034) 91 394 49 47

email: f.pulido@bio.ucm.es web: [http://www.ucm.es/info/zoo/bcv\\_eng/eng\\_fpulido.html](http://www.ucm.es/info/zoo/bcv_eng/eng_fpulido.html) FRANCISCO PULIDO DELGADO <f.pulido@bio.ucm.es>

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## UMissouriColumbia CompGenomics

Graduate research assistantship in computational comparative genomics.

The University of Missouri's Informatics Institute (MUII) is accepting applications to the Doctoral Program in Informatics (<http://muii.missouri.edu/-index.php?pid=3D3>). Deadline for application is March 1. As part of this program, one research assistantship is available in my laboratory. Potential thesis topics include a) developing evolutionary models of the processes of sequence evolution, gene duplication and gene loss in eukaryotes b) assembly and annotation of large scale sequence data (from 454/Solexa instruments) from vertebrates c) inference and analysis of metabolic and protein interaction networks using comparative genomics and d) modeling of the processes of gene duplication and metabolic adaptation in human cancers.

More information on my research interests can be found at <http://web.missouri.edu/~conantg> Infor-

mal enquiries can be made to Gavin Conant, [conantg@missouri.edu](mailto:conantg@missouri.edu)

Detailed application instructions are available at: <http://mii.missouri.edu/index.php?pid=3D14> Gavin Conant

F21C Animal Reproductive Biology Group 163B Animal Science Research Center 920 East Campus Drive University of Missouri Columbia, MO 65211 Phone: 573-882-2931 Email: [conantg@missouri.edu](mailto:conantg@missouri.edu) Web: <http://web.missouri.edu/~conantg> [conantg@missouri.edu](mailto:conantg@missouri.edu)

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## UNeuchatel PlantSystematics

A PhD position on Plant systematics is available in the Department of Evolutionary Botany at the University of Neuchâtel, Switzerland.

Topic: Systematics of the genus *Macrocarpaea* (Gentianaceae) in southern Peru and Bolivia

This research project concerns the biodiversity of the neotropical gentian genus *Macrocarpaea* in the Cordillera Central of central and southern Peru and adjacent Bolivia. Most of the ca. 25 species of *Macrocarpaea* in this region form a monophyletic group of derived position within the genus. This group has several unique characters unknown in any other group of the genus, notably winged seeds and a derived pollen type. In addition to the preparation of a taxonomic revision of the group, this project aims to answer several questions. Why and how have such unique morphological characters evolved in this geographical region? What evolutionary function do they bring to effective pollination and subsequent presumed wind dispersal? To answer such questions, extensive fieldwork will be conducted in Peru and Bolivia. Subsequent laboratory work will include molecular techniques, cytology, and anatomy including scanning electron microscopy.

The successful candidate must hold a MSc degree in Biology, have experience in plant taxonomy preferably including molecular techniques, and be independent to conduct extensive fieldwork in the tropical Andes. Candidates with proficiency in Spanish are highly welcome.

The appointment must lead to the completion of a PhD thesis within three years. The candidate will be supervised by Dr. Jason R. Grant as well as committee members from other institutions in Switzerland and abroad. The candidate will participate in the teaching of sev-

eral undergraduate laboratory exercises and excursions, and will be enrolled in the Interuniversity Doctoral Program in Organismal Biology: <http://www2.unine.ch/-dp-biol/page24151>. This is a 3-year appointment that begins August 1, 2010.

Applicants should send their applications to Dr. Jason R. Grant, e-mail: [jason.grant@unine.ch](mailto:jason.grant@unine.ch). The application should include letter of motivation, CV, copy of academic degree(s), list of publications and conference participations, copies of publications in PDF format, an abstract of research done during the MSc thesis, and the names and addresses of three references. Deadline for application is March 1, 2010.

Dr. Jason R. Grant Laboratoire de botanique évolutive, Institut de biologie Faculté de Sciences, Université de Neuchâtel Rue Émile-Argand 11, Case Postale 158 CH-2009 Neuchâtel SWITZERLAND Tel: (+41) [0] 32 718 39 58 FAX: (+41) [0] 32 718 30 01 [http://www2.unine.ch/evobot/page27279\\_en.html](http://www2.unine.ch/evobot/page27279_en.html) GRANT Jason Randall <[jason.grant@unine.ch](mailto:jason.grant@unine.ch)>

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## UOslo BirdSpermEvolution

Natural History Museum, University of Oslo PhD position: Sperm competition in passerine birds

The PhD candidate will be part of a team working on the project 'Sperm, speciation and promiscuity - An integrated analysis of evolution in passerine birds'. The PhD position is funded by NHM whereas the remaining part of the project is funded by the Research Council of Norway. Throughout the animal kingdom sperm cells are extremely diversified. In passerine birds they show strong signatures of selection by sperm competition induced by female promiscuity. The intensity of sperm competition also varies considerably among passerine species. The main aim of the project is to advance our understanding of how sperm cells evolve and diversify in a sperm competition context. The project will apply a variety of analytical tools, like in-vitro sperm motility analysis, high-resolution microscopy with digital imaging and morphometrics, advanced protein and DNA fragment and sequence analysis, and standard phylogenetic analysis and comparative statistics methods. The project includes comprehensive field work in Norway and abroad.

In addition to the PhD candidate, the project team will consist of two postdocs, on field/lab technician, a network of international collaborators and

two senior NCB scientists: Associate Professor Arild Johnsen and Professor Jan T. Lifjeld (project leader). The NCB is an interdisciplinary research centre in biosystematics and biodiversity which integrates the research groups of 11 faculty working on plants, fungi and animals. More information about NCB can be found at <http://www.nhm.uio.no/forskning-samlinger/forskning/forskningsgrupper/ncb/> The purpose of the position is research training leading to the successful completion of a PhD degree. Applicants must have a Masters degree or the equivalent in ecology or evolutionary biology, and preferably hands-on experience with relevant analytical tools as indicated above. We seek a highly motivated, enthusiastic person with the ambition to become an independent scientist through the doctoral training. The successful candidate must be prepared to spend several months in the field, especially during the first half of the employment period. The employment period is four years; starting date is 1 April 2010. Compulsory service (i.e. duty work) shall represent 25% of nominal working time.

Pay Grade: 45 - 49 (NOK 355 600 - 380 900, depending on qualifications) Application Deadline: 1 February 2010.

Informal inquiries to Professor Jan T. Lifjeld ([j.t.lifjeld@nhm.uio.no](mailto:j.t.lifjeld@nhm.uio.no)).

For further particulars and instructions on how to apply, please see the full announcement text: <http://www.admin.uio.no/opa/ledige-stillinger/-2010/vitenskapelige/phdfellowNHM-2010-102.html>  
[j.t.lifjeld@nhm.uio.no](mailto:j.t.lifjeld@nhm.uio.no) [j.t.lifjeld@nhm.uio.no](mailto:j.t.lifjeld@nhm.uio.no)

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## UOviedo AmphibianEvolution

We offer a predoctoral position funded by the Spanish Government associated to the project "Functional genetic variation and plasticity in amphibian thermal performance; a population approach to predict the impacts of global warming along altitudinal gradients" to work in evolutionary aspects of physiological ecology, growth and development of larval amphibians

Here is the link to the offer:

<http://www.uniovi.es/nicieza/projects.htm> Yours sincerely

David Alvarez Departamento de Biología de Organismos y Sistemas Unidad de Ecología Universidad de Oviedo C/ Rodrigo Uria s/n 33006-Oviedo Spain

Phone: +34-985104830 Fax: +34-985104777

E-mail: [dalvarez@innova.uniovi.es](mailto:dalvarez@innova.uniovi.es) [dalvarezf@gmail.com](mailto:dalvarezf@gmail.com) web: <http://www.uniovi.es/~dalvarez/> <http://naturalezacantabrica.blogspot.com/>  
 David Alvarez <[dalvarez@innova.uniovi.es](mailto:dalvarez@innova.uniovi.es)>

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## USheffield GrassEvolution

Opportunity for PhD study in the UK â Evolutionary Biology

Applications are invited for a PhD studentship in the Department of Animal and Plant Sciences at the University of Sheffield, UK, with the Royal Botanic Gardens, Kew as CASE partner. The studentship is funded by NERC, and provides fees and a maintenance bursary for UK nationals (or residents in the UK for the past 3 years), including an additional Â£1000 per year from the CASE partner. It will be supervised by Colin Osborne and Rob Freckleton (University of Sheffield), David Simpson (Kew), and Pascal-Antoine Christin (Brown University).

The project will investigate how ecological and functional diversity has evolved in the âAllotroopsis-forest shade cladeâ of grasses, an ecologically diverse lineage of 130 extant species. These include the worldâs most productive plant and its most important weeds, two to four evolutionary transitions between the C3 and C4 photosynthetic pathways, and the only species with C3 and C4 subspecies. The C4 pathway is a turbo-charger for photosynthesis that has evolved many times. What sequence of morphological changes and habitat transitions led to C4 evolution in grasses? And was the evolution of C4 photosynthesis associated with a shift in net diversification and the occupation of new niche space? The project is highly relevant to the current global research effort to bioengineer the C4 photosynthetic pathway in rice, which aims to boost yield in this important crop. More generally, the PhD project also aims to advance our fundamental understanding of trait evolution in the grasses.

The objectives of the project are: 1) To sequence DNA for all of the species in the clade, and use these data to construct the first complete species-level phylogeny for any grass lineage of this size; 2) To acquire information on morphological and functional plant traits, ecological niche characteristics (e.g. climate, fire regime, habitat), and geographical range for each species, and map these onto the phylogeny; 3) To reconstruct the evolution-



ary history of each of these characters, and to explore the relationships between morphological and functional trait evolution, the occupation of new ecological niche space, shifts in geographical range, and changes in the net diversification rate.

The student will be trained in the latest techniques in phylogenetics, ecological informatics and comparative methods, and will have an unrivalled opportunity to work closely with some of the world's leading experts on grasses in the herbarium at RBG Kew. The project will exploit GrassPortal a new ecological informatics resource developed by Sheffield and Kew ([www.grassportal.org](http://www.grassportal.org)).

Please feel free to contact Colin Osborne ([c.p.osborne@sheffield.ac.uk](mailto:c.p.osborne@sheffield.ac.uk)) if you have any questions about the project. To apply, please email a CV and covering letter to Colin, then make a formal application following the procedure outlined at <http://www.shef.ac.uk/aps/prospectivepg/applications.html>. The deadline for applications is 31st January 2010.

Colin's webpages: <http://web.me.com/colin.osborne/lab/home.html> Osborne, C.P., Freckleton, R.P. (2009) Ecological selection pressures for C4 photosynthesis. *Proceedings of The Royal Society, Series B*, doi:10.1098/rspb.2008.1762

Ibrahim, D.G., Burke, T., Ripley, B.S., Osborne, C.P. (2009) A molecular phylogeny of the genus *Alloteropsis* (Panicoideae, Poaceae) suggests an evolutionary reversion from C4 to C3 photosynthesis. *Annals of Botany*, 103, 127-136.

Christin, P.A., Besnard, G., Samaritani, E., Duvall, M.R., Hodkinson, T.R., Savolainen, V., Salamin, N. (2008) Oligocene CO2 decline promoted C4 photosynthesis in grasses. *Current Biology* 18, 37-43.

Colin Osborne Dept. Animal and Plant Sciences University of Sheffield

office tel: +44-114-222-0146 lab webpages: <http://web.me.com/colin.osborne/lab/home.html> blog: <http://graminology.blogspot.com/> Colin Osborne <[c.p.osborne@SHEFFIELD.AC.UK](mailto:c.p.osborne@SHEFFIELD.AC.UK)>

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## UStirling ForestConservation

Importance of waterborne seed dispersal for conservation of alder-dominated riparian woodlands

Black alder, *Alnus glutinosa* Gaertn, is the most abun-

dant native tree in Scottish riparian woodlands where it plays a key ecological role. Despite its importance in riparian ecosystem function, the reproduction and dispersal dynamics of the species has been little studied. Seeds are small and equipped with air-filled wings that enable them to float. Long-distance water dispersal of seeds for several km is therefore believed to be driven by flowing water. This project proposes to investigate the relationship between river flow dynamics and river margin colonisation by alder via waterborne seed dispersal in a river catchment using a landscape genetics approach. Field activities will be based in Scotland; in the river Tay catchment which contains large areas of undisturbed alder dominated floodplain habitat of high nature conservation value. Laboratory activities will involve genotyping of microsatellite markers to detect patterns of seed-mediated gene dispersal. The project will offer scope to develop a geographically-explicit model integrating ecological and genetics data in order to investigate how landscape characteristics, such as fragmentation by dams and flood embankments, affects dispersal distance and connectivity of alder-dominated riparian woodlands and thus inform their conservation management.

The project will require a combination of field work, molecular biology, data analysis and modeling. Individuals with an interest in ecological genetics are encouraged to apply. The successful candidate will join the restoration genetics group in the School of Biological and Environmental Sciences at the University of Stirling.

To apply please email Dr Bacles ([c.f.bacles@stir.ac.uk](mailto:c.f.bacles@stir.ac.uk)<<mailto:c.f.bacles@stir.ac.uk>>) a CV and personal statement of research interests with contact details of two referees.

Closing date for application: 15 February 2010.

The applicant MUST have a good 1st degree (at least a 2.1) and/or MSc in a relevant subject. Applications are expected all year round but those sent by 15/02/2010 will be eligible to enter our studentship competition. We expect applications to be highly competitive. Although no deadline has yet been fixed, interviews are likely to take place in February-March 2010. Self-funded students are welcome to apply at anytime (please check <http://www.findaphd.com>< <http://www.findaphd.com/> > or <http://www.sbes.stir.ac.uk/vacancies> for updates).

Cecile FE Bacles Ph.D. Lecturer in Ecological Genetics School of Biological and Environmental Sciences University of Stirling Cottrell Building 4B148 Stirling FK9 4LA Tel: +44 (0) 1786 46 ext 6897 Email:[c.f.bacles@stir.ac.uk](mailto:c.f.bacles@stir.ac.uk) <http://www.sbes.stir.ac.uk>



www.sbes.stir.ac.uk/people/bacles Registration Now Open! Ecological Genetics Group 54th Meeting 6-8 April 2010 <http://www.sbes.stir.ac.uk/egg> Cecile Bacles <c.f.bacles@stir.ac.uk>

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## U Vermont Hymenoptera Phylogenetics

An NSF-funded position for a PhD student is available in the Department of Biology at the University of Vermont (UVM), to be conducted jointly in the labs of Kurt Pickett and Bryan Ballif. Up to three and a half years of graduate research assistant (GRA) funding are available for this position. The position will involve phylogenetic and proteomic research on all yellowjackets and hornets (Insecta: Hymenoptera: Vespidae). The research focuses on the evolution of proteins across the group as it pertains to division of labor and social behavior. The candidate must have an interest in these fields, and preferred students will have experience in at least some. Technical expertise in the following is also preferred: general entomology, phenotypic (behavioral and morphological) and molecular (both genetic and protein) data gathering, phylogenetic analytical techniques, protein biochemistry and proteomic techniques especially SDS-PAGE, peptide HPLC, protein/peptide mass spectrometry and bioinformatic analyses. Interested candidates should apply online to the UVM's Graduate College at the following link: <https://www.applyweb.com/-apply/uvmg/menu.html> Specific requirements of the Department of Biology can be found here: <http://www.uvm.edu/~biology/?Page=applying.html&SM=gradsubmenu.html> The application deadline of January 15 will be waived for applications for this position.

"Kurt M. Pickett" <Kurt.Pickett@uvm.edu>

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## WakeForestU Yeast Experimental Evolution

Graduate position: A position is available in the Zeyl lab in the Department of Biology at Wake Forest University for a PhD student interested in using experimental evolution with yeast to test hypotheses and answer questions of broad relevance in evolutionary genetics. A minimum of four years' support through teaching assistantships is guaranteed, with the possibility of an additional year of support from a research assistantship or a Graduate School fellowship.

Qualifications include, in order of priority, a broad familiarity with evolutionary theory and a keen interest in testing some of it, a strong work ethic, and some experience with lab research (preferably with microbes and/or as part of an MS degree). Some acquaintance with yeast genetics and molecular biology would be an asset but are not necessary.

Western North Carolina offers the southern Appalachian mountains an hour and a half to the northwest, the most beautiful beaches and best surfing on the east coast, and a broad variety of bird, amphibian and reptile life.

Current experimental evolution projects concern the origin and maintenance of sex, the evolution of uniparental inheritance, speciation, and topics in the genetics of adaptation such as tradeoffs, epistasis and adaptive landscapes.

If interested, please contact me at [zeylcw@wfu.edu](mailto:zeylcw@wfu.edu), or visit my web page at <http://darwin.winston.wfu.edu/-zeyl/> Clifford Zeyl Associate Professor, Department of Biology Wake Forest University phone: (336) 758-4292 [zeylcw@wfu.edu](mailto:zeylcw@wfu.edu)

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UBasel FieldAssist NightingaleEvolution .....	45	WoodsHole ResAssist MicrobialEvolution .....	51
UBasel FieldAssist TurtleEvolution .....	45		

## **BamfieldMarineStation ResCoordinator**

We are searching for a research coordinator who could easily be an evolutionary biologist; they will certainly be providing logistical support to evolutionary biologists. I hope this meets your criteria. Ad below in plain text.

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Research Coordinator, Bamfield Marine Sciences Centre

The Bamfield Marine Sciences Centre seeks a motivated, service- oriented person as Research Coordinator that recognizes the time sensitive nature of field-based research. The role of the Coordinator is to facilitate research at BMSC by providing infrastructure and logistical support to a large and diverse array of visiting scientists. The Coordinator ensures regulatory compliance and promotes safe research practices at the Centre. Research at BMSC covers the full range of marine sciences with a focus on marine biology. Research programs in biology range from molecular to ecosystem levels of organization. The Centre is well-equipped with facilities for molecular biology, physiology, biomechanics, ecology and evolutionary biology. Several new buildings have substantially enhanced the available research space. Supervision of assistants during peak times will be required.

BMSC also teaches university courses 8 months/year and runs concurrent Public Education programs. An ability to coordinate conflicting demands among researchers and among programs is essential. The ideal candidate will participate in ongoing research or have

their own independent research program. Some funds and release time are available to support this research.

Desired Qualifications and certifications

PhD in a relevant field SCUBA diver Small Vessel Operator Proficiency (SVOP) Radiation Safety training Hazardous Waste training Laser Safety training Animal Care Certification (especially fish) Industrial First Aid Class 4 Driver's License Database and Website development Ability to maintain, diagnose faults, and repair scientific equipment Experience in maintaining microscopes Excellent record keeping skills Experience writing research grants

It is unlikely any one person will have all of these skills. BMSC prides itself on continuing education of staff. We encourage all talented individuals with a keen interest in Marine Science, and a desire to live in a smaller close-knit community, to apply.

Bamfield is a charming village on the outer west coast of Vancouver Island best known as a summer sport fishing destination and the northern terminus of the West Coast Trail. It has a vibrant arts and music community. In addition, it provides diverse opportunities for outdoor recreation including kayaking and surfing.

Additional information about BMSC can be found on our website [www.bms.bc.ca](http://www.bms.bc.ca) . Links to community websites can be found there.

Review of applications will begin 1.February.2010 and continue until the position is filled. The anticipated starting date is 1.April. 2010. Salary will be commensurate with qualifications with benefits and holidays. Interested applicants should send their curriculum vitae and contact information for three references along with a cover letter to

Dr. Brad Anholt, Director Bamfield Marine Sciences Centre 100 Pachena Rd, Bamfield, BC, V0R 1B0 Canada

an electronic version may be sent to director at bms.bc.ca

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

\*\*\*\*\*

Brad Anholt Director Bamfield Marine Sciences Centre 100 Pachena Road Bamfield, BC V0R 1B0 250-728-3301 x-215

director@bms.bc.ca

BMSC Director <director@bms.bc.ca>

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### East Carolina U EvolBiol Bioinformatics

The Department of Biology at East Carolina University [<http://www.biology.ecu.edu>], the third largest campus in the North Carolina University system, seeks to enhance its strengths in evolutionary biology and bioinformatics by inviting applications for a tenure-track position at the Assistant or Associate Professor level, to begin August 16, 2010. PhD required. We are looking for a broadly trained biologist with expertise in bioinformatics and computational biology. We are particularly interested in individuals with a strong background in comparative or evolutionary genomics, who can contribute to our ongoing initiative in biodiversity research [<http://sites.google.com/site/ncbiodiversity/home>]. Experience with large datasets, such as those generated through next-generation sequencing technologies, is desirable. The successful candidate is expected to develop a vigorous, externally funded research program, contribute to graduate and undergraduate teaching, and participate actively in the University's broader outreach mission. Appropriate service to the university, community and profession is expected. Applicants should submit curriculum vitae, cover letter, statements of research and teaching philosophy, and names and contact information for three current references online <[ecu.peopleadmin.com/applicants/Central?quickFind=2625](http://ecu.peopleadmin.com/applicants/Central?quickFind=2625)>. Review of applications will begin January 31, 2010 and continue until the position is filled. Graduate transcript required upon employment. For more information, please contact Dr. John Stiller, chair of the search committee [stillerj@ecu.edu].

Dr. David Rudel Department of Biology Howell Science Complex, N407A East Carolina University Greenville, NC 27858 Phone: 252-737-4257 Fax: 252-328-4178 E-mail: rudeld@ecu.edu

"Rudel, David" <RUDEL@ECU.EDU>

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### FRANCE-INRA PermanentSeniorResPosition EvolutionaryEcol

Title of the research position: Community ecology in agroecosystems: structure and persistence of communities in response to perturbations by farming, in the context of global change

Research laboratory: CEBC CNRS UPR 1934, Chizé Address: Centre d'Etudes Biologiques de Chizé, 79360, Beauvoir sur Niort, France. Contact: Vincent Bretagnolle (Director) Telephone: +33(0)5 49 09 78 17, E-mail: breta@cebc.cnrs.fr

How to apply: <http://www.inra.fr/drh/cr2010/bdd/-cr1/profil-cr1.php?codeprofil=CR1-2010-7-SPE-1> Job description: based on the current state-of-the-art, the researcher will undertake generate and publish the results of scientific research in the areas of population and community ecology and agroecology.

Level: Researcher Grade: Senior Researcher (INRA CR1)

Themes of research: community ecology in agroecosystems

Competences sought: Solid knowledge in community ecology (plant or animal) and in the ecology of trophic networks. Knowledge in agronomy. Openness towards modelling and spatial analyses. Keen interest on pluridisciplinary approaches and on collaborative research. Training: PhD or equivalent; a post-doctoral experience, preferably abroad, will be appreciated.

Context: The main drivers of global change (land use changes, climate changes, overexploitation of natural resources) operate at regional scales. European agroecosystems are simultaneously affected by these three drivers of global change. Moreover, they interact and covary to such an extent that it is becoming increasingly difficult to disentangle and to predict their joint effects on biological communities. As the dominant land use in France and in Europe, the perturbations due to farming are the key process underlying the

changes in diversity in agroecosystems. The ecological consequences of these perturbations are observable at the individual, population and community levels. The aim is to understand how the spatial heterogeneity of human activities in intensive agroecosystems affects the persistence of natural populations and the local and regional community structures. A second aim is to disentangle the effect climate change and or land use changes by analysing the relationships between landscape-prey-predators and their changes over time. The research program concerns populations and communities of species of agronomic interest because of the ecological or trophic services they provide and/or the control of crop pests (i.e. weeds, small mammals, insects). Within the context of temporally and spatially variable environmental conditions, the researcher will investigate how historic and ecological processes acting upon individuals and populations determine community patterns. The researcher will contribute to the understanding of the ecological interactions determining species coexistence and community structure, notably predation as well as intra- and inter-specific competition. He/she will also address these questions in a broader context: what management practices (notably in grasslands and other semi-natural components of agroecosystems) are compatible with both the maintenance of biodiversity and its associated ecological services at the regional level and with the economic viability of farms at the local level? The researcher will use empirical and/or modelling approaches and he/she will take part in the pluridisciplinary effort integrating biologists, agronomists, economists and sociologists at the long-term study site of the CNRS-Chizé. Resources available for the development of the candidate's research program: the long term study site is large (the cereal plain of Chizé, 450 km<sup>2</sup>) and has been studied for 15 years through the scientific programmes of the CNRS-Chizé. The biological and agronomical monitoring are both annual and exhaustive: the land use of 18 000 agricultural fields is recorded twice (spring and summer) yearly since 1994, and the abundance and distribution of insects (Coleoptera, grasshoppers) are quantified in space (using stratified sampling) and time (seasonal and/or annual); weed data on the main crops are available since 2005. Finally, inquiries on more than 130 individual farms since 2003 will shed light on the determinants (constraints, history) of farming systems and their possibilities of evolution. In total, 23 research teams (mostly from INRA) currently work at the long-term study site of Chizé in the context of many research programs (ECOGER, ADD-ANR, ESF, etc.). The researcher will take part in on-going research programs at the long-term study of Chizé and will profit from its logistics, administration and finances, as well as from

the internal scientific dynamics of the CNRS-Chizé.

Web of AGRIPPOP research team at CEBC (temporary):

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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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## HarvardU Fellowship ConservationBiol

\*About the Award \* The Sarah and Daniel Hrdy Fellowship in Conservation Biology serves to support the study of conservation biology within the Faculty of Arts and Sciences at Harvard University. The fellowship is awarded to an individual who will engage in scientific study and work in the Department of Organismic and Evolutionary Biology. The fellowship commences with an annual lecture in conservation biology by the distinguished individual chosen for the fellowship from outside Harvard University. It is the hope of the benefactors that this fellowship will have a strong and transformative effect on the study of conservation biology at Harvard, from the undergraduate to the senior teaching level.

\*Fellowship Details and How to Apply\*\* \*Each academic year the Department of Organismic and Evolutionary Biology invites both nominations and direct applications for the Hrdy Visiting Fellowship in Conservation Biology. The Hrdy Visiting Fellowship is available either at the senior faculty level or at the junior (i.e., postdoctoral) level for one or two semesters. Duties will include teaching one course and/or giving lectures in conservation biology, as well as research and collaboration with members of the Harvard community. The Fellowship includes a modest travel stipend. Applicants should contact a faculty sponsor(s), with whom they will collaborate, before applying. Applications should include a cover letter with a statement of intent, CV, and representative publications, and applicants should arrange to have three letters of reference sent.

Inquiries and applications may be sent by postal mail to:

C/O Christopher Preheim Phone: 617-384-9271 [cpreheim@oeb.harvard.edu](mailto:cpreheim@oeb.harvard.edu)

Committee for Hrdy Fellowship in Conservation Biology  
Dept of Organismic and Evolutionary Biology  
Harvard University 26 Oxford Street Cambridge, MA  
02138.

Review of applications begins on \*December 1, 2009  
and continues through January 31, 2010\*.

Harvard University is an Affirmative Action/Equal Opportunity Employer.

Christopher Preheim <cpreheim@oeb.harvard.edu>

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## INRA France 6 Population Quantitative Genetics

I thank you for diffusing this offer on Evoldir Web site - there are 6 tenured positions in genetics of population and quantitative genetics:

Ranked the number one agricultural institute in Europe and number two in the world, INRA carries out mission-oriented research for high-quality and healthy foods, competitive and sustainable agriculture and a preserved and valorised environment.

National Institute for Agricultural Research (INRA, France) is recruiting 62 Scientists through open competitions.

These recruitments are open in a wide range of scientific fields such as biochemistry, molecular biology, genomics, genetics, human and animal food and nutrition, microbiology, ecology, agronomy, cell biology, physiology, modelling, mathematics, economics, sociology, immunology, natural environments and many more.

Applications will be available until February 26, 2010.

All useful information to apply (jobs' profiles, guides for applicants) are available on: [www.international.inra.fr](http://www.international.inra.fr) (see "Join us")

For further details: [concours\\_chercheurs@paris.inra.fr](mailto:concours_chercheurs@paris.inra.fr)

Fabienne Giroux Service Recrutement et Mobilité  
[fabienne.giroux@paris.inra.fr](mailto:fabienne.giroux@paris.inra.fr)

inra Direction des Ressources Humaines 147, rue de l'Université  
75338 Paris Cedex 07 - France Tel 01 42 75 90 77 Fax 01 42 75 90 39

[www.inra.fr/les\\_hommes\\_et\\_les\\_femmes](http://www.inra.fr/les_hommes_et_les_femmes)

Fabienne Giroux <[Fabienne.Giroux@paris.inra.fr](mailto:Fabienne.Giroux@paris.inra.fr)>

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## INRA Orleans Tech Simulating Populations

A 16 month position for a computer software engineer is available at the Research Unit on Improvement, Genetics and Physiology of Forest Trees ([http://www.orleans.inra.fr/les\\_unites/ur\\_agpf](http://www.orleans.inra.fr/les_unites/ur_agpf)) at INRA Orleans (France).

Computer programs were developed in FORTRAN (95) to simulate the genetic evolution of populations subjected to artificial selection. The recruited engineer will be in charge of 1) adding new methods for genotypic evaluation to the simulation program on the basis of algorithms provided by the scientific team and testing their implementation with various sets of parameters 2) the development of a graphical interface to facilitate the use of the simulation tool by breeders. The position is opened in the framework of WP3 "Designing and implementation of improved/novel tree breeding strategies" of NovelTree European research project (<http://www.noveltree.eu/index.php>). The simulation tool resulting from this work will be used in priority to optimize the poplar breeding strategies managed by the Research Unit but will also be of interest for other forest tree species.

Starting date should be as soon as possible after March 1st 2010. The application deadline will be February 20 2010.

Job details Collect, adapt and optimize existing statistical routines found in scientific literature or public repositories to implement them in the simulation program. These routines concern the BLUP (Best Linear Unbiased Prediction) methodology, which uses genetic relationships from a given pedigree to predict individual breeding values in a breeding population. In order to use genotypic data to predict breeding values, write routines and test them by simulation in the framework of the existing simulation program. This will comprise the generation of IBD (identity By descent) matrices at marker and QTL positions and their integration in the BLUP evaluation. Some parts of the software will be validated by comparison with commercial tools (AS-Reml, Gibbs samplers for genetic mixed models, etc.). Conceive an interface facilitating the use of the simulation tool by breeders, in connection with potential users, and build it.



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

**Education and training** Master degree in computer sciences

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

**Gross salary:** 1915 euros monthly

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

– Helene Muranty Chargee de Recherches Tel : 33 (0)2 38 41 78 47 - Fax : 33 (0)2 38 41 78 79 UR INRA Amélioration Genetique et Physiologie Forestieres, 2163 avenue de la Pomme de Pin - CS40001 - Ardon, 45075 ORLEANS CEDEX 2, FRANCE

Helene.Muranty@orleans.inra.fr

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### **KewGardens Mycologist**

**Title:** Senior Researcher in Fungal Conservation/Restoration Ecology - Jointly funded by Natural England and The Royal Botanic Gardens, Kew.

**Status:** Permanent. **Salary per annum:** £30,742 - £40,864. **Location:** Kew Gardens. **Closing date:** Friday 15th January 2010 **Interview date:** Tuesday 26th January 2010

**Skills & competencies:** Proven good working knowledge of fungi, especially the larger basidiomycetes. Ability to communicate complex scientific and conservation management issues clearly and simply. Ability to plan and manage research programmes, both in collaboration and with a high degree of independence; to establish a network of collaborators, promote research internationally, and obtain funding. Ability to work efficiently in teams, but also working independently to deliver specific tasks when required. Ability to make convincing and effective public presentations. The self motivation required to successfully complete research

programmes on time and on budget. Ability to use relevant lab-based technical skills and handle specimens with appropriate care. Working knowledge of a GIS package such as MapInfo, use of databases, and web page design and management.

**Application:** [http://www.kew.org/about-kew/jobs/ref\\_SeniorResearcherInFungalConservationRestorationEcologynew243](http://www.kew.org/about-kew/jobs/ref_SeniorResearcherInFungalConservationRestorationEcologynew243).

m.bidartondo@imperial.ac.uk

m.bidartondo@imperial.ac.uk

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### **SmithsonianInst MolecularSystematicsTech**

#### **MOLECULAR SYSTEMATICS TECHNICIAN**

National Museum of Natural History and Laboratories of Analytical Biology, Smithsonian Institution

The Ant Lab at the Smithsonian Institution (<http://entomology.si.edu/SIAntLab.html>) is looking for a technician to assist in molecular systematic research on fungus-growing ants. The work will be carried out primarily at the Smithsonian’s Laboratories of Analytical Biology (LAB) facility in Suitland, MD. Skills required include experience with molecular laboratory techniques (including DNA extraction, PCR, and DNA sequencing) and an ability to work independently. This position is available starting January 15th for a minimum of 6 months with the possibility for renewal. To apply, please email a copy of your CV and contact information for at least two references to Natasha Mehdiabadi (Mehdiabadi@si.edu).

Natasha Mehdiabadi Research Associate

**USPS ADDRESS:** Department of Entomology Smithsonian Institution PO Box 37012 NHB, MRC 188, Rm. CE-518 Washington, DC 20013-7012

**ADDRESS FOR PRIVATE CARRIERS ONLY** (e.g., FedEx, UPS, DHL): Smithsonian Institution National Museum of Natural History, CE-518 10th & Constitution Aves. NW Washington, DC 20560-0188

**Tel.:** 202-633-1002 (Office), 301-238-1078 (Lab) **Fax:** 202-786-2894 **Email:** Mehdiabadi@si.edu **Website:** <http://entomology.si.edu/StaffPages/mehdiabadi.htm> “Mehdiabadi, Natasha” <Mehdiabadi@si.edu>

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## SyracuseU SummerRes PlantInsectEvolution

Undergraduate Summer Research Position Evolutionary Ecology

Syracuse University Syracuse, NY

We are seeking undergraduates interested in gaining hands-on research experience studying the interactions between plants and insects. The project will involve both field and laboratory research. Field research will be conducted at the Archbold Biological Station in Lake Placid, Florida for 4-8 weeks. Travel to and housing in Florida will be paid in addition to an hourly salary (\$8-\$10/hr). Laboratory research will be conducted at Syracuse University in the Department of Biology after returning from Florida. Job duration is 8-10 weeks and is full-time.

On-the-job training will be provided and no research or field experience is required. Applicants should be planning an ecology/evolutionary biology career and have taken at least one of the following courses: Evolution, Ecology, Population Biology, Field Biology, Entomology, Botany, or an OTS course. Applicants must enjoy working outside and should not have an aversion to handling insects. The start date is late April-early May (non-negotiable).

Interested applicants should send a statement of interest, résumé, transcript, one letter of recommendation, and contact information for two additional references. The statement of interest should be less than 500 words with the following information: (i) career goals, (ii) interest in position, and (iii) statement agreeing to commit to the research position for 10 weeks without other obligations.

Send application materials in one PDF or .doc file to Dr. Kari Segraves (ksegrave@syr.edu). Letters should be e-mailed directly from the recommender with the applicants name in the subject line. Incomplete applications will not be considered. The position will be filled no later than Mar 30, 2010.

ksegrave@syr.edu ksegrave@syr.edu

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## UAlgarve BioinformaticsTech

Job: Bioinformatics Technician - CCMAR, UALG, Portugal

The Centre for Marine Science (CCMAR - <http://ccmar.ualg.pt/>) at the University of the Algarve, Portugal (<http://www.ualg.pt>) seeks candidates for a technician level position (with the possibility for committed and qualified candidates to later apply for a PhD fellowship). We seek candidates with a background in computer science and a strong interest in bioinformatics analysis to implement bioinformatic tools to analyze high-throughput transcriptomic (gene expression) data generated by next generation sequencing platforms. The data come from several ongoing projects; transcriptional profiling of polar eukaryotic phytoplankton communities, and krill (crustacea) from the Southern and/or Arctic Oceans, environmental genomics and stress-responsive gene expression in intertidal brown macroalgae. Our group is mainly interested in ecological and evolutionary genomics, in particular the responses of communities / species to predicted global change scenarios. Hence an interest in evolutionary biology, ecology and/or genomics would be an advantage.

The successful applicant will be adaptable and committed, ideally with a working knowledge of relational databasing, a cross-platform scripting language (Python/Perl/Java), and experience working with biological sequence data.

Applications should be submitted by February 15, 2010, to Gareth Pearson (gpearson@ualg.pt) or Cymon J. Cox (cymon@ualg.pt). Applicants should send a covering letter detailing their research interests, a current C.V., copies of their degree certificates, copy of passport or national identity card, and the email addresses for 3 professional referees. Informal enquires are welcome to the same address.

The technician position is a tax-free fellowship, starting at 750 euros per month for 6 months initially, which may be renewed for an extended period pending on performance assessment.

CCMAR is located on the Gambelas campus, 4km from Faro, the capital city of the Algarve and close to Faro International Airport (FAO). ([http://www.ualg.pt/-index.php?option=3Dcom\\_google\\_maps&Itemid=3D2311&lang=en](http://www.ualg.pt/-index.php?option=3Dcom_google_maps&Itemid=3D2311&lang=en))

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 cymon.cox@googlemail.com

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## UBasel FieldAssist NightingaleEvolution

Field assistants in Evolutionary Ecology of Nightingales

Four field assistant positions are available in an international research project on communication and evolutionary ecology of nightingales (*Luscinia megarhynchos*).

The project is run by the Research Station Petite Camargue Alsacienne, University of Basel ([www.camargue.unibas.ch](http://www.camargue.unibas.ch), PD 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 May 2010, 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.

Field assistants will participate in systematic surveys of territory settlement and in an extensive radio telemetry study. 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 for the entire field season, which should cover travel and food expenses. Applicants are expected to stay for the entire field season from the beginning of April until the end of May. 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. 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 address:

Valentin Amrhein [v.amrhein@t-online.de](mailto:v.amrhein@t-online.de)  
 valentin amrhein <[v.amrhein@t-online.de](mailto:v.amrhein@t-online.de)>

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## UBasel FieldAssist TurtleEvolution

Field assistant in evolutionary ecology of European swamp turtles

We are looking for a field assistant to participate in a conservation project on European swamp turtles (*Emys orbicularis*) from May to July 2010 at the Research Station Petite Camargue Alsacienne in France ([www.camargue.unibas.ch](http://www.camargue.unibas.ch)).

The work will include caring for the about 80 swamp turtles living in the station's outdoor enclosures, capturing the turtles, observing breeding behaviour, locating nests and collecting eggs for artificial incubation in the lab. The applicant is expected to stay for the entire field season from the beginning of May until the end of July. Applicants should have some knowledge of French or German.

The field site is situated in the nature reserve Petite Camargue Alsacienne in France, about 10 km north of Basel (Switzerland). We cannot cover travel expenses, but we offer free accommodation and use of the infrastructure at the research station. The assistant will receive 400 Euros to cover living expenses.

The position will be filled as soon as possible. Applications should be in English, French or German, and should include, in one single pdf or word file, a curriculum vitae and a letter of motivation. 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 address:

Valentin Amrhein [v.amrhein@t-online.de](mailto:v.amrhein@t-online.de)  
 valentin amrhein <[v.amrhein@t-online.de](mailto:v.amrhein@t-online.de)>

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## UBern BirdFertility

University\_\*\*\_of Bern\_\*\*\_: Field assistants Bird fertility / Maternal effects

We are seeking 4 enthusiastic field assistants interested in taking part in field studies in Bern, Switzerland. Applicants will be part of the evolutionary ecology team (Institute of Ecology and Evolution, University of Bern). Our study models are the great tit and the house sparrow. The tits are a good model system since they are hole nesting birds, breeding in forests near Bern, and 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.

Two studies will aim at investigating the relationship between sperm quality, secondary sexual signals and oxidative stress and heritability of these traits in the great tit and the house sparrow. Another experiment with great tits will be assessing the effects of maternal hormones and hatching asynchrony on offspring fitness.

We will require 4 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, takes place in changing weather and requires long hours at times. The study will start at the end of March 2010 until the beginning of June 2010. Fluent English or French speaking and a valid European driving license are required.

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

\*Sylvain Losdat\* Institute of Ecology and Evolution University of Bern Baltzerstr. 6 3012 Bern Switzerland Email: [sylvain.losdat@iee.unibe.ch](mailto:sylvain.losdat@iee.unibe.ch) Phone: +41316313020 Mobile: +41774565214

\*Katarzyna Podlas\* Institute of Ecology and Evolution University of Bern Baltzerstr. 6 3012 Bern Switzerland Email: [podlas.kasia@gmail.com](mailto:podlas.kasia@gmail.com) Phone: +41316313020 Mobile: +41787695209

Sylvain Losdat <[sylvain.losdat@iee.unibe.ch](mailto:sylvain.losdat@iee.unibe.ch)>

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## UBritishColumbia ComparativeZoologyInstructor

### TENURE TRACK INSTRUCTOR POSITION IN COMPARATIVE ZOOLOGY

The Department of Zoology at the University of British Columbia (Vancouver, Canada) is seeking candidates to fill a tenure-track Instructor position to coordinate and teach the laboratory portions of courses in Vertebrate Structure and Function and Comparative Invertebrate Zoology.

Successful candidates will demonstrate (1) evidence of outstanding teaching, (2) a high level of expertise in the subject areas, and (3) the ability to contribute to ongoing course redevelopment. Teaching experience in

comparative zoology (e.g., comparative anatomy, animal diversity, evolutionary morphology, phylogenetics, and marine biology) and a PhD in a relevant area of biology or a combination of qualifications and experience is required.

The duties of the position include coordinating and teaching the laboratory portions of two large-enrolment (approximately 250 student) courses in “Vertebrate Structure and Function” and “Comparative Invertebrate Zoology”, contributing to course redevelopment, and to the training and supervision of graduate student teaching assistants. There are also opportunities to work in collaboration with the Carl Wieman Science Education Initiative ([www.cwsei.ubc.ca](http://www.cwsei.ubc.ca)).

Interested candidates should submit a letter of application, a curriculum vitae, a statement of teaching philosophy, an outline of teaching interests, evidence of teaching effectiveness, and the names and contact information for at least three individuals who would be willing to provide letters of reference. An explicit outline of the courses taught, the year in which each course was taught, course class size, and student evaluations should be included in the application. Candidates are particularly encouraged to highlight previous experience in fostering the education of students from diverse backgrounds. Please send applications to <http://hr.ubc.ca/careers/faculty.html> All application packages should be sent in electronic format as a single PDF document. Questions may be sent to [jobs@zoology.ubc.ca](mailto:jobs@zoology.ubc.ca)

The closing date for applications is February 28, 2010, with appointments anticipated to begin by September 1, 2010.

The University of British Columbia hires on the basis of merit and is committed to employment equity. All qualified persons are encouraged to apply; however, priority will be given to Canadian citizens and permanent residents of Canada.

Brian S. Leander Associate Professor Department of Zoology University of British Columbia #3529-6270 University Blvd. Vancouver, BC V6T 1Z4 CANADA

Web: <http://www.botany.ubc.ca/bleander/-index.html> Email: [leander@zoology.ubc.ca](mailto:leander@zoology.ubc.ca) or [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)

[bleander@interchange.ubc.ca](mailto:bleander@interchange.ubc.ca)

702-1533 <http://pondside.uchicago.edu/ecol-evol/people/ruvinsky.html> Ilya Ruvinsky  
<ruvinsky@uchicago.edu>

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## UChicago ResTech NematodeEvolution

A full-time Research Technologist position is available for a scientist in the Department of Ecology and Evolution at the University of Chicago.

<http://ruvinskylab.uchicago.edu/index.html> Job responsibilities include manipulation of nematode strains, basic molecular biology techniques (PCR, cloning, etc.) and microscopy. In addition, ordering of supplies and laboratory maintenance will be expected.

Bachelor's degree in biology or related field required; previous laboratory experience with molecular biology is required; experience with model organism genetics preferred; familiarity with genetics is required; knowledge of computers, including word processing, spreadsheet and database programs, is required; excellent communication and organizational skills are required; high level of motivation and strong interpersonal skills required; desire to learn new skills and work independently required.

Salary will be commensurate with experience and will include benefits.

The University of Chicago is a premier research institution located in Hyde Park, a vibrant and diverse community within close distance of the downtown Chicago. This location offers unparalleled access to intellectual, cultural and recreational resources of a major metropolitan center.

A cover letter, curriculum vitae/resume and reference contact information (names and contact information, including phone numbers, of three people who agreed to be references) are required to be considered for this position.

Please apply online at:

[jobopportunities.uchicago.edu](http://jobopportunities.uchicago.edu)

Requisition # 083910

The University of Chicago is an Affirmative Action/Equal Employment Opportunity Employer

– 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)

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## UNorthCarolina Wilmington NatHistoryAssistCurator

The University of North Carolina Wilmington has created a temporary full time position (up to 24 months) for an Assistant Curator of Natural History Collections, part of an NSF Biological Infrastructure grant. This is an opportunity for an individual to assist in upgrading and enhancing the availability of the university's collections and to support the university in training and mentoring undergraduate students in professional scientific curating. The ad follows below:

Assistant Curator of Natural History Collections, UNC-Wilmington

The University of North Carolina Wilmington (UNCW) seeks an Assistant Curator for the David J. Sieren Herbarium. The position will be a temporary full-time 12-month appointment with full benefits. The position is subject to renewal for an additional 12 months depending on the incumbent's performance. The annual salary will be \$35,000 and the starting date for the position is March 2010.

This position involves working closely with faculty curators of the various university natural history collections (algae, fish, birds, etc.) and directing undergraduate students. The successful applicant will oversee the transition of UNCW's collections to an electronic format using the program Specify to create databases of specimens, digitized images of specimens, and georeference information. He/she will also catalog and curate specimens, order and organize new equipment, update safety protocols, and direct the design of web pages for the collections.

Organizational and effective verbal communication skills, basic computer knowledge, database management, and related skills are required. Applicants with a minimum MS or MA degree in biology or a related discipline and a strong background in plant taxonomy are especially encouraged to apply. Previous experience with Specify is preferable. To apply, complete the online application process at <http://consensus.uncw.edu> <<https://mail.uncw.edu/exchweb/bin/redir.asp?URL=http://consensus.uncw.edu>> by electronically submitting separately (1) a letter



of application including a statement of collection-based experience and research interests, (2) a curriculum vitae, and (3) contact information for three professional references. MS Word or PDF attachments are preferred. For questions about the position, contact Paul E. Hosier, Search Chair, [hosier@uncw.edu](mailto:hosier@uncw.edu) <<mailto:hosier@uncw.edu%20>> or (910) 962-2642. For questions about the online application process, contact Ms. Tracie Chadwick, [chadwickt@uncw.edu](mailto:chadwickt@uncw.edu) <<mailto:chadwickt@uncw.edu>> or (910) 962-3536. The application process will close on 15 February 2010. UNCW actively fosters a diverse and inclusive working and learning environment and is an equal opportunity employer. Qualified men and women from all racial, ethnic, or other minority groups are strongly encouraged to apply.

Thanks,

Dr. Marcel van Tuinen, Assistant Professor 1051 Friday Hall, Department of Biology & Marine Biology, University of North Carolina at Wilmington, office: 910-962-2178

“Van Tuinen, Marcel” <[vantuinenm@uncw.edu](mailto:vantuinenm@uncw.edu)>

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### UOxford ResearchFellowship PlantEvolution

Department of Plant Sciences, University of Oxford,  
Independent Research Fellows Event 2010

The Plant Sciences Department, University of Oxford, is an internationally leading centre of excellence in plant sciences, ranked equal third of 52 UK Biological Sciences research institutions in RAE 2008 and 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 on 4th and 5th May 2010. 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 are available on the Department of Plant Sciences website [www.plants.ox.ac.uk](http://www.plants.ox.ac.uk) Please email a two-page summary of your research plan and your CV and arrange for two letters of recommendation to be emailed to [debbie.reeves@plants.ox.ac.uk](mailto:debbie.reeves@plants.ox.ac.uk) by noon on Friday 12th March.

John Pannell <[john.pannell@plants.ox.ac.uk](mailto:john.pannell@plants.ox.ac.uk)>

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### UPennsylvania SummerResAssist DiseaseEvolution

Job announcement Disease Ecology and Evolution Project Assistant (April-September) University of Pennsylvania

Full-time Project Assistants (paid) are needed for research on the ecology and evolution of the Lyme disease bacterium in Southeastern Pennsylvania. Research in the Brisson laboratory focuses on the evolving interactions among bacteria, ticks, and animal hosts, that influence Lyme disease prevalence. Duties include live-trapping small mammals and birds and sampling tick abundance to assess infection status. Early morning, moderately strenuous activity is required. Field research is conducted in small teams in Crow's Nest Preserve, PA - about 45 minutes west of Philadelphia. Prior experience handling wild small mammals or birds is highly desirable; strong work ethic, meticulousness, and ability to work both independently and in small teams is required. The project offers research and learning experiences for Project Assistants, particularly with regard to the ecology and evolution of infectious diseases.

Desired dates of employment (35 hours/week): April 12 to September 12, 2010, although applicants available during summer break from college are also welcome. Wage is commensurate with education experience. Near-site housing is available.

Consideration of applications will begin on Feb 23rd. Please submit via email a brief letter of application, a resume, and 2-3 letters of recommendation from professional supervisors or academic instructors to:

Dustin Brisson [dbrisson@sas.upenn.edu](mailto:dbrisson@sas.upenn.edu)

Department of Biology University of Pennsylvania  
Leidy Laboratories, 209 433 South University  
Avenue Philadelphia PA 19104-6018 V:215.746.1731

F:215.898.8780

dbrisson@sas.upenn.edu dbrisson@sas.upenn.edu

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## UPoitiers France SymbiosisEvoEcol

Assistant professor position available in the Ecology Evolution Symbiosis laboratory at the University of Poitiers, France.

The research group in Evolution Ecology and Symbiosis led by Professor Didier Bouchon (<http://ecoevol.labo.univ-poitiers.fr/>) is seeking an assistant professor to fill in a permanent position, starting November 2011, in relation with a project investigating the impact of Wolbachia symbiosis on terrestrial isopods.

The host lab, 'Ecology, Evolution, and Symbiosis (UMR CNRS 6556)', is co-funded by the University of Poitiers and the Centre National de la Recherche Scientifique (CNRS). Our area of expertise is the peculiar symbiosis involving feminizing Wolbachia and their terrestrial isopod hosts. The multiple competences of the research members converge into an integrative approach of host-symbiont interactions.

Key-words: Evolutionary Ecology, functional Genomics, Bacterial Symbiosis, Environmental Biology

Teaching: The Department of Organismal and Population Biology is coordinating its own Bachelor (1) and Master (3) courses (<http://sfa.univ-poitiers.fr/bop/>). The ideal applicant shall teach in the areas of population and community ecology, and agroecology in the context of global change. Professional skills in Ecology, Population Biology and Biostatistics are sought. Good knowledge of the professional context of ecological management will be appreciated. Moreover, we offer the opportunity to teach the international Master Erasmus Mundus in Applied Ecology (<http://www.master-ema.org/>) (teaching language is English).

Research project: The ideal applicant shall work in the field of evolutionary ecology of host-parasite interactions, which can also include the study of host immune defenses. Interest in using arthropods as a model and experience in molecular techniques is advantageous. The successful candidate will be expected to develop a research programme in functional genomics and gene expression studies of host-parasite interactions. Research experience in emerging fields such as next generation sequencing data (RNASeq, 454), func-

tional genomics and metagenomics of symbiotic systems will be appreciated. We expect willingness to collaborate with others in the group.

French regulations require that applicant first qualify with the National Council of Universities. Any questions on the position can be directed to Didier Bouchon.

Interested candidates should submit a Curriculum vitae and statement of research interests, along with a list of references, by email or post to:

Didier Bouchon Universite de Poitiers Ecologie Evolution Symbiose, UMR CNRS 6556 40 avenue du Recteur Pineau F-86022 POITIERS Cedex tel : +33 (0)5 49 45 38 95 fax : +33 (0)5 49 45 40 15 <http://ecoevol.labo.univ-poitiers.fr/> <http://pbildb3.univ-lyon1.fr/endosymbart/> mailto:didier.bouchon@univ-poitiers.fr

Didier Bouchon <didier.bouchon@univ-poitiers.fr>

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## UToronto Mississauga EvoBioLecturer

Biology Lecturer, Department of Biology - Job # 0901107

The Department of Biology at the University of Toronto Mississauga invites applications for a full-time appointment at the rank of Lecturer effective July 1, 2010. Appointments at the rank of Lecturer may be renewed annually to a maximum of five years. In the fifth year of service, Lecturers shall be reviewed and a recommendation made with respect to promotion to the rank of Senior Lecturer. Applicants must have demonstrated excellence in teaching and have a Ph.D. degree in biological sciences. The successful candidate will be expected to have a strong interest in innovative teaching methods for large undergraduate classes and in novel approaches to pedagogy and student education in general. In addition to teaching in introductory core courses, the position will involve the development and promotion of new teaching methods. The ideal candidate will have teaching expertise that complements existing faculty and will be expected to take a leadership role in the undergraduate biology program, curriculum development and other undergraduate matters within the Biology Community. Salary will be commensurate with qualifications and experience.

All qualified candidates are encouraged to apply; however, Canadian and permanent residents will be given

priority. The University of Toronto is strongly committed to diversity within its community. The University especially welcomes applications from visible minority group members, women, aboriginal persons, persons with disabilities, members of sexual minority groups, and others who may contribute to the further diversification of ideas.

Applicants should submit a curriculum vitae, a teaching portfolio and names and e-mail addresses of three referees. We strongly encourage you to submit your application online at <http://www.jobs.utoronto.ca/-faculty.htm>. If you are unable to apply online, please submit your application and other materials to the following address: Professor Robert Reisz, Chair Department of Biology University of Toronto Mississauga Mississauga, Ontario, Canada L5L 1C6

Email: [robert.reisz@utoronto.ca](mailto:robert.reisz@utoronto.ca)

Closing date for submissions is March 5, 2010.

For more information about the Department of Biology at UTM, please visit our home page <http://www.utm.utoronto.ca/~w3bio/homepage/index.htm>  
Sasa Stefanovic Assistant Professor Department of Biology University of Toronto Mississauga 3359 Mississauga Rd N Mississauga, ON, Canada, L5L 1C6

Stefanovic Sasa <[sasa.stefanovic@utoronto.ca](mailto:sasa.stefanovic@utoronto.ca)>

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## Valencia Tech Comparative Genomics

### Post description

A technician position is now available for a programmer, biologist or bioinformatics to serve as an integral part of the Comparative Genomics Unit of Hernán Dopazo at Bioinformatics & Genomics Department at CIPF in Valencia, Spain. Our group focuses on the comparative analysis of complete genome sequences of mammals and *Drosophila* species using evolutionary and computational methods. The position is for an enthusiastic person interested to be included in a research programme for the analysis of adaptation at genomic level, the development of web based tools for molecular evolution, phylogenetics and adaptation and a national and international teaching programme. Our group collaborates with different research lines developed in reproductive biology, developmental biology, theoretical biology, metagenomics and population genetics in different labs of Spain (Madrid, Barcelona,

Vigo) and International labs at Buenos Aires University (Argentina) and Cambridge University (UK). The duties of the position will include implementing and improving the computational speed of algorithms, building analysis pipelines, database construction and management, web-based tools and software development. If you have any additional questions please contact Hernán Dopazo at [hdopazo@cipf.es](mailto:hdopazo@cipf.es)

### Candidate requirements

Ideal candidates will have a computer science, or bioinformatics background, proven programming skills in C/C++, Python, Java, and PERL, experience with relational databases (mysql or similar), basic knowledge of web programming, and experience working with publically available genomic data.

Professional training qualification in the Bioinformatics/Biology sector

Language: English or Spanish. Computer literacy is essential

Employment conditions The employment contract is directly linked to the following research project: "Selección natural en genomas completos de especies de mamíferos y *Drosophila*. Una aproximación desde la Biología de Sistemas, con un nom. de referencia BFU2009-13409-C02-01 (subprograma BMC), financiado por el MICINN y con cofinanciación del Plan-Ea. The contract will last the duration of the project, renewed on a yearly basis up until 31/12/2012. Salary according to the current Private Health Collective Agreement of Valencia Full-time Start date: March 2010

Application procedure Applications from interested parties can only be submitted by completing the online application form, which can be accessed through this link: <http://www.cipf.es/aplicacion.html> The period for the receipt of applications ends on 12th of February 2010 The candidate is responsible for the accuracy of the information on the application form, their C.V. and relevant documentation, and assumes the consequences of any false information, amongst which are the immediate exclusion from the selection process or termination of the contract.

Hernán J. Dopazo, PhD Head of the Comparative Genomics Unit Bioinformatics & Genomics Department Centro de Investigación Príncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanográfico) 46012, Valencia, España Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 [hdopazo@cipf.es](mailto:hdopazo@cipf.es) <http://hdopazo.bioinfo.cipf.es/> Hernán Dopazo <[hdopazo@cipf.es](mailto:hdopazo@cipf.es)>

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## Vienna AdminManager PopGeneticsProgram

We are searching for a communicative, independent person, who has very strong management skills and enjoys working in an international environment. The position is based at the Institute of Population Genetics at the Vetmeduni Vienna (<http://i122server.vu-wien.ac.at/pop>) and embedded in the evolutionary research community in Vienna (<http://www.evovienna.at>).

Requirements: - fluent in German and English - PhD in one of the following disciplines: Life sciences, statistics, informatics; previous experience with population genetics and/or evolutionary biology is a bonus

Duties: - Management of research grants and active participation on securing further funding for the PhD program - Planning and coordination of training activities, workshops and meetings - International networking with other institutions operating similar training program - PR activities - Administrative support of the PhD students (visa, housing, health agendas) - Support of the PhD students in basic statistics, programming, IT - Some limited teaching

The successful applicant will receive a postdoctoral salary including health benefits, contribution to pension funds etc. according to the FWF rules (<http://www.fwf.ac.at/de/projects/personalkostensaetze.html>). The position is initially for one year, but can be extended up to 12 years.

Please send your CV together with a motivation letter to Christian Schlotterer (Christian.schloetterer@vetmeduni.ac.at) by January, 31. The position is available from beginning of February, but later starting dates could be negotiated.

schlotc@gmail.com

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## WoodsHole ResAssist MicrobialEvolution

RESEARCH ASSISTANT I/II, MARINE BIOLOGICAL LABORATORY, WOODS HOLE MA

**\*\*Please apply online at <http://mbl.simplehire.com>\*\***  
Posting Number: 0000254 Department: Bay Paul Center Position Type: Research Position Title: Research Assistant I/II- Evolutionary Dynamics

Position Summary: The MBL seeks a highly motivated individual to join the Simmons lab as a full time Research Assistant I or II beginning in the spring of 2010. The successful applicant will contribute to projects that employ molecular, bioinformatic, cultivation, and field-based approaches to understanding short-term evolutionary dynamics in microbial communities. The Simmons lab is housed within the Marine Biological Laboratory's Josephine Bay Paul Center, a collaborative research group with interests in microbial diversity, molecular evolution, and comparative genomics.

Additional Information: Responsibilities will include but are not limited to: DNA and RNA extractions, standard and quantitative PCR, in situ hybridization, laser microdissection microscopy, preparation of libraries for 454 and Illumina sequencing, bioinformatic analyses, cultivation of bacteria and/or archaea, general lab organization and maintenance. Opportunities for locally based field work may also be available.

Basic Qualifications: EDUCATION, SKILLS, EXPERIENCE REQUIRED: Applicants should have an interest in microbiology, genomics, and evolution and possess a genuine drive to perform basic research. This position requires an independent, organized, and very motivated individual with experience in molecular techniques and ideally some experience with bioinformatics as well. Educational requirements include a B.A., B.S., or M.S. in microbiology/molecular biology/evolutionary biology or a related field and prior experience in an active research lab. Excellent written, verbal, and interpersonal skills, attention to detail, and a superb work ethic are essential. Position level and salary will depend upon education and experience.

Required Applicant Documents: Resume/CV Cover Letter References Unofficial Transcripts

Special Instructions to Applicants: The application process consists of four items: (1) a letter describing your interests, skills, and prior research experience, including any specific experience with the job responsibilities listed above; (2) a curriculum vitae; (3) copies of your transcripts from undergraduate and, if applicable, graduate work; (4) the name and contact information of three referees.

Sheri Simmons Assistant Scientist Bay Paul Center Marine Biological Laboratory 7 MBL St Woods Hole, MA 02543 <http://jbpc.mbl.edu/cv-simmons.html>  
Sheri Simmons <ssimmons@mbl.edu>

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### ABISequencer 377 Supplies GiveAway

\*ABI Prism DNA Sequencer 377 supplies and accessories to give away:\*

We are offering the following items for free on a first come first serve basis, but we would appreciate it if you would only claim what you really need, so more people can benefit from it. Also we ask that the receiver pays for shipping, if it comes to more than just send-

ing them out in a letter and any packaging costs should they arise.

8 x 96 well combs, catalog-no: CAK 96U-040, sharkstooth, 4mm thick 3 x 64 well combs, catalog-no: CAK64-040, sharkstooth, 4 mm thick 2 x 48 well combs, catalog-no: CAK48040, sharkstooth, 4 mm thick 2 sets of 96 + 4 well Combs, catalog-no: CAM96, Menb, unlaminated, upgrade 18 sets (36 pcs) of 377 Spacer, 48 cm WTR, 0.2mm thick 2 sets (4 pcs) of 377 Spacer, 36 WTR, 0.2 mm thick 1 set of Wedge Plate Separator (4 pcs), catalog-no: MJJ-4 3 rubber stripes to slant the plates for easier gel distribution

1 heat plate to be put over glass plates with gel for



the 48 well short gel run 1 extra upper buffer holding reservoir with lid

Contact information: Katrin Sommerfeld Dalhousie University Dept. of Biochemistry & Molecular Biology  
Email: [ksommerf\[at\]dal\[dot\]ca](mailto:ksommerf[at]dal[dot]ca) Phone: (02) 494-3569

– Katrin Sommerfeld W. Ford Doolittle Lab / John Archibald Lab Dalhousie University Dept. of Biochemistry & Molecular Biology 5850 College Street Halifax, NS, B3H 1X5, Canada

Phone: (902) 494-3569 Fax: (902) 494-1355 web site: <http://doolittle.biochem.dal.ca/> <http://myweb.dal.ca/jmarchib/> Katrin Sommerfeld <[ksommerf@dal.ca](mailto:ksommerf@dal.ca)>

## ALFP background noise answers

Here the answers to my questions. Thanks

- Which are the main causes of background noise and how to correct it?

You will undoubtedly get a mix of high quality markers and low quality markers and anything in between. Some markers can be quite sensitive to reaction conditions, while others are very robust. Slight inconsistencies between the different tips of a multichannel pipette may cause markers to drop out and I even had some markers that only worked at the edges of a 96 well plate due to minute differences in PCR block temperature response between centre and edges! (i.e. column 1, column 12, row 1, and row 8 gave peaks while the rest of the wells did not). Don't be scared by all this. Most markers will perform fine. If a marker is suspect, just leave it out.

- May the dye colour influence the magnitude of the background noise?

Don't think so

- How can protein / phenol contamination of the extracted DNA affect AFLP quality?

Some people get the best results with DNA extracted with qiagen DNeasy kit. Also phenol extracted DNA pellet diluted in H<sub>2</sub>O often works better than diluted in TE (but the DNA will be less stable over long periods of time in water).

- Is there any problem to overlay multiple primers with different dye labels? May peaks in one dye interfere with detection of other dyes?

Should be OK, but you will get spectral bleeding for the strongest peaks. They (the real marker and the background peak) will give the same present-absent pattern in and should be easy to identify.

Good luck

These aren't elementary questions. We are all still working to figure out the best way to cut out noise from AFLPs. I find running at least one pre-amp and one selective amp (some people only run the selective amp) helps cut back on some of the noise. Also, make sure you set your threshold above the noise. (You can usually eye-ball that one.) One last note on that part: stick with larger peaks, as they're less likely to be affected by things other than your typical DNA.

I don't know if dye color can affect the noise. We don't have a lot of money, so we only run one dye (and a different dye-ladder) at a time. Hopefully someone else can get back to you on that one. I also don't know if the different dyes can affect each other, but considering a lot of people use this approach, I would like to assume any effect is minimal.

As for the protein/phenol contamination, typically it causes problems in repeatability. Therefore, make sure you run many of your samples multiple times (the rule of thumb is 10%, but I typically run any of my "trouble" samples multiple times) and discard bins where the peaks are not replicable.

My favorite reference for fluorescently-labeled AFLPs is Meudt and Clarke 2007, Almost forgotten or latest practice? AFLP applications, analyses and advances. Trends in Plant Science 12(3): 106-117. Even though it is a couple years old, it hits on most of the major questions to be considered with AFLPs.

Good luck!

Subject: Other: question about AFLP background noise

Dear all,

Maybe these are very elementary questions for this list, but I am beginning with AFLP analysis and I have some doubts (probably elementary ones as I said)

- Which are the main causes of background noise and how to correct it? - May the dye colour influence the magnitude of the background noise? - How can protein / phenol contamination of the extracted DNA affect AFLP quality? - Is there any problem to overlay multiple primers with different dye labels? May peaks in one dye interfere with detection of other dyes?

Any references you could advise me to get into this subject and clarify my doubts?

Thanks.

anidras\_ayu@yahoo.com

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### Alternatives for GenBank Submission

Dear Colleagues,

Has anyone found a less cumbersome interface than Sequin for preparing large batches (>200 individuals) of sequence data to GenBank. I've spent days tearing my hair out in the past trying to make Sequin work, and am dreading doing it again.

Along those lines, I would be interested in hearing about the experience of other submitters in dealing with GenBank submissions and subsequent processing of your annotations.

Regards,

Christopher Irwin Smith Assistant Professor Department of Biology Willamette University Salem, OR 97301 ph: 503-370-6181 fax: 503-375-5425

email: csmith@willamette.edu csmith@uidaho.edu  
chris.smith@post.harvard.edu

<http://www.willamette.edu/~csmith/ChrisSmith.htm>  
Chris Smith <csmith@willamette.edu>

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### AmerSocMammalogists Student Research Awards

The Honoraria Committee of the American Society of Mammalogists welcomes applications for graduate honoraria and undergraduate research awards. The application process for the graduate awards has changed from previous years but that for the undergraduate awards remains the same. For more information, see the Honoraria Committee webpage at <http://www.mammalsociety.org/committees/indexhonor.asp>  
**CALL FOR GRADUATE STUDENT HONORARIA**

Graduate students are encouraged to submit a summary of a research project on any aspect of mammalogy for consideration by the Honoraria Committee. The Anna M. Jackson, A. Brazier Howell, and Elmer C.

Birney Awards recognize outstanding research projects completed by the Society's graduate student members and are among the Society's highest student honors. Winners will present their research to the Society at the Plenary Session of the Annual Meeting, to be held at the University of Wyoming in June 2010. Please note that application procedures have changed for the 2010 competition.

Detailed instructions:

**Eligibility:** The competition is open to all graduate student members of the American Society of Mammalogists, regardless of nationality or current institutional affiliation. To become a member of the Society visit the ASM membership page at <http://www.mammalsociety.org/membership/index.html>. Applicants must be Masters or doctoral students (or have completed their degrees during the previous Fall term) when they apply. Applicants must not have received a previous Graduate Honorarium from ASM, or a Shadle or ASM Fellowship. However, recipients of ASM Grant-in-Aid of Research and Latin American Student Field Research awards are eligible and encouraged to apply. Students unsure of their eligibility are encouraged to contact the Honoraria Committee ([honoraria@mammalsociety.org](mailto:honoraria@mammalsociety.org)) well in advance of the application deadline.

**Research Statement:** Applicants should submit a summary of their graduate research not exceeding 1000 words (excluding Literature Cited, figures, or tables) with the following clearly labeled sections: Title, Project Significance/ Theoretical Context, Methods, Results, and Discussion/Interpretation. Please include key figures/tables (3 items maximum) with concise captions to support your results. Research currently under review or 'in press' may be submitted. Applicants should note that the Honoraria Committee is composed of members from across different subdisciplines of mammalogy, and therefore are urged to write for a broad, scientifically literate audience and to avoid excessive jargon or technical terms. Collaborative work with multiple authors may be submitted, so long as the applicant has played the primary role in designing and conducting the research (the reference letter, see below, should address this issue).

**Reference Letter:** A letter should be addressed to the committee and be written by an individual familiar with the applicant's research, ideally, the research advisor/mentor or major professor. Beyond comments concerning the student's general strengths, the letter must address the following: 1) if the student will be prepared to present the research project in the Plenary Session of the upcoming Annual Meeting and 2) the student's role

in designing and conducting the research, especially in the case of collaborative research. We seek to recognize students that have been primarily responsible for the design and/or conduct of the submitted research project (normally the student's thesis or dissertation research). Any letter that does not clearly address the two points stated above will result in disqualification of the applicant.

Evaluation criteria: Members of the Honoraria Committee review and rank applications based on originality, quality, and presentation of the research and the advisor's letter of support. The three proposals with the highest overall ranking will be awarded. Each award carries an Honorarium of \$1000, intended to subsidize attendance at the meeting

Submit your research statement (and ask your advisor to send his/her letter separately) in PDF or Microsoft Word format, electronically to [www.mammalsociety.org/applications/](http://www.mammalsociety.org/applications/) by 11:59 p.m. Eastern Standard Time on 15 February. Please also email the chair of the committee [Virginia Hayssen, [vhayssen@science.smith.edu](mailto:vhayssen@science.smith.edu)] at the time that you submit your application. Questions should be directed to [honoraria@mammalsociety.org](mailto:honoraria@mammalsociety.org) (or via snail mail to Virginia Hayssen, Biology Department, Smith College, Northampton, MA 01063 [413 585 3856]). Applications that do not meet the above requirements or are received after the deadline will not be considered. Applicants will be notified of the committee's decision around 15 March.

— / —

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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## AnimalGenetics paper

Dear Colleagues,

I am looking for the following paper which is cited in so many places but I couldn't find it in the mentioned Vol and Issue, may I request you to help me if any send a copy of it to me:

Paper title: A novel polymorphism in the bovine insulin-like growth factor binding protein-3 (IGFBP3) gene.

Maciulla JH Zhang HM DeNise SK Animal Genetics, 1997 Vol. 28, No.5, 1997

Regards

Nasrollah Pirany Assistant Professor University of Tabriz Faculty of Agriculture Dept. of Animal Science 29th Bahman Bolvard, East Azarbaiejan, Tabriz, Iran. Phone (Office): +98-411-3392060- Mobile: +98-9144177930 Fax: +98-411-3356004-3345332 Alternative Email: [n.pirani@tabrizu.ac.ir](mailto:n.pirani@tabrizu.ac.ir)

Nasrollah Pirany <[npirany@gmail.com](mailto:npirany@gmail.com)>

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## Astrobiology SummerProgram 2010

Please announce to your undergraduates:

Penn State's Astrobiology Summer Program - 2010 (An NSF-REU Site)

Each summer the program supports 10 students from universities and colleges across the U.S., between their freshman and senior years, to conduct research with astrobiologists (including evolutionary biologists) for 10 weeks at Penn State (6 June to 14 August, 2010). Activities also include a behind-the-scenes field trip to NASA-Goddard Space Flight Center, NASA Headquarters, the Smithsonian Air and Space Museum, as well as weekly seminars, discussion groups and a research symposium. The program covers the cost of travel (up to \$500), room, and meals and provides a \$4,000 stipend. For further information see <http://evo.bio.psu.edu/asp/>. Review of applications begins February 19th.

[sbh1@psu.edu](mailto:sbh1@psu.edu) [sbh1@psu.edu](mailto:sbh1@psu.edu)

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## Austria SummerFellowships

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

Funding is available for PhD students interested in three months of collaborative research during June-August 2010 on

Evolutionary and Ecological Modeling

in population ecology, evolutionary ecology, community

ecology, spatial ecology, biodiversity research, fishery science, and vegetation science.

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

Summer research projects are invited in any of the following areas:

Models for Fisheries Management Fisheries-induced Evolution

Adaptive Speciation Food-Web Evolution

Vegetation Models Evolutionary Conservation Biology

Evolution of Cooperation

Adaptive Dynamics SpatialEcological andEvolutionary Models

Applicants prepare a research proposal that corresponds to their professional plans and to the agenda of their hosting IIASA Program. Accepted applicants begin work before the summer by planning their research in close collaboration with their IIASA supervisors. Previous experiences with implementing and studying evolutionary or ecological models are important assets. To improve their chances of being selected, potential applicants are encouraged to send informal inquiries regarding their specific research interests and plans to EEP's program leader Ulf Dieckmann ([dieckmann@iiasa.ac.at](mailto:dieckmann@iiasa.ac.at)).

Online applications need to be submitted before Monday, January 18, 2010.

Since 1977, the annual Young Scientists Summer Program (YSSP) of the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria, has attracted 1500+ students from 70+ countries. The YSSP 2010 will take place from June 1 to August 27, 2010. IIASA is located in the former summer palace of Austria's royal family, ca. 15 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on regular personal interaction with advising scientists, and typically leads to a publication in an international journal, as well as to a chapter in a candidate's PhD thesis.

Some useful links:

+ [www.iiasa.ac.at/Admin/YSP/reg-info/](http://www.iiasa.ac.at/Admin/YSP/reg-info/)-

[more\\_about\\_the\\_program.html](#) Details about the summer program, and online application

+ [www.iiasa.ac.at/Research/EEP/](http://www.iiasa.ac.at/Research/EEP/) Information about IIASA's Evolution and Ecology Program

+ [www.iiasa.ac.at/Research/EEP/Students.html](http://www.iiasa.ac.at/Research/EEP/Students.html) Examples of successful YSSP projects

+ [www.iiasa.ac.at/docs/IIASA\\_Info.html](http://www.iiasa.ac.at/docs/IIASA_Info.html) General information about IIASA

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

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

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

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## Chicago Botanic Garden Summer Res Positions

Summer field research internships

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

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

If you want more information or wish to apply, please visit this website <http://echinacea.umn.edu/> or contact Stuart Wagenius. Applications due 5 March 2010.

Stuart Wagenius, Ph.D. Conservation Scientist Division of Plant Science and Conservation Chicago Botanic Garden 1000 Lake Cook Road Glencoe, IL 60022 phone: 847 835 6978 fax: 847 835 6975

email: [stuart09@echinaceaproject.org](mailto:stuart09@echinaceaproject.org) web: <http://echinacea.umn.edu/> [SWagenius@chicagobotanic.org](mailto:SWagenius@chicagobotanic.org)

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## Darwin biopic

Dear Colleagues

Many of you will have heard about or seen the new Darwin biopic "Creation," which opened last Friday across North America. Here in Atlantic Canada, and I understand elsewhere in Canada, the film has been given only extremely 'limited release.' I suspect the same is true elsewhere [NCSE: please advise]. From all accounts, the film deserves to be widely seen as a part of a balanced consideration of science and faith; the starring cast will no doubt bring in many who might not otherwise attend.

We urge everyone to check local availability, and to lobby for the widest possible distribution. The following letter has prompted attention from CBC, and may lead to a local 'Darwin Fest' if there is no other means to ensure local viewing.

Steve

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Open Letter to the Editor, St John's "Telegram" 27 Jan 2010

The year 2009 marked the 200th anniversary of the birth of Charles Darwin and the 150th anniversary of the publication of his seminal work, "On the Origin of Species," regarded as the most influential book in the history of biology. These events have been commemorated across the world, for example by publication of new editions of the "Origin," and special lectures here and elsewhere on Charles Darwin the man, his scientific work, and the impact of evolutionary thinking on society.

One such event is the release last Friday of the film "Creation," starring Paul Bettany and Jennifer Connelly as Charles and Emma Darwin. It examines the marriage of the deeply religious Emma and her scientist husband Charles, as they grapple with the implications of his new theory for themselves and others. There are flashbacks to Charles' five-year voyage around the

world, in which the evidence for evolutionary change and natural selection first became clear to him. As such it combines biopic, adventure film, and an exploration of faith and science. "Creation" premiered at the Toronto International Film Festival last Fall, to rave reviews.

We are therefore dismayed to find "Creation" in only "limited release" in Atlantic Canada, at a handful of theatres in Halifax and nowhere at all in PEI, New Brunswick, or Newfoundland and Labrador. We suppose the reasons are economic: however, at a time when the federal Minister of Science has expressed doubts about the reality of evolutionary change, more education is needed rather than less.

As instructors in evolutionary biology at Memorial University, we urge Empire Theatres to reconsider its decision, and release "Creation" as widely as possible in Atlantic Canada, for the education and entertainment of all students of science and others interested in the very human story of this fascinating and important scientist.

Sincerely,

Steven M. Carr, Ph.D. Professor of Biology Tom W. Chapman, Ph.D. Asst Professor of Biology David J. Innes, Ph.D. Professor of Biology H. Dawn Marshall, Ph.D. Asst Professor of Biology Edward H. Miller, Ph.D. Professor of Biology

Dr Steven M Carr, Professor of Biology Department of Biology Memorial University of Newfoundland St John's NL A1B 3X9 CANADA

e-mail: [scarr@mun.ca](mailto:scarr@mun.ca) <http://www.mun.ca/biology/-scarr/Research.html> (709) 737 - 4776 office / -4713 lab / -3018 FAX

Dr Steven M Carr <[scarr@mun.ca](mailto:scarr@mun.ca)>

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## Disappearing DNA

Hello all,

In November '09 I extracted DNA using Wizard SV 96 Genomic DNA purification system in the 96 well plate format. All steps were followed as per the protocol with minor alterations (e.g. elution volume etc.). 1microL of the DNA obtained was loaded onto a 0.8% agarose gel (containing EtBr) soon after extraction. Typical DNA yield was in the region of 20ng/microL. Recently I have begun optimization for Microsatellite work, and



reloaded a few of the DNA plates on an Agrose gel (Same as above). I've found that my DNA concentration is decreasing over time without intermediate degradation i.e. the DNA does not appear as a smear but a discrete band of the same size as the previous test.

Has anyone ever experienced this before, and if so could you enlighten me as to what might be happening.

N.B. I have been reusing promega DNA binding plates (in most cases for the third time). I have tested for contamination with previous DNA and results were negative.

Thanks

Kevin Keenan 13928058

kkeenan02@qub.ac.uk

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## Dobzhansky and Fisher Awards

The Society for the Study of Evolution solicits applications/nominations for the Dobzhansky and Fisher Awards. The Fisher Award deadline for an excellent student paper in Evolution is January 31, 2010. The Dobzhansky Award deadline for an outstanding early-career evolutionary biologist is February 15, 2010. See [www.evolutionarysociety.org](http://www.evolutionarysociety.org) for details.

Judy Stone <jstone@colby.edu>

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## Drosophila santomea genome

Drosophila santomea genome sequence (release 1.0)

Dear Evolution community,

This is to announce the release of a first draft of the Drosophila santomea genome sequence (release 1.0), which can be downloaded at

<http://genomics.princeton.edu/AndolfattoLab/Links.html> D. santomea was first described by Lachaise et al (2000) as a new melanogaster-group sister species endemic to the island of São Tomé off the coast of West Africa. D. santomea is most closely related to D. yakuba and the two species diverged ~0.5 Mya (Cariou et al. 2001; Llopart et al. 2005; Bachtrog et al. 2006). The species has a number of derived

characters relative to D. yakuba, including highly reduced pigmentation and mating and temperature preferences, making it fertile ground for studies of the evolution of novel characters (Llopart et al. 2002; Coyne et al. 2004; Carbone et al. 2005; Llopart et al. 2005; Mas and Jallon 2005; Moehring et al. 2006; Jeong et al. 2008; Matute and Coyne 2009). The species is only partially reproductively isolated from D. yakuba, facilitating the genetic dissection of the factors underlying reproductive isolation and other derived phenotypic traits of interest.

The current draft genome represents a bwa (<http://bio-bwa.sourceforge.net/bwa.shtml>) assembly of 65.9 million 54 bp Illumina sequence reads to the D. yakuba reference genome sequence (release 1.3) yielding an average coverage of ~10X. Further updates are expected soon, including higher coverage with paired-end reads and a de novo assembly in collaboration with Mike Eisen at UC Berkeley.

We hope this will stimulate evolutionary genetic research on D. santomea and other Drosophila species - enjoy!

Peter Andolfatto, [pandolfa@princeton.edu](mailto:pandolfa@princeton.edu) Tina Hu  
Kevin Thornton

Peter Andolfatto <[pandolfa@Princeton.EDU](mailto:pandolfa@Princeton.EDU)>

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## Estimating reproducibility of AFLP genotyping

Dear EvolDir readers:

I am curious to know if there is any method or software available to check and estimate the reproducibility (or error rate) of AFLP genotyping. I have seen people citing Bonin et al. 2004 for this purpose. Your suggestion is highly appreciated.

Thank you.

Apurba Barman

Dept. of Entomology Texas A & M University 2475  
TAMU, College Station Texas 77843

[apurbabarman@neo.tamu.edu](mailto:apurbabarman@neo.tamu.edu)

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## EuropeanSocEvolBiol Outreach fund

Dear Colleagues

The European Society for Evolutionary Biology (ESEB) is pleased to announce a new Outreach Fund available globally to promote evolution-related activities, with a total annual budget of 10000 euros. The goal of this initiative is to promote knowledge about evolution to general public. Applications for funding will be accepted for educational initiatives that promote evolution, translation of evolutionary material (books, films, websites) intended for a general audience, public outreach seminars, public exhibitions, etc. The application form can be found on [www.eseb.org](http://www.eseb.org) (click on the "Outreach Fund" link). Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to ESEB Secretarial Assistant, Mrs. Olga Vos <office@eseb.org> (Subject: Outreach).

Tadeusz Kawecki Secretary , European Society for Evolutionary Biology

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lausanne, Switzerland [tadeusz.kawecki@unil.ch](mailto:tadeusz.kawecki@unil.ch)

[tadeusz.kawecki@unil.ch](mailto:tadeusz.kawecki@unil.ch) [tadeusz.kawecki@unil.ch](mailto:tadeusz.kawecki@unil.ch)

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## Evolutionary addictions

I am a Spanish Biology student. After contacting the ESEB, they suggested I could try to find an answer to my query at EvoDir.

I would like to kindly ask you if you could help me find a European research group dealing with addictions from an evolutionary point of view.

Thank you very much for your help. I am looking forward to your answer.

Regards,

Mariona Casals

Mariona Casals <[marionacasals@hotmail.com](mailto:marionacasals@hotmail.com)>

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## Faunmap question

I have been using the online version of Faunmap (<http://www.museum.state.il.us/research/faunmap/-query/>), and although it seems to process the queries fine, none of the map images actually show up (I just get an X, ? or broken picture symbol. I have tried Safari, Firefox and Explorer. If anyone has information on what the problem/solution is, please email me directly at: [arbogastb@uncw.edu](mailto:arbogastb@uncw.edu)

Best, Brian

Brian S. Arbogast, PhD Department of Biology and Marine Biology University of North Carolina Wilmington, NC 28403

(910) 962 2644 [arbogastb@uncw.edu](mailto:arbogastb@uncw.edu) <http://people.uncw.edu/arbogast/> "Arbogast, Brian S." <[Arbogastb@uncw.edu](mailto:Arbogastb@uncw.edu)>

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## FieldMuseum Chicago SummerUndergraduateFellowships

Field Museum summer 2010 undergraduate research internship opportunities:

The Field Museum in Chicago, Illinois is pleased to announce its 2010 Research Experiences for Undergraduate (REU) internship grants. Go to <http://www.fieldmuseum.org/research.collections/-scholarships/reu.html> for details.

Application deadline: February 1st, 2010

Potential 2010 REU Projects for undergraduate students include: CT Reconstruction at the sub-micron-level Scaling analyses of mammalian sensory capacities based on Synchrotron X-Ray imaging The Bivalve Tree of Life – understanding the evolution of clams, mussels, oysters and their relatives Evolution and patterns of reproduction in Philippine mammals Phylum Bryozoa: Developing a Global Taxonomy on the Web Understanding the evolution of secondary chemistry in lichens The evolution of an ant-plant mutualism Island gigantism or dwarfism? Phylogeny and taxonomy of Madagascar's chirping Giant Pill-Millipedes, describ-

ing newly discovered, micro-endemic species An island giant: describing a new species of rove beetle from the Chatham Islands Do some nocturnal Malaysian mammals see in color? Morphological integration of the turtle shell: the effects of plastral hinging

2010 Program Dates Start of 2010 REU Program: Monday, June 7, 2010 Phylogenetic workshop series (weekly), and introductory lectures: June 9- July 28, 2010 (evening class, participation mandatory) End of 2010 REU Program: Friday, August 13, 2010 2010 REU research symposium: Saturday, August 14 (participation mandatory)

Stipend and allowances: REU student participants receive a salary of \$4,500 for the 10- week program, and additionally \$2,500 subsistence and \$500 travel allowance.

Program Director: Petra Sierwald, Associate Curator - Zoology, Insects Field Museum of Natural History, 1400 S Lake Shore Drive Chicago, IL 60605, USA E-mail: psierwald@fieldmuseum.org Phone: (312) 665-7744; Fax: (312) 665-7754

Corrie Saux Moreau, Ph.D. Assistant Curator, Division of Insects Department of Zoology Field Museum of Natural History 1400 South Lake Shore Drive Chicago, IL 60605 USA Office: (312) 665-7743 Fax: (312) 665-7754 cmoreau@fieldmuseum.org [http://fm1.fieldmuseum.org/aa/staff\\_page.cgi?staff=3Dcmoreau](http://fm1.fieldmuseum.org/aa/staff_page.cgi?staff=3Dcmoreau) cmoreau@fieldmuseum.org

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## Gel extraction advice

Dear All,

I need to extract and purify quite a few PCR products from agarose gels. I've used Qiagen kits in the distant past for this, but was hoping others have more recent experience with this technique and could suggest protocols or kits that have worked well for them.

Thanks for your help!

SJM

Stacy J. Mantooth Ecology and Evolutionary Biology Section School of Life Sciences University of Nevada, Las Vegas 4505 Maryland Parkway Las Vegas, NV 89154-4004 (702) 895-5373 / (702) 895-3956 (fax)

mantooth@unlv.nevada.edu <http://faculty.unlv.edu/~mantooth/> mantooth@unlv.nevada.edu mantooth@unlv.nevada.edu

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## GenGIS version1 05 for Mac

Hi everyone,

We have released a version of our GenGIS software for geospatial analysis of environmental genomic data that works on both Mac OS X 10.5 (Leopard) and 10.6 (Snow Leopard). It can be accessed at the page <http://kiwi.cs.dal.ca/GenGIS/Download> under 'Mac OSX Release'.

Source code and a Windows installable version are also available from the same page.

The GenGIS reference is: Parks DH, Porter M, Churcher S, Wang S, Blouin C, Whalley J, Brooks S, Beiko RG. (2009) GenGIS: A geospatial information system for genomic data. *Genome Res.* 19(10):1896-904.

Best wishes, Rob Beiko Faculty of Computer Science, Dalhousie University

beiko@cs.dal.ca beiko@cs.dal.ca

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## GlasgowU BlueTitEvolution

RESEARCH ASSISTANTS NEEDED  
SPRING/SUMMER 2010

We are currently looking to recruit enthusiastic field assistants to work on a research project investigating individual variation in steroid hormones and fitness in a population of blue tits. Research will be conducted in stunning oak woodland on the banks of Loch Lomond, Scotland, UK.

Positions are available between April-June 2010. Although starting and ending dates are flexible, you must be available to work for at least 2 weeks. You will be working as part of a team with Dr Kathryn Arnold of the University of Glasgow ([www.gla.ac.uk:443//ibls/-staff/staff.php?who=PGe~Pn](http://www.gla.ac.uk:443//ibls/-staff/staff.php?who=PGe~Pn)). This is a great opportunity to gain valuable experience in several field research techniques including: nest box monitoring, measuring eggs and nestlings, invertebrate sampling and behavioural observations. Basic living costs will be covered and accommodation during fieldwork will be

provided at the University of Glasgow field station, SCENE, within Loch Lomond National Park (<http://www.gla.ac.uk/departments/scene/>).

Requirements: A strong interest in animal ecology and behaviour. Applicants must be reasonably fit and able to climb ladders (for fieldwork). Preference will be given to candidates with a background in biological sciences and experience handling birds but this is not essential.

General inquires and formal applications should be sent to: Lindsay Henderson (E-mail: [l.henderson.1@research.gla.ac.uk](mailto:l.henderson.1@research.gla.ac.uk)). Applications must include: a CV, cover letter and two referees (academic or field biology related with e-mail addresses). Be sure to indicate the dates that you are available. If it is not possible to send applications via email, please send them by post to: Lindsay Henderson, Division of Environmental and Evolutionary Biology, Graham Kerr Building, University of Glasgow, G12 8QQ Scotland, UK

Closing date: Friday 19th March.

LINDSAY JENNIFER HENDERSON  
<[l.henderson.1@research.gla.ac.uk](mailto:l.henderson.1@research.gla.ac.uk)>

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## Hornworm parasitoid

Dear EvoDir readers,

I am teaching a lab class this spring and plan to include a section on the development and metamorphosis of the hornworm *Manduca sexta*. I was wondering if anyone knew of a commercial supplier of small numbers of a parasitoid wasp that infects this species?

Thanks! -Dave Angelini

David R. Angelini, Ph.D. American University  
Department of Biology [angelini@american.edu](mailto:angelini@american.edu)  
<http://www1.american.edu/cas/bio/people/faculty/angelini/> [angelini@american.edu](mailto:angelini@american.edu) [angelini@american.edu](mailto:angelini@american.edu)

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## Ideas Ecol Evolution

Volume 2 (2009) for Ideas in Ecology and Evolu-

tion is now complete (<http://library.queensu.ca/ojs/index.php/IEE/issue/current>), including a year-end editorial with reflection on the journal's first full year of operation, the ongoing mission of the journal, and anticipation for future growth. IEE is a peer-reviewed, open-access journal published at Queen's University, welcoming submissions of forum-style papers involving new ideas and commentaries from all areas of study in ecology and evolution.

Lonnie W. Aarssen Professor Dept. of Biology Queen's University Kingston, ON Canada, K7L 3N6

Editor Ideas in Ecology and Evolution <http://library.queensu.ca/ojs/index.php/IEE> Campus Office: Room 4326, Biosciences Complex

email: [aarssenl@queensu.ca](mailto:aarssenl@queensu.ca) web: <http://biology.queensu.ca/%7Eaarssenl/> tel: 613-533-6133 fax: 613-533-6617

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## LERN group selection debate online

Dear all

The London Evolution Research Network's group selection debate is now online at <http://www.vimeo.com/user2795743> The motion was:

Is natural selection at the group level an important evolutionary force? Four eminent speakers discussed the motion:

- Stuart West Professor of Evolutionary Biology, University of Oxford
- Herbert Gintis Professor of Economics, Santa Fe Institute, University of Siena, and Central European University
- Samir Okasha Professor of Philosophy of Science, University of Bristol
- Mark Pagel Professor of Biology, University of Reading

Best wishes

Gillian

Gillian Pepper MSc Student - Evolutionary Psychology Brunel University

Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Mobile: 07951 295 751 Email: [ht08ggp1@brunel.ac.uk](mailto:ht08ggp1@brunel.ac.uk) [<mailto:ht08ggp1@brunel.ac.uk>](mailto:ht08ggp1@brunel.ac.uk) Personal

web page: <http://www.scienceandsociety.info>  
 < <http://www.scienceandsociety.info/> >  
 Science Policy UK Network: <http://network.nature.com/groups/ukpolicy/forum/topics>  
<http://network.nature.com/groups/ukpolicy/forum/topics>  
 > London Evolution Research Network:  
 work: <http://londonevolution.net/> Re-  
 search and Media Network: <http://researchandmedia.ning.com/profile/GillianPepper>  
<http://researchandmedia.ning.com/profile/GillianPepper>  
 >  
 ht08ggp1@brunel.ac.uk ht08ggp1@brunel.ac.uk

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## Lizard video

Hello everyone,

I disturb you, just to comment that, with the aim of spreading in an "extra-scientific" area, some aspects of the work we have done on a project that evaluates the role of lizards as seed dispersers in insular environments, we conducted a 3D video. Unfortunately, we have not yet been able to incorporate a version in English, but we will try to do so shortly. If anyone is interested, can see the video on the web:

<http://webs.uvigo.es/plantecology/-divulgacion.en.html> If anyone is interested, can also download high definition version freely accessing the platform Vimeo:

<http://vimeo.com/8612833> I hope you enjoy it.

Luis Navarro

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

Luis Navarro <[lnavarro@uvigo.es](mailto:lnavarro@uvigo.es)>

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## LondonEvolutionNetwork AGM ChristmasSocial Dec3

Dear all,

The LERN year will be coming to a close at the end of the year 2009 and we would like to invite all members and potential new members to join us for our Annual General Meeting which will be followed by a Christmas Social.

LERN AGM & Christmas Social

December 3rd 2009, at 18:30

Anthropology Postgraduate Common Room  
 (Anthropology Department - 14 Taviton Street)

The event is free all are welcome!

Wine and mince pies will be served!

This will be a good opportunity to meet fellow LERN members and learn a bit more about LERN's activities.

We are currently looking for new LERN committee members as well as new LERN representatives for 2010, so if you think you would like to be involved in organizing LERN activities either as part of the committee or as a rep, or if you are simply curious about LERN in general and would like to meet other members join us on December 3rd.

Alternatively, if you know that you would like to be part of the next committee, you can email us at [info@londonevolution.net](mailto:info@londonevolution.net) to obtain more information on what this entails.

Opportunities to fill the following positions for 2010:

Treasurer (currently, Shakti Lamba)

Events Coordinator (currently, Gillian Pepper)

Secretary (currently, Anna Barros)

Webmaster (currently, Anna Barros)

Chair (currently, Michael DeBarra and Sandra Virgo)

Visit website <http://londonevolution.net/> for information on how the event and how to get there.

We hope to see you there!

The LERN Committee

–

LERN: the London Evolutionary Research Network. E-mail [info@londonevolution.net](mailto:info@londonevolution.net) or visit <http://londonevolution.net> for events and further information. New members and suggestions for speakers are always welcome!

If you do not want to receive any more emails from LERN, <http://londonevolution.net/-mailinglist/?p=3Dunsubscribe&uid=-3D8d9cce993952a0074a870e7af9e6d4c0> To update your preferences and to unsub-



scribe visit <http://londonevolution.net/-mailinglist/?p=3Dpreferences&uid=-3D8d9cce993952a0074a870e7af9e6d4c0> – Powered by PHPlist, [www.phplist.com](http://www.phplist.com) –

Gillian Pepper MSc Student - Evolutionary Psychology Brunel University

Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Mobile: 07951 295 751 Email: [ht08ggp1@brunel.ac.uk](mailto:ht08ggp1@brunel.ac.uk) Personal web page: <http://www.scienceandsociety.info> Science Policy UK Network: <http://network.nature.com/-groups/ukpolicy/forum/topics> London Evolution Research Network: [http://londonevolution.net/-Research and Media Network: <http://researchandmedia.ning.com/profile/GillianPepper>](http://londonevolution.net/-Research%20and%20Media%20Network) [ht08ggp1@brunel.ac.uk](mailto:ht08ggp1@brunel.ac.uk) [ht08ggp1@brunel.ac.uk](mailto:ht08ggp1@brunel.ac.uk)

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## Microsat clustering

Greetings,

I am generating a microsatellite dataset across a large genus of flowering plants and am interested in using a model-based clustering approach to guide species delimitation. My situation involves a large number (ca. 70) of morphologically distinctive but relatively young diploid lineages that have presumably achieved pairwise reproductive isolation but which still exhibit plenty of trans-specific alleles.

I know that there are a number of model-based clustering programs available, but that they differ in their underlying assumptions. Is there a good review discussing clustering at this level of divergence (above the species level)? Any personal experiences with software would also be greatly appreciated.

Thanks! James – James Beck Department of Biology Duke University Durham, NC 27708 <http://www.duke.edu/~jbb31/> “Choose your enemies carefully ’cause they will define you.” -U2 “Cedars of Lebanon” (2009)

[jbb31@duke.edu](mailto:jbb31@duke.edu) [jbb31@duke.edu](mailto:jbb31@duke.edu)

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## Mimulus guttatus genome release1 0

We are please to announce the initial release of the *Mimulus guttatus* genome from the DOE Joint Genome Institute. *Mimulus* is one of the first completely sequenced plants in the large asterid clade of eudicots, and is a long-standing model organism for ecological and evolutionary genetics.

The assembly and annotation of the IM62 inbred line are available from Phytozome (<http://www.phytozome.net/mimulus>) for browsing, BLAST, and download. The assembly consists of 321.7Mb arranged in 2216 scaffolds, with 6.5% gaps. For scaffolds, N50 and L50=1.1 Mbp. 95.7% of the genome is in scaffolds larger than 50 Kbp. The genome annotation contains 25,530 protein-coding loci. There is a separate collection of 27,504 protein-coding transcripts from EST sequencing of IM62 and other genotypes (and species). These data are also being incorporated into a forthcoming update of the [mimulusevolution.org](http://mimulusevolution.org) database, which integrates the sequence data with genetic markers, maps and other information.

Terms of Use The Fort Lauderdale guidelines aim to balance the value of rapid release of genomic data with respect for the scientific interests of the generators of that data. We ask that you respect these terms. Please feel free to use these data to advance biology e.g. help clone a gene, analyse a gene family, etc., though note that this is a preliminary release, and undoubtedly includes various errors. Our plans for publication of the *Mimulus* genome are focused on the large-scale analysis of the gene and repetitive content of the genome and its evolutionary dynamics (including synteny and chromosomal/segmental duplication, gene family evolution, gene structure evolution) relative to other angiosperms. The initial manuscript describing the assembly, annotation, and first global analysis of the *mimulus* genome will be based on an improved, chromosome-scale assembly currently in development. If you have an interest in using these data for large-scale analysis, or contributing to a companion manuscript, please contact one of us.

Todd Vision John Willis Dan Rokhsar

[tjv@bio.unc.edu](mailto:tjv@bio.unc.edu)

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## Pedigree software for parental reconstruction

Hello,

Does anyone know what has happened to the website

hosting the Pedigree v2.0 or 2.2 software for parental reconstruction. The web-address that is widely cited no longer works (<http://herbinger.biology.dal.ca:5080/-Pedigree/>) and I cannot find an alternative address. I would be very grateful if someone could direct me to a functional address.

Many thanks

Sean

F1502202@qub.ac.uk

Sean Fitzpatrick <F1502202@qub.ac.uk>

Felicity Davie Tou-can Marketing The Holly 42 Heath Hill Road South Crowthorne Berkshire RG45 7BW

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E-mail: [felicity@tou-can.co.uk](mailto:felicity@tou-can.co.uk) < <http://www.tou-can.co.uk> > www.tou-can.co.uk

[felicity@tou-can.co.uk](mailto:felicity@tou-can.co.uk) [felicity@tou-can.co.uk](mailto:felicity@tou-can.co.uk)

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## SequenceMachine ForSale

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## Recoding pedigree file for VCE

Hi all;

Do you know some program for recode pedigree file. I know that PEST could do that but is unavailable in the net... do you know some link or other software??

Thanks in advance

Regards Rodrigo

Rodrigo Badilla <[rodrigo.badilla@gmail.com](mailto:rodrigo.badilla@gmail.com)>

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## Royal Society LifeCycles

Royal Society Publishing has just published 'From polyphenism to complex metazoan life cycles' compiled and edited by Giuseppe Fusco and Alessandro Minelli. See - <http://rstb.royalsocietypublishing.org/site/2010/metazoa.xhtml> for further details or you can go straight to the issue contents which are freely available online until the end of February 2010 at <http://rstb.royalsocietypublishing.org/content/365/1540.toc> The print issue is available at the special price of £47.50. You can order this online via the above web page (enter special code TB1540 when prompted) or, alternatively, you can contact [deb-bie.vaughan@royalsociety.org](mailto:deb-bie.vaughan@royalsociety.org)

All Royal Society content (65,000+ articles dating back to 1665) is FREE to access until 28 February 2010 in celebration of the Royal Society's 350th anniversary (<http://royalsocietypublishing.org/seefurther>)

\*2 Beckman Coulter CEQ 8000 capillary DNA sequencing machines for sale (new price)\*

We purchased these 2 instruments in early 2004 and have been very satisfied with their performance over the years, but they are no longer needed since we have a 3rd Beckman CEQ 8000, which is sufficient for our day to day sequencing needs.

Developed using Beckman Coulter's extensive experience in laboratory automation and leadership in capillary electrophoresis technology, the CEQ 8000 is a fully automated genetic analysis system. It can be used for DNA sequencing as well as fragment analysis (e.g., genotyping). This system automatically fills the capillary array with a patented linear polyacrylamide (LPA) gel, denatures and loads the sample, applies the voltage program, and analyzes the data. Software tools let you rapidly review data quality and even customize automated data assessment. With the CEQ 8000, you can perform virtually all-genetic analysis functions with one Gel, one Array and One Software Package.

2 units (complete with dedicated PCs, software and user manuals) are available at \$10,000 CAD each or OBO. Machines were well looked after and professionally serviced. Beckman Coulter maintenance and training is recommended. Buyer is responsible for packaging and shipping costs.

If you are interested or have any further questions, please contact: Katrin Sommerfeld Archibald/Doolittle Labs Dalhousie University Dept. of Biochemistry & Molecular Biology Phone: (902) 494-3569 Email: [ksommerf@dal.ca](mailto:ksommerf@dal.ca)

Thanks, Katrin

Katrin Sommerfeld <[ksommerf@dal.ca](mailto:ksommerf@dal.ca)>

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## Software DAMBE update

Dear Colleague,

I just noticed that the DAMBE version I uploaded two days ago included a test module instead of a release module. It affects the FastME method and a few functions based on the maximum likelihood method. If you do use these, please download the new version that I have just uploaded.

I apologize for this inconvenience.

Best Xuhua

Xuhua Xia, Professor of Biology CAREG and Biology Department University of Ottawa 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 Fax: (613) 562-5486 URL: <http://dambe.bio.uottawa.ca>

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## Software for drawing MSTs

Greetings, Evoldir:

I have generated a bunch of minimum-spanning trees in Arlequin and would like to make figures of these. Currently I am generating individual MST figures from the Nexus data (using FigTree) and then editing this in graphics software to make my figure. This is a very time-consuming exercise (I am drawing the nodes as circles with diameter proportional to the number of sequences at that node) and I was wondering if anyone knows of a software package that can make this more efficient. It would be nice if the software could also incorporate the information about alternative connections, but any level of help would be greatly appreciated.

Cheers, Kurt Wollenberg, Ph.D. Contractor, Lockheed Martin Phylogenetics Specialist Biocomputing Research Consulting Section Bioinformatics and Computational Biosciences Branch (BCBB) OCICB/OSMO/OD/NIAID/NIH

31 Center Drive, Room 3B62 Bethesda, MD 20892-0485 <http://bioinformatics.niaid.nih.gov> “Wollenberg, Kurt (NIH/NIAID) [C]” <wollenbergk@niaid.nih.gov>

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## Software GeoPhyloBuilder ArcGIS

GeoPhyloBuilder v1.1 for ArcGIS is now available. GeoPhyloBuilder is an add-on for ESRI's ArcGIS geographical information system that builds 3D spatial trees from a tree file and associated geographical data. v1.1 supports two new methods for node positioning based on minimum convex polygon centroids and the centroids of overlap and disjunction between sister nodes.

The installation file, VB.net source code and reference manual can be downloaded from <http://sourceforge.net/projects/geophylobuilder/> . Project web pages [https://www.nescent.org/wg\\_EvoViz/-GeoPhyloBuilder#Software-Information](https://www.nescent.org/wg_EvoViz/-GeoPhyloBuilder#Software-Information) David M. Kidd

Research Associate Center for Population Biology Silwood Park Campus Imperial College London O207 594 2470

d.kidd@imperial.ac.uk<mailto:d.kidd@imperial.ac.uk>

“Kidd, David M” <d.kidd@imperial.ac.uk>

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## Software TESS MacOSX Version

A Mac OSX version of TESS is now available. The TESS program computes individual admixture proportions and cluster membership coefficients using multi-locus genotypes and geographical coordinates. It supports both dominant and codominant markers.

Windows and Mac versions, C++ sources codes and the reference manual can be downloaded from Olivier Francois's web site

<http://membres-timc.imag.fr/Olivier.Francois/-tess.html> The method is described here:

Durand E, Jay F, Gaggiotti OE, François O (2009) Spatial inference of admixture proportions and secondary contact zones. *Molecular Biology and Evolution*, 26:1963-1973.

Olivier Francois Computational and Mathematical Biology Group TIMC, Faculty of Medicine Grenoble INP, University of Grenoble F38706 La Tronche, France

best regards, olivier

Olivier Francois <olivier.francois@imag.fr>

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## SSB Graduate Student Research Awards

Society of Systematic Biology Graduate Student Research Award

The Society of Systematic Biologists (SSB) announces the 2010 annual Graduate Student Research Award 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 - \$2000 and approximately seven to nine awards will be made. The list of awardees below includes examples of successful proposals for you to download.

How to apply All application materials must be in electronic format. Applicants and their recommenders are required to use pdf format, rather than Word or some other application, to minimize difficulties in file transfer. Applicants should 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 recommendation letters.

Applicants must submit

1. a 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. and arrange for 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 APPLICANT'S CONTACT E-MAIL ADDRESS AT THE TOP OF THE APPLICATION ITSELF. Both Masters and Ph.D. students in their FIRST TWO YEARS 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 Awards Committee [ssb-apps@life.uiuc.edu](mailto:ssb-apps@life.uiuc.edu). IN THE SUBJECT LINE OF THE E-MAIL, PLEASE INDICATE "Student Research" FOLLOWED BY FIRST INITIAL AND LAST NAME.

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2010.

Sydney Cameron <[scameron@life.illinois.edu](mailto:scameron@life.illinois.edu)>

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## SSB Mayr Award

Society of Systematic Biology Award 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 E-MAIL, please indicate the SSB award category as "Mayr Award" followed by first name initial and last name.

Applicants should: 1. 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 NO LATER THAN 19

APRIL, preferably before the deadline. All candidates will be notified of their participation status no later than 26 April. 2. Register for the meeting using the meeting registration process (<http://www.evolutionssociety.org/SSE2010/>). When you login to the Evolution 2010 Presentation Submission site and submit your title and keywords, you will be given an option to declare your candidacy for the SSB Ernst Mayr Award. Please note that deadline for submission of presentation titles for Evolution 2010 is 19 April.

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 2010 Portland, OR meetings, which will be held at a single venue in a separate session. Talks will be judged on creativity, quality, and excellence of research, and on 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 Portland, again during the banquet or awards ceremony at the conclusion of the Evolution Meetings, and an announcement will be published in Systematic Biology.

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

ofc ph. 217-333-2340 lab ph 217-333-2170 cell ph 217 766-5631 [scameron@life.illinois.edu](mailto:scameron@life.illinois.edu)

[www.life.illinois.edu/scameron](http://www.life.illinois.edu/scameron) Sydney Cameron  
<[scameron@life.illinois.edu](mailto:scameron@life.illinois.edu)>

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## SYNTAX grant scheme

### SYNTAX RESEARCH GRANT SCHEME

The Systematics and Taxonomy (SynTax) research

grant is a new programme for supporting Systematics and Taxonomy research in the UK. The grant scheme is designed to provide short-term funding for preliminary research with a view to stimulating high quality taxonomy and systematics-related research proposals to the UK's Research Councils. The scheme is supported by the BBSRC and NERC UK research councils with additional funding available from DEFRA for work that focuses upon UK BAP priority species. The scheme follows on from the Collaborative Systematics (CoSyst) scheme, through which a number of projects have gone on to receive responsive mode funding. The grant can provide funding of £5k to £30k for projects with a substantial systematic/phylogenetic/taxonomic component. Closing date for applications is the 31st January 2010.

Details of the scheme, can be found at: <http://www.systass.org/awards/-syntax.shtml>  
T.A.Richards@exeter.ac.uk  
T.A.Richards@exeter.ac.uk

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## Systematic research fund

### SYSTEMATIC RESEARCH FUND IS OPEN FOR APPLICATIONS

The SRF fund is jointly administered by the councils of the Linnean Society of London and the Systematics Association.

Applications of all nationalities are welcome and need not be members of either the Systematics Association or the Linnean Society of London. Typical activities supported include contributions to fieldwork expenditure, the purchase of scientific equipment or expertise (e.g. buying time on analytical equipment), specimen preparation (including the cost of temporary technical assistance), and contributions to publication costs. Projects of a more general or educational nature will also be considered, provided that they include a strong systematics component. Typical activities not supported include attendance at scientific meetings and contributions to student maintenance or tuition fees. The fund does not provide payments for Bench Fees and projects already substantially funded by other bodies may be disadvantaged.

Successful projects are selected by a panel of six systematists who represent a wide range of conceptual interests and taxonomic groups. The value of any single award will not exceed £1500.



Applications deadline is the 31st of January. Decisions will be posted March-April. Please read the "Guidelines for applying for SRF funding" before completing the online application form below. Please note that only applications made using the form below are acceptable.

Application forms are accessible at: <http://www.linnean.org/index.php?id=3D331> or <http://www.systass.org/awards/> T.A.Richards@exeter.ac.uk  
T.A.Richards@exeter.ac.uk

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### Systematics Association Meeting Support

The Systematics Association offers small grants (up to £2000) to support scientific meetings on any subject likely to be of interest to members of the Systematics Association, and who wish to publish a proceedings volume through the Association's book series with Cambridge University Press. The application process initially involves only filling in a brief form on the SA website. See <http://www.systass.org/events/-conference-proposal.shtml> for more details, or visit <http://www.systass.org/publications/catalogue.shtml> for some idea of the range of meetings we have supported in the past.

James Cotton School of Biological and Chemical Sciences Queen Mary, University of London +44 (0)207 882 3645 [j.a.cotton@qmul.ac.uk](mailto:j.a.cotton@qmul.ac.uk)  
<http://webspaces.qmul.ac.uk/jacotton/index.html>  
<http://www.sbcs.qmul.ac.uk/staff/jamescotton.html>  
[j.a.cotton@qmul.ac.uk](mailto:j.a.cotton@qmul.ac.uk)

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### UAkron Summer Undergraduates Evolution Ecol

We invite undergraduate students to participate in a summer 2010 Research Experiences for Undergraduates (REU) Program at the University of Akron, sponsored by the National Science Foundation.

This REU site program supports collaborative research on Evolution and Ecology at the Urban-Rural Interface, with opportunities to investigate species, interac-

tions, and ecosystems within human dominated landscapes. Students will be immersed in their own research projects that are part of a larger, interactive team of students and faculty. We offer a stipend, housing, and support for research supplies.

Review of applications will begin February 16, 2009. Women and minorities are strongly encouraged to apply.

For more information, and an application: visit us on the web at <http://www3.uakron.edu/biology/-fieldstation/reu.htm>, contact the Program Director, Dr. Randy Mitchell (330-972-5122 or [rjm2@uakron.edu](mailto:rjm2@uakron.edu)), or write to Biology REU Program, Department of Biology, The University of Akron, Akron, OH 44325-3908.

Dr. Randy Mitchell, Dr. Jean Pan, Dr. Greg Smith  
"Mitchell,Randall J" <[rjm2@uakron.edu](mailto:rjm2@uakron.edu)>

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### UNotre Dame Undergrad Research Speciation Biology

GLOBES SUMMER 2010 UNDERGRADUATE RESEARCH PROGRAM UNIVERSITY OF NOTRE DAME

June 1 - August 6, 2010

The Program: The GLOBES (Global Linkages of Biology, the Environment, and Society) program at the University of Notre Dame is pleased to sponsor a Research Experience for Undergraduates (REU) program during the summer of 2010. Funded by an NSF-IGERT training grant, GLOBES undergraduate research fellowships provide an exciting opportunity to be involved in cutting-edge research with the intent of providing real world solutions to environmental and human health issues. Research projects mentored by GLOBES faculty and students include speciation biology, ecological genetics and the evolutionary consequences of climate change.

Program Activities: The program consists of 10 weeks of full-time research, developed and mentored by GLOBES fellows and faculty. Applicants are encouraged to contact faculty and fellows about potential projects before submitting applications (go to website <http://globes.nd.edu>). Other activities include a weekly seminar program and journal club, regular research lab meetings, workshops on career choices in the sciences, research ethics, problem solving, and scien-

tific writing. Lastly, participants have the opportunity to give formal presentations at the end of the summer REU Symposium.

**Support:** The award consists of a \$4200 stipend and includes housing on campus, meals, lab supplies and travel (up to \$500).

**Eligibility:** Current sophomores and juniors, who are U.S. citizens or permanent residents, are eligible to apply; exceptionally well qualified freshmen may be considered. Women, minority students, students with disabilities, and students from small colleges are encouraged to apply.

**Application Materials:** Priority will be given to applications postmarked by February 12, 2010. Application forms can be found at [globes.nd.edu](http://globes.nd.edu) and must include (1) a cover letter stating your career goals and research interests; (2) a completed application form; (3), an official transcript, and (4) two recommendation letters from science faculty. Incomplete applications will not be considered.

**Selection:** Preference will be given to sophomores and juniors whose primary interest is a research career, and who will likely pursue a Ph.D. Award notifications will occur in late March/early April.

**Send Application Materials to:** Virginia Anderson, GLOBES Administrative Coordinator University of Notre Dame Department of Biological Sciences Notre Dame, Indiana 46556-0369 Phone: (574) 631-3287 Email: [g.anderso@nd.edu](mailto:g.anderso@nd.edu)<<mailto:g.anderso@nd.edu>>

If you need to express mail, only send via FedEx or UPS, not the US post office.

Ginna Anderson GLOBES Program University of Notre Dame Department of Biological Sciences Rm 180 Galvin PH: 574-631-3287 EMail: [g.anderso@nd.edu](mailto:g.anderso@nd.edu)<<mailto:g.anderso@nd.edu>> Mail to: P.O. Box 369 Notre Dame, Indiana 46556 Web: <http://globes.nd.edu>< <http://globes.nd.edu/> >

Ginna Anderson <[g.anderso@nd.edu](mailto:g.anderso@nd.edu)>

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## USouthCarolina EvolutionREU

The University of South Carolina hosts an REU site in Integrative Evolutionary Biology. Applications for this summer's program are due February 24, 2010.

This program is for undergraduate students interested in gaining a hands-on experience in research in evolu-

tionary biology. The program emphasizes the interface between molecular genetics and organismal-level processes. Students will learn about hypothesis generation and testing, as well as the techniques and experimental designs employed in molecular biology and one or more other subspecialty areas - including behavior, life history evolution, systematics, population biology, or ecological physiology. Students will present summaries of their work in mini-symposium at the end of the summer. Undergraduate students from any academic institution except the Columbia campus of the University of South Carolina are invited to apply. Students from underrepresented groups and smaller undergraduate institutions are especially encouraged to apply. US citizenship or permanent residency is required.

For more information, go to <http://www.biol.sc.edu/~elygen/reu/evolution.html> Jeffrey L. Dudycha Assistant Professor Dept. of Biological Sciences University of South Carolina Columbia, SC 29208 [dudycha](mailto:dudycha@biol.sc.edu) [at] <http://www.biol.sc.edu/~dudycha> [dudycha@biol.sc.edu](mailto:dudycha@biol.sc.edu)

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## UWyoming Bioinformatics UndergradSummerResearch

<http://www.wyomingbioinformatics.org/-SummerSchool/> Bioinformatics and Computational Molecular Biology Undergraduate Summer Research Program University of Wyoming The University of Wyoming is proud to offer summer research opportunities to external undergraduate students to engage in research in bioinformatics and computational molecular biology in Laramie. The summer research program will last from May 24, 2010 to August 6, 2010 and will include a stipend of \$3500 for the period.

The program in 2007-2008 included students from Amherst College, Oberlin College, Grinnell College, Juniata College, SUNY-Buffalo, and CUNY.

Information on the 2009 students and their research can be found here.

The program includes both lectures and educational opportunities as well as a focus on a research experience. Lectures will be given by both University of Wyoming faculty and external speakers. During the summer, Nikolay Dokholyan (University of North Carolina) will give a presentation on protein structure prediction. Keith Crandall (Brigham Young University)

will give a presentation on phylogenetic methods.

Several labs that will host bioinformatics/computational molecular biology students include:

- \* Alex Buerkle: Statistical genetics and models of adaptation and speciation
- \* Rex Gantenbein: Computational resources for rural health and education
- \* Mark Gomelsky: Statistical analysis of microarray data; microbiology
- \* Snehalata Huzurbazar: Birth-death processes in biology
- \* Jan Kubelka: Protein folding
- \* David Liberles: Comparative genomics and molecular evolution
- \* Jessica Siltberg-Liberles: Protein structural bioinformatics
- \* Anne Sylvester: Comparative genomics of maize
- \* Dan Wall: Genetics of bacterial motility
- \* Naomi Ward: Metagenomics and Microbial Genomics
- \* Cynthia Weinig: Environmental Genetics and Adaptation in Plants

To apply, send a resume, cover letter, and statement of research interests to liberles@uwyo.edu, arrange to have 2 letters of recommendation sent directly by the letter writer to liberles@uwyo.edu, and arrange to have an official transcript sent to:

David Liberles Department of Molecular Biology Dept. 3944 University of Wyoming Laramie, WY 82071

Your cover letter should indicate: 1). Any prior experience in computer programming and if none, any interest in a mini-tutorial on programming; 2). Your plans (if known) immediately after graduation and if they include immediately attending graduate or professional school; 3). If your ultimate career plans involve a Ph.D., an M.D., or an M.D./Ph.D., and 4). Your top two choices of research group to work in over the

summer.

Applications for Summer, 2010 are now being accepted. Review of applications will begin on February 5, 2010 and continue until the class is filled.

“David A. Liberles” <liberles@uwyo.edu>

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### Volunteer StKilda mouse project

Volunteer wanted for 5 weeks from 5th March 2010, to help with live trapping of field mice on St Kilda, a small archipelago 180km off the west coast of Scotland.

Responsibilities consist of helping to set up trapping grids on remote parts of the island, prepping and cleaning traps, handling mice and recording data. You will be living as part of a small group of researchers in restored cottages on the remotest field site in the British Isles; the accommodation is fairly basic but the scenery is spectacular! A great opportunity to acquire small mammal field experience.

You must be available for the full duration of the field work, and should have a background in biological sciences. A good level of fitness and head for heights are essential, as the field work will involve carrying heavy equipment packs over steep and precipitous terrain in all weathers (and we do mean all weathers!).

Helicopter flights between St Kilda and Benbecula (Outer Hebrides) will be provided, as will food and board whilst on St Kilda. Reasonable travel expenses within Scotland will also be reimbursed.

To apply for this volunteer position, please send a CV and covering letter, plus details of two referees who can be contacted at short notice by email to: Tom Black (t.w.black@sms.ed.ac.uk).

T.W.Black@sms.ed.ac.uk T.W.Black@sms.ed.ac.uk

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## AustralianNatIU ComputationalGenomics

The Computational Genomics Group in the John Curtin School of Medical Research, Australian National University (Canberra, Australia) have made pioneering contributions to our understanding of genetic diversity within and between mammal species in areas including: the genomic distribution of linkage disequilibrium, human molecular adaptation, the influence of sex on mutation rates, the relationship between epigenetic state and genetic variation, and the radiation of mammals. These contributions have been accompanied by significant methodology developments in the form of both novel statistical models and open source software for analyses of genomic diversity. Our recent advances in models of context-dependent substitution, for instance, represent a significant advance in robust estimation of the mode of natural selection.

We are seeking outstanding applicants for a postdoctoral fellowship. The individual will work on the development and application of improved models of sequence divergence, joining a highly productive collaboration between Associate Professor Gavin Huttley and Dr Von Bing Yap (Department of Statistics and Applied Probability, National University of Singapore). The work will build on the PyCogent open source software toolkit for

statistical modelling of molecular evolution developed in the Huttley lab.

Application deadline: 7 February 2010 Full position description: <http://jobs.anu.edu.au/PositionDetail.aspx?p=3D1074> For more details, please contact Gavin Huttley (Gavin.Huttley@anu.edu.au).

Gavin.Huttley@anu.edu.au Gavin.Huttley@anu.edu.au

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## AustralianNatIU ComputationalGenomics 2

The Computational Genomics Group in the John Curtin School of Medical Research, Australian National University (Canberra, Australia) have made pioneering contributions to our understanding of genetic diversity within and between mammal species in areas including: the genomic distribution of linkage disequilibrium, human molecular adaptation, the influence of sex on mutation rates, the relationship between epigenetic state and genetic variation, and the radiation of mammals. These contributions have been accompanied by significant methodology developments in the form of both novel statistical models and open source software for analyses of genomic diversity. Our recent advances in

models of context-dependent substitution, for instance, represent a significant advance in robust estimation of the mode of natural selection.

We are seeking outstanding applicants for a postdoctoral fellowship. The individual will work on the development and application of improved models of sequence divergence, joining a highly productive collaboration between Associate Professor Gavin Huttley and Dr Von Bing Yap (Department of Statistics and Applied Probability, National University of Singapore). The work will build on the PyCogent open source software toolkit for statistical modelling of molecular evolution developed in the Huttley lab.

Application deadline: 28 February 2010 Full position description: <http://jobs.anu.edu.au/PositionDetail.aspx?p=1074> For more details, please contact Gavin Huttley (Gavin.Huttley@anu.edu.au).

Gavin Huttley <Gavin.Huttley@anu.edu.au>

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## BigelowLabs Maine Phylogenomics

January 14, 2010

### Position Description

Post-doctoral position in bioinformatics / phylogenomics Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, Maine

A full-time post-doctoral position is available in the lab of Dr. Hwan Su Yoon at Bigelow Laboratory for Ocean Sciences in West Boothbay Harbor, Maine. This position involves participation in an NSF-funded project, "RedToL: Phylogenetic and Genomic Approaches to Reconstructing the Red Algal (Rhodophyta) Tree of Life" to study phylogenetic relationships of red algae using multi-gene dataset, and plastid genomes and transcriptome sequence data. Therefore, a post-doc with a strong background in evolutionary genomics, molecular evolution, bioinformatics, or genome analysis is requested to start in March 2010. Primary duties include plastid DNA isolation, EST library construction, phylogenomics and bioinformatics analysis. Candidate with a Ph.D. degree in evolutionary genomics, computational biology or a relevant field is required. Experience with next generation sequence analysis (454, Illumina, or SOLiD) is desirable. Funding is available for three years.

Applicants should send their CV, a letter of intent de-

scribing candidate's motivation, qualifications, skills, and experience relevant to this position, and contact information for two references to [jobs@bigelow.org](mailto:jobs@bigelow.org). Please reference #PD10-1 in the subject line. For full consideration, the application should be received by January 31st, 2010. Bigelow Laboratory is an Equal Opportunity Employer.

Jane Gardner <jgardner@bigelow.org>

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## CambridgeExeter TransgenerationalEvolution

Research associate vacancy at Cambridge/Exeter: 'Transgenerational effects in evolution'

We invite applications for a postdoctoral Research Associate position, to start on 1 April 2010 or as soon as possible thereafter. Funds are available for up to 36 months. The successful candidate will join an interdisciplinary research team, funded by the EPSRC to explore the role of transgenerational effects in evolution, which involves mathematicians and biologists at the Universities of Cambridge, Exeter, University College London and Surrey. They will be based for the first 18 months of the project in the Behaviour and Evolution Group in the Department of Zoology, University of Cambridge. Subsequently, it is intended that they will be based in the School of Engineering, Mathematics and Physical Sciences at the University of Exeter.

The successful candidate will have a PhD, or equivalent, and substantial experience in mathematical modelling and preferably expertise in dynamical systems or control theory.

Closing date for applications: January 29th, 2010.

Details at

<http://www.zoo.cam.ac.uk/zooone/administration/vacancy.html>

Stuart Townley

<S.B.Townley@exeter.ac.uk>

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## FinnishMuseumNH BirdEvolution

The Finnish Museum of Natural History invites applications for the position of



A Postdoctoral Researcher

to the project Origin and maintenance of phenotypic variation. The project is funded by the Academy of Finland and the Principal Investigator is Academy Research Fellow Toni Laaksonen. The assignment will begin on the 1st of February 2010 (or as otherwise agreed) and last until the end of 2011.

The main aim of the project is to understand mechanisms creating and maintaining variation in coloration and other phenotypic traits, using as a model species a passerine bird, the pied flycatcher (*Ficedula hypoleuca*). The males in this species exhibit a plumage trait complex that varies extensively both among and within populations. The project uses a combination of field experiments, lab studies and analyses of long-term data to reveal the roles of spatially and temporally varying selection, gene flow, and variable mating strategies in the maintenance of this variation. Another main question in the project is to examine the role of seasonal interactions in life history and population dynamics.

The long-term monitoring data from the Museums extensive monitoring schemes furthermore provide a number of exciting possibilities to work on issues related to avian responses to environmental change. The Post doc project plan can be tailored according to the interest and experience of the candidate within this broad framework. An important aspect of the post doctoral work is to support a PhD project on the migratory connectivity between wintering and breeding areas (i.e. on how the conditions experienced on the wintering grounds in Africa carry over to the breeding grounds and vice versa).

A person selected for the post of postdoctoral researcher is required to have a doctoral degree and the ability to do independent scientific work.

The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities and the job-specific component of the salary will thus be EUR 2 578,53 per month. In addition, the appointee will be paid a salary component based on personal work performance.

The application should include a complete CV including education and degrees obtained, prior research experience, publication list, a max. one page letter of motivation explaining why you are interested in the position and why you would be suitable for it, and contact information for referees.

The application with the attachments should be addressed to the Director Juhani Lokki and sent to [hkirjaamo@helsinki.fi](mailto:hkirjaamo@helsinki.fi). The deadline for applications is 21 January 2010 at 15.45 local Helsinki time.

For further information, please contact Toni Laaksonen, Academy Research Fellow, +358 9 191 28664 or +358 50 5288117, [toni.k.laaksonen\(AT\)helsinki.fi](mailto:toni.k.laaksonen(AT)helsinki.fi).

Additional information can be found from the following web-pages: Research environment: Monitoring team at the Finnish Museum of Natural History: <http://www.fmmh.helsinki.fi/english/zoology/monitoring/index.htm> Personal web-page of Toni Laaksonen: <http://users.utu.fi/tokrla/toni/> Web-page of the part of the group working at the University of Turku: <http://users.utu.fi/tokrla/toni.k.laaksonen@helsinki.fi>

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## Gainesville ComputationalBiol

I have an opening in my laboratory for a geneticist/computational biologist.

POSITION: Computational Biologist/Research Geneticist

LOCATION: Gainesville, FL

DESCRIPTION OF DUTIES: The position is located in the Center for Medical, Agricultural, and Veterinary Entomology, Imported Fire Ant and Household Insects Research Unit at Gainesville, Florida. The researcher will interact closely with a dynamic group of researchers (including collaborators from University of Lausanne and elsewhere) with expertise in population and evolutionary genetics, functional genomics, and bioinformatics. The incumbent will be a member of a team investigating the population and evolutionary genomics of fire ants through large-scale analysis of whole-genome sequence data. The project will involve comparative genomic studies in fire ants as well as across Hymenoptera, design and use of SNP markers for genetic mapping and population genomic studies, characterization and study of genomic sequence for features of interest (e.g., repetitive elements, regulatory regions), and numerous molecular evolutionary studies (e.g., evolution of gene families, origin and fate of gene duplications). The incumbent will be responsible for providing bioinformatics support to the research group by participating in several of the above studies and will interact closely with other collaborators with bioinformatics experience. The incumbent will have the opportunity to pursue additional molecular evolutionary genomic studies of fire ants, including one or more laboratory experiments, under the supervision of the lead scientist and will be responsible for data analyses and

writing scientific manuscripts for publication.

**QUALIFICATION REQUIREMENTS:** Recent Ph.D. in Genetics, Bioinformatics/Computational Biology or closely related discipline appropriate to the position. The applicant must have an interest in population and evolutionary genetics and ideally should be familiarized with bioinformatics approaches relating to population and evolutionary genetics as well as experience analyzing next generation sequencing data. Applicants with a strong computational background should have demonstrated experience (e.g., refereed publications, Ph.D. thesis) in at least one programming language (Python/Perl/Ruby, C/C++), as well as experience in analysis of genomic (or transcriptomics) data and whole-genome level study. Applicants with mainly an experimental background should have demonstrated experience in standard molecular genetic techniques (PCR, fluorescent-based genotyping and next generation DNA sequencing, gene expression, bioinformatics) as well as experience in basic programming (in any language) and large-scale data analysis (e.g. high-throughput genotyping, comparative genomics).

The full advertisement and description can be found at: [jobview.usajobs.gov/GetJob.aspx?JobID989339&JobTitle=RESEARCH+GENETICIST+%2f+COMPUTATIONAL+BIOLOGIST++\(Postdoctoral+Research+Associate\)&sort=rv&vw=d&brd876&ss=0&FedEmp=N&FedPub=Y&q=ra-10-036-L&AVSDM09-12-07+10%3a04%3a00](http://jobview.usajobs.gov/GetJob.aspx?JobID989339&JobTitle=RESEARCH+GENETICIST+%2f+COMPUTATIONAL+BIOLOGIST++(Postdoctoral+Research+Associate)&sort=rv&vw=d&brd876&ss=0&FedEmp=N&FedPub=Y&q=ra-10-036-L&AVSDM09-12-07+10%3a04%3a00)

For additional information or queries, please contact DeWayne Shoemaker by email at: [dewayne.shoemaker@ars.usda.gov](mailto:dewayne.shoemaker@ars.usda.gov)

DeWayne Shoemaker <[dewayne.shoemaker@ARS.USDA.GOV](mailto:dewayne.shoemaker@ARS.USDA.GOV)>

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## Madrid Diversity Conservation

Within the framework of a research project titled 'Analysis and management of the diversity in structured populations in the conservation of genetic resources and breeding programmes: theoretical studies' we offer a grant for four years to develop a PhD thesis in the Animal Breeding Department of the Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA) in Madrid (Spain). Net salary is around 1,000 euros per month and free fees for the doctorate courses.

Within the same project we also offer a postdoctoral

contract for three years. Main task of that position will be to carry out computer simulations on different aspects of the general objective of the project. Therefore, a requisite for the candidates is the ability for computer programming (FORTRAN preferred). A sound background on quantitative and population genetics is also required. Net salary is around 1,500 euros per month and two extra pays (fourteen in total).

For further information contact:

Jesús Fernández Martín 34 913471487 Departamento de Mejora Genética Animal 34 913572293 (FAX) Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria Ctra. Coruña Km 7,5 28040 Madrid, Spain.

[jmj@inia.es](mailto:jmj@inia.es)

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## MichiganStateU PhytoplanktonPhylogenies

Two postdoctoral positions in phytoplankton traits and models of community structure

We are looking for two postdoctoral researchers to develop trait-based approaches to plankton ecology. One position will focus on applying statistical approaches to relate traits to phylogenies, environmental gradients, and each other. The other position will develop trait-based mathematical models. Ideally these two positions will find ways to collaborate.

Basic qualifications are a PhD in ecology, oceanography, limnology or related field and a strong interest in trait-based approaches and quantitative ecology. The first position requires familiarity with multivariate statistics, the second position requires modeling experience, preferably trait-based modeling approaches (e.g., adaptive dynamics). For both positions, knowledge of phytoplankton ecology, limnology, or oceanography is a plus. These positions are supported by a recently funded NSF grant "Phytoplankton Traits, Functional Groups and Community Organization: A Synthesis" and a grant from the James S. McDonnell Foundation, "Plankton Community Assembly: Theory and Practice."

The postdocs will be based at the Kellogg Biological Station of Michigan State University ([www.kbs.msu.edu](http://www.kbs.msu.edu)). Each position is for one year with a possibility of renewal, given satisfactory performance. Send a cover letter describing your research interests

and experience, current CV and names of 3 references to Elena Litchman (litchman@msu.edu) by January 31, 2010. For questions, please contact Elena Litchman or Chris Klausmeier (klausme1@msu.edu).

litchman@msu.edu

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## MississippiStateU CrocodilianGenomeEvolution

Position Title: Post Doctoral Associate

Area of Specialization: Genome analysis/Bioinformatics

Position Function: To perform a variety of routine and specialized duties in the laboratory requiring considerable knowledge of the principles and theories of bioinformatics and genome analysis including the analysis of whole genome shotgun (WGS) sequence data as well as assembly and analysis of 454 and Illumina next-generation sequence data and including transposable element analysis.

Essential Duties and Responsibilities: Candidates should have demonstrated research experience in bioinformatics and preference will be given to those with experience working with WGS data, next-generation sequence data, and transposable element sequences. Duties include the creation of custom scripts (Perl, Python, C++, etc.) to analyze large sequence databases from a variety of taxa including crocodilians and other reptiles (including birds), mammals, and insects (see <http://www.crocodile.bch.msstate.edu/-Research.htm> for additional details). The successful candidate may also train students in the use of computational tools and procedures.

Minimum Qualifications: Ph.D. degree with major course work in curriculum appropriate for the field of assignment - bioinformatics, molecular biology, etc.

Preferred Qualifications: Experience with genome annotation techniques, custom scripting, and intergenomic analysis.

Instructions for Applying Please submit a letter of application, curriculum vitae, transcripts and names of three references to:

Dr. David A. Ray Department of Biochemistry and Molecular Biology Box 9560 - Dorman Hall Mississippi State University Mississippi State, MS 39762 Contact E-mail: dray@bch.msstate.edu Contact Phone: 662-

325-7740

Screening will begin on January 10, 2009 and will continue until the position is filled.

Mississippi State University is an affirmative action/equal opportunity employer

Department Profile The Department of Biochemistry and Molecular Biology is a comprehensive department with an academic, research and service mission. The Department offers B.S., M.S., and Ph.D. degrees from within the College of Agriculture and Life Sciences, and currently advises approximately 150 undergraduate and 25 graduate students.

– David A. Ray Assistant Professor Department of Biochemistry and Molecular Biology Mississippi State University University Starkville, MS 39762

Website: <http://www.crocodile.bch.msstate.edu> E-mail: dray@bch.msstate.edu Office phone: 662-325-7740 Laboratory phone: 662-325-7746 Fax: 663-325-8664

Benjamin Franklin, after witnessing the ascent of one of the first hot-air balloons, was challenged about the use of human flight. Franklin reportedly replied, “What’s the use of a newborn baby?”

dray@bch.msstate.edu dray@bch.msstate.edu

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## Nairobi EmergingDiseaseEvolution

Post Doctoral Fellow - Molecular Biology and Biotechnology Department

icipe is an independent, intergovernmental organization funded by government aid agencies, UN organisations and private foundations to carry out research and training in the environmentally sound and sustainable management of arthropods for improving health and agricultural productivity in Africa. icipe has approximately 300 staff to support its research and capacity building programmes, located at various sites in Kenya, and other locations in Africa, including Ethiopia and Sudan.

icipe seeks to recruit a young and highly motivated Post Doctoral Fellow to work in its Molecular Biology and Biotechnology Department and be part of the new collaborative project entitled “An Integrated Response System For Emerging Infectious Diseases in East Africa (AVID)” (<http://avid.icipe.org>; <http://sites.google.com/site/arbovirusdynamicsprojectsite>). AVID aims to bring

current molecular and epidemiological approaches to the detection of pathogens - both known and unknown in field samples. One of icipe's critical roles in this project is to develop a platform of wet-lab technologies enabling high-throughput screening and detection of known and unknown arthropod transmitted viruses (arboviruses).

This position is an opportunity for a dynamic and highly motivated post-doc who is capable of working in dispersed and complex teams, to make important contributions to the understanding of disease in Africa - particularly epidemic viral disease. This job is based in Nairobi. Requirements

\* PhD in molecular biology/genetics. \* Experience in molecular analysis of complex biological material. \* Hands on experience of highly multiplexed PCR. \* Quantitative PCR and mass spectrometry, e.g. for diagnostics and of working with complex, mixed biological samples. \* Phylogenetic/population analysis in prokaryotes or eukaryotes would be an advantage. \* Excellent communication and interpersonal skills. \* Ability to reason independently. \* A track record of publications and report writing. \* Fluency in spoken and written English. Knowledge of French would be an added advantage.

#### Responsibilities

\* Designing and testing highly multiplexed assays for host/vector/pathogen identification. \* Establishing QPCR and other analytical protocols including mass-spectrometry for detection of known viruses. \* Develop protocols for the identification of unknown pathogens.

This appointment is for two years with the possibility to renew subject to performance and funding availability. Benefits including a competitive international compensation package will be offered to the successful candidate.

Applications will be accepted up to 15th February, 2010, or when the position gets filled whichever is the earlier. Please send an application with a detailed CV and names and addresses of 3 referees including e-mail addresses and Fax numbers to [hr@icipe.org](mailto:hr@icipe.org) This e-mail address is being protected from spambots. You need JavaScript enabled to view it or:

The Human Resources Department icipe - African Insect Science for Food and Health P.O. Box 30772-00100 Nairobi Kenya

"Masiga, Daniel" <[dmasiga@icipe.org](mailto:dmasiga@icipe.org)>

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## NatIUireland Maynooth NetworkEvolution

Two-year Science Foundation Ireland post-doctoral position at the National University of Ireland, Maynooth on the evolution of microbial genomes.

We have funding available for one position for two years, with a salary of approximately 44,000 Euro (approximately 64,000 USD), which includes 10.75% PRSI payment.

The research will focus on the evolution of microbial genomes, concentrating in the first instance on the evolution of the YESS group (Yersinia, Escherichia, Salmonella and Shigella), but will broaden to encompass all completed genomic sequences of prokaryotes.

The ideal candidate should be able to program in the Python or PERL languages and should be familiar with the construction of phylogenetic trees and the analysis of network diagrams.

The research group at NUI Maynooth is part of a small collection of bioinformatics and Molecular Evolution groups, composed of approximately 20 researchers. You can find out more about our groups at <http://bioinf.nuim.ie/> This position is available to be filled immediately, but will remain open until the right person is found for the position.

Any enquiries can be directed to me at [james.o.mcinerney@nuim.ie](mailto:james.o.mcinerney@nuim.ie)

Regards,

James

- James McInerney, Institute for Chemical Biology, NUI Maynooth, Co. Kildare, Ireland. P: +353 1 7083860 F: +353 1 7083845 W: <http://bioinf.nuim.ie/> James McInerney <[james.o.mcinerney@nuim.ie](mailto:james.o.mcinerney@nuim.ie)>

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## NEON ResAssoc GeneticBioinformatics

The National Ecological Observatory Network (NEON, Inc.) is a nonprofit science corporation dedicated to un-

derstanding how changes in climate, land use and invasive species impact ecology. Currently under design is the NEON project - an observatory comprising more than 60 environmental and biological monitoring locations distributed throughout twenty domains across the United States, Hawaii, Alaska & Puerto Rico. These observations will be monitored and controlled in real-time from our headquarters in Boulder, Colorado.

#### Term Appointment:

This position will be funded for two years initially with the possibility of one year extension as deemed appropriate based on the success of the tasks performed during the first year.

#### Essential Duties and Responsibilities:

\* Coordinate and oversee data processing and analyses for two prototype studies: 1) soil microbial diversity and 2) insect DNA barcoding. \* Coordinate data management between outsourced analytical facilities and NEON cyberinfrastructure team. \* Work with NEON scientists to develop appropriate ways to maintain genetic data and formats for public data access. \* Work with NEON scientists to develop useful data products and analyses for the NEON genetic data. \* Work with collaborating laboratories and NEON scientists to facilitate publication of results from the prototype studies, and collaborate with the NEON microbiology and barcode working groups to prepare reports and develop recommendations for future analyses and data processing.

#### Education:

\* PhD in computational biology, bioinformatics, computer science or related field (Life science, Ecology, Evolution, etc.)

#### Required Experience:

\* Experience analyzing high-throughput (454, Illumina, or SOLiD) data \* Experience working in a collaborative scientific enterprise \* Scientific writing and review

#### Preferred Experience:

\* Experience or familiarity with DNA barcoding.

#### Skills and Abilities:

\* Strong communication and interpersonal skills \* Undertake responsibilities beyond those associated with individual research projects \* Ability to work independently and as part of an active science team \* Problem solver who can successfully apply experience, judgment, and creativity to both short- and long-term challenges \* Self-starter who can create new opportunities within this field and use novel methods, analyses and approaches to tackle continental- scale research

#### TO APPLY:

Please send your cover letter and CV/resume to [Careers@NeonInc.org](mailto:Careers@NeonInc.org) with Bioinformatics Research Associate in the subject line.

NEON Inc. is an Equal Opportunity Employer. Women, Minorities, Veterans and Disabled Persons are encouraged to apply.

Laura Reynolds <[lreynolds@neoninc.org](mailto:lreynolds@neoninc.org)>

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### PennStateU Adaptation

An NSF-funded postdoctoral position is available immediately in the laboratory of Tracy Langkilde (<<http://homes.bio.psu.edu/people/faculty/langkilde/>>) at The Pennsylvania State University. The aim of this project is to understand the ecology and evolution of adaptive responses to rapid global change.

The main duties of the postdoc will be to conduct field and lab experiments and surveys aimed at unraveling the causes and consequences of changes in lizard anti-predator behavior following the invasion of red imported fire ants. The postdoc will be expected to play an important role in developing this research, in collaboration with the lab manager and graduate and undergraduate students involved in the project.

The successful candidate will have a PhD in behavioral ecology, ecology, evolutionary biology or a related field. Previous extensive field experience and publication of papers in leading journals in the field is a must. Candidates with prior experience in mark-recapture, population genetics, and research in reptilian systems are especially encouraged to apply.

The postdoc will be based at the University Park campus of Penn State. Field research trips totaling up to 3 months per year will be conducted in semi-remote locations throughout the Southeastern USA. A valid driver's license and willingness to drive long distances is required.

Target start date is April 1, 2010, with the first field trip taking place in early May 2010. The initial contract is for one year; with possible extensions up to three years pending satisfactory performance and available funding.

Interested applicants should send pdfs with CV, a short (less than one page) statement of research interests and experience, and contact information of three references



to <mailto:tll30@psu.edu>, indicating a postdoctoral position in the subject line. The review of applications will begin immediately and continue until the position is filled.

Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

nafl1@psu.edu naf11@psu.edu

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## Portugal Celegans ExperEvolution

ERC POSTDOCTORAL POSITION ON C. EL-EGANS EXPERIMENTAL EVOLUTION SECOND CALL 18 JANUARY 2010

A postdoctoral position is available in the laboratory of Henrique Teotonio at the Instituto Gulbenkian de Ciencia (IGC), Oeiras Portugal ([www.igc.gulbenkian.pt](http://www.igc.gulbenkian.pt)).

**PROJECT:** The research will be focused on the genetic basis of adaptation to novel environments, in particular on the evolution of phenotype distributions in heterogeneous environments using populations of *C. elegans* manipulated in their mating system and standing levels of genetic variation. We aim to describe adaptation in life-history, behavioral and gene expression phenotypes, and correlate them with genome-wide patterns of DNA sequence variation during long-term experimental evolution. The specifics of the postdoctoral project will be defined according to the applicant's interests and experience, and collaborations with labs in the USA and Europe are envisaged.

**REQUIREMENTS:** PhD in evolutionary genetics and interest in the topics of adaptation from standing genetic variation, evolution of phenotypic plasticity, and mating system evolution. The ideal candidate will have a strong background in quantitative genetics (analysis of selection gradients, estimation of breeding values, QTL mapping) and the population genetics of DNA sequence data (comparative analysis of heterozygosity and linkage disequilibria). Although not essential, experience with culturing model organisms in the lab is preferred, as well as experience with basic molecular biology techniques. The candidates are expected to have the computational skills to conduct multivariate statistical analysis and data management. Candidates with a PhD in theoretical evolutionary genetics are invited to apply.

**FUNDING and STARTING DATE:** The postdoc-

toral position is funded by the European Research Council (ERC), for a monthly salary of about 2000, plus social benefits. The successful applicant can start as soon as

**APPLICATIONS:** Applications should be composed of a CV including professional experience, list of relevant publications, and list of technical competencies. CVs are to be accompanied by a letter of motivation and the contact information of two referees. Applications should be sent by email to: [teotonio@igc.gulbenkian.pt](mailto:teotonio@igc.gulbenkian.pt). The call for the position will remain open until a suitable candidate is found.

Henrique Teotonio <[teotonio@igc.gulbenkian.pt](mailto:teotonio@igc.gulbenkian.pt)>

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## UAntwerp BirdParasite

Call for applicants on bird-parasite research

In the framework of its research on host-parasite interactions between birds and Ixodid ticks, the Evolutionary Ecology Group of the University of Antwerp is looking for candidates who want to apply for either a PhD scholarship (4 years) or a visiting postdoc fellowship (6 to 12 months). Applications will be submitted to and evaluated by the Belgian Fund for Scientific Research.

We welcome applications on the following topics, or a combination of them: (1) ecology of ectoparasite transmission in a guild of cavity-nesting birds, using field studies and/or cage experiments; (2) life-cycle and host preference of nidicolous cavity-dwelling ticks (3) population structure and host differentiation in ticks using molecular markers; (4) molecular identification of hosts in blood meals; (5) individual-based modelling of tick transmission and evolution of host specialization in relation to resource use by hosts.

PhD scholarships can be awarded for 4 years, starting 1st October 2010, with application deadline 1 February 2010. Candidates should have an MSc degree from an EU university and have excellent student grades (ranking among the top 10% of their graduation cohort). Publications also increase the chance of being selected. Specific expertise is not required.

Visiting postdoctoral fellowships can be awarded to non-Belgian postdocs for a maximum of 12 months. Candidates are selected based on publication record and expertise. Applications can be submitted at any time with a minimum of three months before the starting date.

If you are interested or need further information, contact Prof. Erik Matthysen at [erik.matthysen@ua.ac.be](mailto:erik.matthysen@ua.ac.be) <<mailto:erik.matthysen@ua.ac.be>>

Prof. Dr. Erik Matthysen Evolutionary Ecology Group  
Department of Biology, University of Antwerp

Groenenborgerlaan 171, 2020 Antwerpen +32 3 265  
3464

[erik.matthysen@ua.ac.be](mailto:erik.matthysen@ua.ac.be) [erik.matthysen@ua.ac.be](mailto:erik.matthysen@ua.ac.be)

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## UCalgary Biodiversity

POSTDOCTORAL POSITION in Pollination and Biodiversity, combined appointment through Departments of Biological Sciences at University of Calgary and Simon Fraser University.

As part of the NSERC-funded Canadian Pollinators Initiative (CANPOLIN), researchers Jana Vamosi [<http://homepages.ucalgary.ca/~jvamosi/>] and Elizabeth Elle [<http://www.sfu.ca/biology/faculty/elle/>] invite applications for a two-year postdoctoral position requiring skills in pollination research. Individuals with experience in the development of datasets from disparate sources, considerable capacity for independent research, and strong quantitative abilities are preferred. Taxonomic skills in both plants and insects are a plus. The successful applicant will be responsible for developing and analyzing a dataset of pollination in native and nonnative Canadian plant species, and for helping to coordinate the efforts of ~20 researchers situated throughout Canada, all studying the abundance and diversity of pollinators and how they affect pollination within native and agroecosystems. This appointment is shared between University of Calgary and Simon Fraser University, but it is expected that the successful applicant will perform the majority of their responsibilities at the University of Calgary. The NSERC-CANPOLIN network is a consortium of 50 researchers in pollination biology and provides many collaborative opportunities [see <http://www.uoguelph.ca/canpolin/> for more details]. To apply, please arrange to have a curriculum vitae, statement of research interests and plans, copies of two publications, and contact information for three references sent by email to Jana Vamosi [[jvamosi@ucalgary.ca](mailto:jvamosi@ucalgary.ca) <<mailto:jvamosi@ucalgary.ca>>] and Elizabeth Elle [[elizabeth\\_elle@sfu.ca](mailto:elizabeth_elle@sfu.ca) <[mailto:elizabeth\\_elle@sfu.ca](mailto:elizabeth_elle@sfu.ca)>] or by post to: Jana Vamosi, Department of Biological Sciences, University of Calgary, 2500 University Dr.

NW, Calgary AB T2N1N4, Canada. Review of applications will begin on Feb 1, 2010 and continue until a suitable candidate is identified. Starting date is anticipated to be this spring or summer and is contingent on release of network funds. Salary and benefits will be competitive with NSERC postdoctoral fellowships and may include some additional funding for travel related to fulfilling responsibilities to CANPOLIN. Equity is a University policy; women, aboriginal peoples, members of visible minorities and persons with disabilities are encouraged to apply.

[jvamosi@ucalgary.ca](mailto:jvamosi@ucalgary.ca)

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## UCaliforniaLosAngeles PlantEvolution

POST-DOCTORAL SCHOLAR POSITION in Plant Evolutionary Biology/Molecular Ecology Department of Ecology and Evolutionary Biology UCLA

A postdoctoral scholar position is available in the lab of Prof. Victoria Sork to conduct research on the environmental genomics of oaks (2/3) and to manage the lab (1/3 time). Current, on-going lab projects include: population genomics, landscape genetics, and phylogeography of California oaks; co-evolution of lichen fungal-algae symbioses; and molecular ecology of pollen and seed dispersal. The lab is an intellectually dynamic environment consisting of students, postdocs, and visiting researchers working on a diverse range of questions. We meet weekly to discuss projects and articles, and have annual field trips and retreats. UCLA offers an exciting environment for evolutionary biologists, ecologists, conservation biologists, and bioinformaticians through its myriad seminars, colloquia, and informal activities within the department and across campus.

The specific post-doctoral project will be developed jointly. The lab management component will include data management, statistical analyses, grant preparation, and manuscript preparation, with their relative emphasis varying during the year. The successful candidate will also oversee day-to-day management of the laboratory and mentor undergraduate and graduate students working in the lab. Despite the diverse range of responsibilities, they would be balanced to ensure that the candidate could spend time on his/her own project.

Requirements for the position include: a Ph.D. in biology; experience with DNA sequencing and microsatel-

lite markers; statistical skills in population genetics and genomics; and good project management skills. Experience with high throughput technology and data management is desirable. Knowledge of US funding sources is also a plus.

Please apply by emailing as attachments your c.v., cover letter, contact information for references, and a statement of research interests and experience to Sork Research Position, c/o Ms. Bobbi Fenske, LSSA Personnel Manager, rfenske@lifesci.ucla.edu. Screening of applications will begin February 22, 2010, and will continue until filled. Ideally, the position would start May 2010, but the start date is flexible. The initial appointment is for one year, with renewal based on performance. Salary is commensurate with years of post-doctoral experience and education and in accordance with University policy, starting around \$45,000. For more information, please contact Victoria Sork (vlsork@ucla.edu).

UCLA is an Equal Opportunity/Affirmative Action Employer.

Victoria Sork <vlsork@ucla.edu>

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## UCalifornia SantaCruz 10K Genomes

UNIVERSITY OF CALIFORNIA, SANTA CRUZ,  
JACK BASKIN SCHOOL OF ENGINEERING, DE-  
PARTMENT OF BIOMOLECULAR ENGINEERING

Postdoctoral Scholar, Genome 10K Sample Collection

Applications are invited for a Postdoctoral Scholar position to undertake a pilot sequencing project in the laboratory of David Haussler, Professor of Biomolecular Engineering at UCSC, in conjunction with Oliver Ryder, Kleberg Chair of Genetics of the Zoological Society of San Diego and Adjunct Professor of Biology at UCSD, and Stephen OBrien, Chief of the Laboratory of Genomic Diversity at the National Cancer Institute.

The Genome 10K project aims to assemble a genomic zooXa collection of DNA sequences for 10,000 vertebrate species, approximately one for every vertebrate genus. The trajectory of cost reduction in DNA sequencing suggests that within a few years it will be feasible to sequence a fully representative set of more than 10,000 genomes, capturing much of the genetic diversity of vertebrate species. This would represent an unprecedented resource for the life sciences and for worldwide

conservation efforts. The growing Genome 10K Community of Scientists (G10KCOS), made up of leading scientists representing major zoos, museums, research centers, and universities around the world, is dedicated to coordinating efforts in tissue specimen collection that will lay the groundwork for a large-scale sequencing and analysis project. The project will capture biodiversity available from the worlds vertebrate species such that the resulting sample collection is as comprehensive as possible, well-documented, available for general research use, and suitable for accurate whole-genome sequencing with current and anticipated high-throughput DNA sequencing technologies (Journal of Heredity, November 2009, <http://jhered.oxfordjournals.org/cgi/content/full/100/6/659>).

The successful candidate will work cooperatively with the G10KCOS to achieve the following:

Develop and improve a web-searchable database that documents the major international holdings of vertebrate tissues.

Undertake a pilot project in which samples from all 130 orders of vertebrates are collected and portions of their genomes sequenced. This includes designing and executing the pilot as well as analyzing the results.

Help with further curation and verification of the specimen database.

Contribute to the planning for the main Genome 10K project to sequence and analyze 10,000 species.

RANK: Postdoctoral ScholarXEmployee

SALARY RANGE: From \$38,088 to \$50,628; commensurate with qualifications and experience

MINIMUM QUALIFICATIONS: A Ph.D. in evolutionary biology, bioinformatics, computer science, genomics, population genetics, or other relevant fields of biology is required along with relevant bioinformatics experience and demonstrated record of accomplishment. Familiarity with SQL and web tools and the ability to write new code in a UNIX environment are essential. Some experience with DNA sequencing is necessary. Other requirements include excellent organizational, verbal communication, and collaboration skills and willingness to do extensive international travel.

PREFERRED QUALIFICATIONS: The ideal candidate will have some experience with sample collection, classification, and analysis in evolutionary biology, experience in relational databases, and experience with high-throughput DNA sequencing.

POSITION AVAILABLE: As soon as possible.

TERM OF APPOINTMENT: One year, with possible

extension, contingent upon funding and a positive performance review.

TO APPLY: Applicants should submit a letter of application, curriculum vitae, research statement, and contact information for three references. Please apply online at <http://genome10k.org/postdocposition>. Electronic submission is preferred.

Alternative mailing addresses:

Search Committee, Genome 10K Postdoc cb-sehr@soe.ucsc.edu or

Search Committee, Genome 10K Postdoc University of California Mail Stop: CBSE-ITI 1156 High Street Santa Cruz, CA 95064

Please refer to position #PS-G10K in your reply.

CLOSING DATE: Position is open until filled.

The University of California, Santa Cruz is an Affirmative Action/Equal Employment Opportunity Employer, committed to excellence through diversity. We strive to establish a climate that welcomes, celebrates, and promotes respect for the contributions of all students and employees.

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Rochelle Fuller Administrative Specialist Center for Biomolecular Science and Engineering MS: CBSE/ITI 501C Engineering 2 Bldg UC Santa Cruz 95064 Phone: 831-459-1597 Fax: 831-459-1809 rochelle@soe.ucsc.edu

Rochelle Fuller <rochelle@soe.ucsc.edu>

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## UGeorgia PlantEvolution

Postdoctoral position in Plant Evolutionary Biology We have National Science Foundation funding for a postdoctoral associate (2-3 year appointment), with a start date as early as June 1, 2010. Our groups conduct research in the areas of natural hybridization, evolutionary genetics and speciation. Most of our research studies have involved plant taxa. Current projects continue to emphasize both natural and experimental populations, and address conceptual issues from evolutionary biology and ecology.

The successful candidate will have a strong background in evolutionary biology and the ability to 1) collect habitat data from natural plant populations, 2) genotype plants using microsatellite loci, and 3) analyze the habitat and genotype data to test various evolutionary

hypotheses. They will work with the PIs and undergraduate and graduate students in order to test the effects of ???reproductive isolation QTL??? on the fitness of plants in natural microhabitats and on introgression in natural hybrid zones between the Louisiana Iris species, *Iris fulva* and *Iris brevicaulis*. Each of the studies is designed to reveal the factors that promote and limit introgressive hybridization between these species and thus affect the evolutionary outcome of genetic transfer events. These studies will thus test hypotheses concerning the evolutionary importance of natural hybridization and the processes leading to speciation.

Applications should arrive no later than April 1, 2010. Applicants should e-mail a CV and a brief summary of research experience and interests to Mike Arnold (arnold@plantbio.uga.edu) and Noland Martin (nm14@txstate.edu). They should also have at least two letters of recommendation sent to these same e-mail addresses.

For more information feel free to contact Mike Arnold or Noland Martin via e-mail or telephone (Mike A.: 706-542-1407; Noland M.: 512-245-2111).

Mike Arnold

Michael L. Arnold Professor Department of Genetics Life Sciences Building University of Georgia Athens, GA 30602 Office Phone: 706-542-1407 Cell Phone: 706-207-6056 Fax: 706-542-3910

Michael Arnold <arnold@plantbio.uga.edu>

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## UGuelph Barcoding

Biodiversity Institute of Ontario, University of Guelph  
Postdoctoral position: DNA barcoding of Canadas endangered species

DNA barcode studies employ a 650-base sequence near the 5' end of the mitochondrial gene COI to differentiate animal species. Over the past five years, over 750K DNA barcode records have been collected from approximately 100K species. This information is building a capacity to rapidly identify organisms, aiding efforts to monitor global biodiversity patterns. The International Barcode of Life Project ([www.ibolproject.org](http://www.ibolproject.org)) scheduled for launch in late 2010 will allow coverage in the DNA barcode reference library to rise to 500K species by 2015.

Environment Canada has provided funding for a post-

doctoral position based at the Biodiversity Institute of Ontario focused on the assembly of DNA barcode records for rare and endangered species. This position involves four key activities linked to project organization and oversight: - Work with researchers at Environment Canada to identify a target list of species that should be barcoded - Interact with museum curators and other external collaborators to obtain samples for analysis - Work with our core sequencing laboratory, the Canadian Centre for DNA Barcoding ([www.dnabarcoding.ca](http://www.dnabarcoding.ca)), to gather sequence records - Create, organize, and manage projects in the Barcode of Life Data Systems ([www.boldsystems.org](http://www.boldsystems.org))

The DNA barcode data gathered in this work will provide the opportunity for high-quality publications in areas such as taxonomy, biogeography, evolutionary biology, or molecular evolution depending upon the expertise of the successful candidate.

To apply, please send a cover letter, CV, and contact information for three references to [gsinger@ibolproject.org](mailto:gsinger@ibolproject.org). As the position is available immediately, the review process will commence as applications are received.

Greg Singer <[gsinger@uoguelph.ca](mailto:gsinger@uoguelph.ca)>

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## UGuelph LepidopteraBarcoding

Biodiversity Institute of Ontario, University of Guelph  
Postdoctoral position: DNA barcoding of Lepidoptera  
DNA barcode studies employ a 650-base sequence near the 5' end of the mitochondrial gene COI to differentiate animal species. Over the past five years, over 750K DNA barcode records have been collected from approximately 100K species. This information is building a capacity to rapidly identify organisms, aiding efforts to monitor global biodiversity patterns. The International Barcode of Life Project ([www.ibolproject.org](http://www.ibolproject.org)), scheduled for launch in late 2010, will allow coverage in the DNA barcode reference library to rise to 500K species by 2015.

Species of Lepidoptera have long been a major focus for DNA barcoding, and DNA barcodes are now available from nearly a quarter of the worlds 160K described species. We are seeking a postdoctoral fellow to advance efforts to build comprehensive barcode coverage for the Lepidoptera faunas of Australia and North America. This position involves four key ac-

tivities linked to project organization and oversight: - Interact with external collaborators to obtain samples/specimens - Coordinate the submission of samples/specimens to the Canadian Centre for DNA Barcoding ([www.dnabarcoding.ca](http://www.dnabarcoding.ca)), located within our Institute - Perform quality checks such as comparing image records to the collaborator-provided taxonomy and examining genetic distance trees built from the barcode records - Organize and manage data in the online DNA barcoding database, the Barcode of Life Data Systems (BOLD; [www.boldsystems.org](http://www.boldsystems.org))

Candidates for this position should have a strong background in Lepidoptera taxonomy; experience in molecular phylogenetics is also desirable. The DNA barcode data gathered in this work will provide the opportunity for high-quality publications in areas such as integrative taxonomy, evolutionary biology, molecular ecology, or phylo-geography depending upon the expertise of the successful candidate.

To apply, please send a cover letter, CV, and contact information for three references to [gsinger@ibolproject.org](mailto:gsinger@ibolproject.org). As the position is available immediately, the review process will commence as applications are received.

Greg Singer <[gsinger@uoguelph.ca](mailto:gsinger@uoguelph.ca)>

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## UGuelph MarineBiodiversity

Postdoctoral position in Marine Biodiversity analysis through Next-Gen sequencing

Biodiversity Institute of Ontario, University of Guelph

A postdoctoral position is available to work with Dirk Steinke and Mehrdad Hajibabaei at the Biodiversity Institute of Ontario, on developing molecular biodiversity approaches based on Next-Gen sequencing platforms.

The position is part of the Marine Barcoding of Life (MarBOL) project that is affiliated with the Census of Marine Life and the International Barcode of Life Project (iBOL) and focuses on comparative ecosystem analysis by massive parallel sequencing of ecosystem samples from different oceanic regions. The candidate will contribute to the data generation and the design of probabilistic algorithms to analyze the sequence data generated.

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. Candidates for this position should have a strong background in bioinformatics (including experience in scripting languages such as python). Experience in molecular evolutionary biology and phylogenetics is also desirable.

The position is initially 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 Dirk Steinke (dsteinke@uoguelph.ca <mailto:dsteinke@uoguelph.ca>). As the position is available immediately, the review process will commence as applications are received.

Dr. Dirk Steinke Lead Scientist Barcoding of Marine Life Biodiversity Institute of Ontario University of Guelph 50 Stone Road East Guelph, Ontario N1G 2W1 Canada tel. 1-519-824-4120 ext. 53759 fax 1-519-767-1656 eMail: dsteinke@uoguelph.ca

dsteinke@uoguelph.ca dsteinke@uoguelph.ca

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## UHawaii DengueEvolution

DEPARTMENT OF TROPICAL MEDICINE, MEDICAL MICROBIOLOGY AND PHARMACOLOGY, UNIVERSITY OF HAWAII

Postdoctoral Researcher - Dengue Evolution and Virus-Vector Interactions

A postdoctoral position is available immediately for two or more years to study dengue virus evolution and mosquito-virus interactions. The study will build upon molecular epidemiologic and evolutionary research on dengue viruses from several distinct transmission arenas and involve the evolutionary genomics of flavivirus/mosquito interactions using natural and genetically engineered viral genomes. The position will be held in the Asia-Pacific Institute of Tropical Medicine and Infectious Diseases, Department of Tropical Medicine, University of Hawaii, in the laboratory of Dr. Shannon Bennett, in which we combine evolutionary biology with molecular genetics and bioinformatic approaches to study how viruses responsible for resurging human disease evolve.

Candidates should have a PhD in evolutionary biology, virology, or a related subject, with a strong background in molecular genetics and evolution. Specific experi-

ence in the following areas is desirable: arbovirology, mosquito infection/inoculations, molecular genetic approaches (qRT-PCR, reverse genetics & cloning, next-generation sequencing and transcriptomics), virologic approaches (isolation, culture, and plaque assays), and bioinformatics (phylogenetics, R, Perl or Python). The candidate will also assist with grant writing to further support this and related projects. We are housed in the new medical school facility at Kaka'ako in Honolulu, Hawaii, and interact with the Kapan and Carlon labs (University of HawaiiManoa) studying evolutionary genomics and next generation sequencing applications to evolutionary questions.

Funding is available for at least two years, subject to annual review. Salary starting at \$45,000, depending on experience, plus benefits. Applications require a cover letter explaining how candidate meets the requirements, CV, a brief statement of research interests, reprints of relevant publications, and contact information for three references. Send applications or inquiries by email to sbennett@hawaii.edu. Review of applications begins February 16, 2010, until position has been filled.

Shannon N. Bennett, PhD. Assistant Professor, Asia-Pacific Institute of Tropical Medicine and Infectious Diseases Department of Tropical Medicine, Medical Microbiology and Pharmacology John A. Burns School of Medicine 651 Ilalo Street, BSB 3rd Floor Honolulu, HI 96813 Phone: (808) 692-1603 Fax: (808) 692-1979 sbennett@hawaii.edu

sbennett@hawaii.edu sbennett@hawaii.edu

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## UHelsinki ButterflyGenomics

Post Doctoral Research Associate in life-history ecology and evolution of the Glanville fritillary butterfly, University of Helsinki

We are seeking an outstanding young post doc with background in population or evolutionary biology or population genetics to join a large research group working on metapopulation ecology, evolution and functional genomics of the Glanville fritillary butterfly. The successful candidate has strong quantitative skills. We are currently sequencing the genome of the Glanville fritillary and plan extensive association and linkage analyses of phenotypic and life history traits. The project is funded by the European Research Council and the Academy of Finland.

Description of the position: The post doc will conduct common garden experiments in large out-door population cages using butterfly material originating from different types of populations and landscapes. In addition to conventional life-history studies, the project involves analyses of variation in the coding region and gene expression in relation to individual performance and the structure of the population of origin. The position is initially for 2 years but may be extended for up to 4 years.

Deadline for applications is February 19. To apply, send a CV, a cover letter explaining your background and research interests and contact information for three references to Ilkka Hanski (ilkka.hanski@helsinki.fi). Further information about the project may be obtained from him. The web-site of the Metapopulation Research Group is [www.helsinki.fi/science/metapop](http://www.helsinki.fi/science/metapop) . ilkka.hanski@helsinki.fi

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## Uillinois Pollinator PopGenetics

PhD or Postdoc position in Population Genetics, Phylogeography and Conservation of Pollinators Cameron Lab, Department of Entomology, University of Illinois

A postdoctoral or PhD student position is available beginning June 2010 to work on conservation genetics of wild pollinators. We are looking for someone excited about interdisciplinary work in population genetics. The focus of the research will be to untangle the recent evolutionary history of bumble bee (*Bombus*) pathogens that may be a factor in the population decline of these wild pollinators across North America. Those able to integrate phylogeographic theory and statistical modeling into data analysis are particularly encouraged to apply. Candidates should have a strong interest in the use of DNA sequence markers to understand recent evolutionary history, including questions regarding host/pathogen interactions, biodiversity, population structure, phylogeography, and ecology of invasion. Field work will be conducted in Europe and North America, and lab work will involve sequencing DNA from contemporary samples and historical museum specimens. Motivated individuals with experience in the fields of ecology, evolution, or genetics are preferred. The position is best suited to a person who has independent initiative for problem-solving, is well organized and works well with a team and can work effectively under pressure.

In the Cameron Lab (see <http://www.life.uiuc.edu/~scameron> for further information on the lab), the successful applicant will work closely with a postdoc and graduate students working on *Bombus* population structure, ecology and phylogeography. You may contact Sydney Cameron directly if you have additional questions. For information about the Department of Entomology see <http://www.life.illinois.edu/entomology> . Application Procedure: The position is initially funded for two years. Interested applicants should send the following required materials as a single attachment: 1) CV, 2) statement of research interests and explanation of why this position is suitable to your experience and skills, 3) informal transcripts, and 4) names and contact information for at least three referees with whom you have done research. Please email the application file to Jeffrey Lozier (jdlazier@life.illinois.edu), a postdoctoral collaborator on the project (<http://www-u.life.uiuc.edu/~jdlazier/index.html>).

APPLICATIONS ARE DUE 31 MARCH 2010

The University of Illinois is committed to equal opportunity and the diversity of its workforce.

– Jeffrey D. Lozier, Ph.D. Post doctoral researcher Department of Entomology University of Illinois 320 Morrill Hall 505 S. Goodwin Ave. Urbana, IL 61801

phone 217-333-7811 jdlazier@life.uiuc.edu

<http://www-u.life.uiuc.edu/~jdlazier/> jdlazier@life.uiuc.edu

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## ULondon Adaptation

Dear All

We are seeking an enthusiastic, well-organized and experienced Postdoctoral Research Assistant for a two-year position in the School of Biological Sciences, Royal Holloway, University of London. This individual will work on the NERC-funded UK portion of the CLIMIGRATE project, a part of the FP7 ERA-NET program BiodivERsA.

The CLIMIGRATE project will generate ancient DNA data from a suite of taxa to determine how species respond to climate change at the population level. We will use these data to evaluate, adjust and improve existing forecasting models to more accurately predict future responses. This work forms part of an inter-

national collaboration between Dr Ian Barnes (RHUL, London), Professor Nigel Yoccoz (Tromsø, Norway) and Dr Love Dalen (Stockholm, Sweden) and will likely lead to high quality publications.

The appointed researcher will work in a small dynamic group and be responsible for their own research, in addition to playing a significant role in running the laboratory and supervising students. The exact focus of the research is flexible - several different lines of research are possible depending on the candidate's background, experience and interests. Our general research involves the use of DNA recovered from palaeontological and archaeological remains - ancient DNA. We have previously employed ancient DNA techniques to investigate mobility and population change in a range of taxa including brown bears (Valdiosera et al. 2007, *Molecular Ecology* 16, 5140; Barnes et al. 2002, *Science* 295, 2267) and woolly mammoth (Barnes et al. 2007, *Current Biology* 17 1072); our current research expands our taxonomic focus and methodological approach. We plan to develop our protocols to utilise next-generation sequencing (particularly 454), and so candidates with such experience would be particularly well placed. However, the CLIMIGRATE project also involves a significant modelling component, so candidates with experience in bioinformatics/climate or species distribution modelling, and an interest in integrating genetic data into this framework, are particularly welcome (to work in collaboration with Nigel Yoccoz, Norway).

Candidates must be highly motivated, capable of independent work, and have a relevant degree and experience. Proven ability with the application of molecular biology and/or modelling to ecological and evolutionary questions is also essential. The position is available for 2 years and is available from February 2010. Salary £31,838 pa inclusive of London allowance. For informal enquiries please contact Dr Ian Barnes (ian.barnes@rhul.ac.uk). The closing date for applications is midday, 29th January, 2010.

Further details and an application form are available online at <http://www.rhul.ac.uk/personnel/Ads/-X0110-5255.html>.

Ian Barnes Reader in Molecular Palaeobiology School of Biological Sciences Royal Holloway, University of London Egham, TW20 0EX +44 1784 443562 AIM: drian-barnes

ian.barnes@rhul.ac.uk ian.barnes@rhul.ac.uk

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## UMichigan EvolutionaryGenomics

Postdoctoral Position in Evolutionary Genomics at University of Michigan

A postdoctoral position is available in the lab of Jianzhi George Zhang to use the budding yeast *Saccharomyces cerevisiae* and its relatives as model organisms for the study of evolutionary processes. Potential topics include but are not limited to (1) the molecular basis of adaptation, (2) genic and genomic bases of reproductive isolation, (3) mechanisms of retention and functional divergence of duplicate genes after gene/genome duplication, and (4) driving forces and molecular mechanisms of transcriptome evolution. Potential approaches include experimental evolution and next-generation sequencing, in addition to yeast molecular genetics.

The position requires a motivated individual with an interest in evolutionary genetics and experience in molecular genetics or genomics. Prior training in yeast genetics is a plus but not required. Experience in analyzing genome-wide data of DNA sequences, transcriptomes, and/or gene functions will be a plus.

Applicants should email a short statement of research interests, CV, and contact information of three references to [jianzhi@umich.edu](mailto:jianzhi@umich.edu). The position is funded by NIH and is available immediately.

For further information about the Zhang lab, see <http://www.umich.edu/~zhanglab/> Jianzhi George Zhang Professor of Ecology and Evolutionary Biology University of Michigan 1075 Natural Science Building 830 North University Avenue Ann Arbor, MI 48109, USA Tel: 734-763-0527 Email: [jianzhi@umich.edu](mailto:jianzhi@umich.edu) <http://www.umich.edu/~zhanglab/> [jianzhi@umich.edu](mailto:jianzhi@umich.edu)

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## UMunster PlantAdaptiveEvolution

\*Postdoc on Adaptive Evolution in Plants\*

\*University of M<sup>1</sup>nster\*\*, Germany\*\*\*

\*A postdoc position is available at University of M<sup>1</sup>nster, in the Institute for Evolution and Biodiversity.

The postdoc will join the lab of Juliette de Meaux and work on the molecular basis of genetic adaptation in *Arabidopsis thaliana* and its relatives. We are looking for a talented evolutionary geneticist interested in the molecular details of genetic adaptation. The skills of the applicants should be documented by high rank publications in international journals. The successful applicant will initially work on the consequences of life-history evolution on the investment into immune competence and defense. \*The position is for two to five years.\* \*The successful applicant will be encouraged to develop his/her own research project within the framework of our research. We especially encourage population geneticists interested in testing the effect of natural selection on functional variants. Experience with the specificities of *A. thaliana* as a model system is NOT a pre-requisite. \*\*

Since Fall 2005, the de Meaux lab has dedicated its efforts to dissecting the molecular basis of genetic adaptation in *A. thaliana*. We combine population genetics approaches with the tool kit of molecular biology and functional genetics (and biochemistry) to characterize the functional consequences of natural variation and determine its evolutionary significance. Work in the lab has focused on various traits (seed dormancy, innate immunity). Transversal approaches using newly developed genomics tools are also used to understand the evolutionary dynamics of specific types of molecular functions, e.g. *cis*-regulation. Initially located at the Max Planck Institute for Plant Breeding Research in Cologne, our lab is about to join the IEB in M<sup>1</sup>nster.

The IEB in M<sup>1</sup>nster is unique in Germany (<http://ieb.uni-muenster.de/>). Its marked focus on Evolution places it at the forefront of education and research in diverse sectors of evolutionary biology, from evolutionary ecology to phylogenetics, population genetics and evolutionary bioinformatics. This interdisciplinary environment, the diversity of model organisms as well as close proximity to world class research at the nearby Institute of Botany promises to bring you a highly interactive environment in which both your theoretical and experimental skills can be harmoniously developed.

\*M<sup>1</sup>nster is a multi-faceted city. It is a city of science and learning. Westphalia's long-standing regional capital is a young city; one of 7 of its inhabitants is either studying or employed by university and half of its inhabitants are below 30 years of age. Compared to other German cities, M<sup>1</sup>nster is a forerunner in the field of environment and climate protection. It is Germany's bicycle metropolis with more bikes than inhabitants, more than 250 kilometres of bicycle paths and an underground bicycle parking area in front of the main train station. High-tech and traditional trade coexist

in this city, as well as baroque noble residences and modern architecture, or a historic city centre and progressive urban development. This is how M<sup>1</sup>nster can guarantee you the highest quality of life. \*

\* \*

\*Applicants should send a detailed cover letter presenting their past research as well as their current research interest to Juliette de Meaux ([demeaux@mpiz-koeln.mpg.de](mailto:demeaux@mpiz-koeln.mpg.de)). They should also send a detailed CV and the contact information of three referees. Review of applications will begin on January 22<sup>nd</sup> and continue until the position is filled. The position is available from April 1<sup>st</sup>, but a later starting date can be negotiated. Fluency in German is NOT a pre-requisite for joining the lab. Applicants are encouraged to check our website prior to application: <http://www.mpiz-koeln.mpg.de/english/research/koornneefGroup/demeaux/index.html>\*

Juliette de Meaux <[demeaux@mpiz-koeln.mpg.de](mailto:demeaux@mpiz-koeln.mpg.de)>

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## UNebraska AphidEvolutionaryGenetics

Postdoc in aphid evolutionary genetics

A postdoctoral position is available in the lab of Jenn Brisson in the School of Biological Sciences at the University of Nebraska, Lincoln (UNL). Our lab uses genetic, developmental, and genomic approaches to study how pea aphids produce winged and wingless morphs. The postdoctoral project can be tailored to the specific interests of the successful candidate, but will focus on one or more of the following areas: 1. transcriptomics and metabolomics of the wing polyphenism 2. pea aphid population genomics, 3. the role of epigenetics in the pea aphid wing polyphenism.

Candidates should have a background in molecular genetics, bioinformatics, or a related field. Experience with next generation sequence analysis is desirable but not required. Funding is available for up to three years, subject to review after each year. The position is available immediately and the start date is flexible.

For additional information, including informal inquiries, please contact Jenn Brisson at [jbrisson2@unl.edu](mailto:jbrisson2@unl.edu). To apply, please send a CV, short letter of research interests and accomplishments, and contact information for three references to [jbrisson2@unl.edu](mailto:jbrisson2@unl.edu).

Further information about the School of Biological Sciences at UNL can be found at: <http://www.biosci.unl.edu/> jbrisson2@unl.edu jbrisson2@unl.edu

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## UNebraska Bioinformatics

Post Doctoral Research Associate in Bioinformatics

The University of Nebraska - Lincoln is seeking outstanding candidates for a non-tenure leading, post doctoral research associate position. The successful candidate will work under the direct supervision of Dr. Janos Zempleni (Nutrition and Health Sciences and Nebraska Gateway for Nutrigenomics) and Dr. Andrew Benson (Food Science and Technology, Core for Applied Genomics and Ecology, and UNL Gut Function Initiative). The initial appointment to this position is for one year and continuation of the position from year to year (with a maximum of 5 years) will depend on availability of funds, satisfactory performance and continued employability in the United States. Research will include:

Developing algorithms and pipelines for analysis of high-throughput microbiome, metagenome, and transcriptome data from Next Generation sequencing platforms.

Quantitative genetic analyses of gut microbiome traits.

Developing algorithms for analysis of data ChIP-Seq and ChIP-chip datasets.

Analysis of Auta ChIP-Seq, DNA chip hybridization to detect chromosomal abnormalities, SNP and miRNA profiling, and disease risk analysis.

To be considered for this position and for further details, go to <http://employment.unl.edu>, requisition 090676 and complete the Faculty/Academic Administrative form and attach letter of application, curriculum vitae, and professional references. Review of applications will begin January 18, 2010 and continue until the position is filled. The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers.

emoriyama2@unlnotes.unl.edu  
emoriyama2@unlnotes.unl.edu

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## UNebraska PopulationBiology

Population Biology - Post-doctoral Fellowships

The University of Nebraska Program Of Excellence in Population Biology announces two-year Postdoctoral Fellowships in Population Biology. Applicant selection will be based on previous research and potential for successful collaboration with an established Population Biologist at UNL (<file:///see:%20http://popbio.unl.edu><http://popbio.unl.edu>). Once in residence post-docs will be expected to interact more broadly and participate in instruction through graduate seminars. Qualified candidates must contact a potential faculty advisor from the list of core faculty associated with the program. A Ph.D. and expertise in any aspect of population biology are required. Applications should include: a CV, a 1-page research proposal, 1-page description of previous research, and a 1-page description of potential graduate seminars. Also arrange for three letters of reference, one of which must be from the proposed faculty sponsor. Send application materials to: Population Biology Post-doctoral Fellowship Selection Committee, School of Biological Sciences, University of Nebraska- Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118. Application review will begin on February 15, 2010 and Post-doctoral Fellows may start between April and September, 2010. Fellowship positions will remain open until suitable candidates are selected. UNL is committed to a pluralistic campus community through Affirmative Action and Equal Opportunity, and is responsive to the needs of dual career couples. We assure responsible accommodation under the Americans with Disabilities Act.

Diana Pilson <dpilson1@unl.edu>

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## UOslo BirdSpermEvolution

Natural History Museum, University of Oslo Postdoctoral position: Sperm evolution in passerine birds

The postdoc fellow will work on the project 'Sperm, speciation and promiscuity - An integrated analysis of evolution in passerine birds', funded by the Research



Council of Norway and NHM. Throughout the animal kingdom sperm cells are extremely diversified. In passerine birds they show strong signatures of selection by sperm competition induced by female promiscuity. The intensity of sperm competition also varies considerably among passerine species. The main aim of the project is to advance our understanding of how sperm cells evolve and diversify in a sperm competition context. The postdoctoral fellow will study the evolutionary differentiation of sperm morphology and behaviour within and among passerine species and assess the importance of sperm competition as a driving force in sperm evolution. The project will require the use of a variety of analytical tools, like in-vitro sperm motility analysis, high-resolution microscopy with digital imaging and morphometrics, and standard phylogenetic analysis and comparative statistics methods. The project will include comprehensive field work, especially in the Macaronesian islands (Canary Islands, Madeira and the Azores) where a selection of passerine species will be used as a comparative model system for sperm evolution.

The project team will consist of two postdocs, one PhD student and one field/lab technician, in addition to a network of international collaborators and two senior NCB scientists: Associate Professor Arild Johnsen and Professor Jan T. Lifjeld (project leader). The NCB is an interdisciplinary research centre in biosystematics and biodiversity which integrates the research groups of 11 faculty working on plants, fungi and animals. More information about NCB can be found at <http://www.nhm.uio.no/forskning-samlinger/forskning/forskningsgrupper/ncb/>. Applicants must hold a degree equivalent to a Norwegian PhD/doctoral degree. The successful applicant should be an evolutionary biologist with a scientific record in molecular systematics and/or comparative trait analysis in a phylogenetic framework. Experience with the analysis of sperm motility and sperm morphology will be an advantage. The postdoc fellow will be expected to participate in the supervision of PhD and Masters students and should have good training in ornithological field methods. The postdoc fellow must also be prepared to spend several months in the field during the first half of the employment period.

Employment is for three years, starting from 1 April 2010. Pay Grade: 57 - 64 (NOK 438 700 - NOK 499 700, depending on qualifications and seniority) Application Deadline: 1 February 2010.

Informal inquiries to Professor Jan T. Lifjeld ([j.t.lifjeld@nhm.uio.no](mailto:j.t.lifjeld@nhm.uio.no)).

For further particulars and instructions on how

to apply, please see <http://www.admin.uio.no/-opa/ledige-stillinger/2010/vitenskapelige/-postdocresearchfellowNHM-2010-100.html>  
[j.t.lifjeld@nhm.uio.no](mailto:j.t.lifjeld@nhm.uio.no) [j.t.lifjeld@nhm.uio.no](mailto:j.t.lifjeld@nhm.uio.no)

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## UOttawa SexualSelection

Reposting, with alteration to start date. Candidates that have already applied do not need to reapply.

Funding is available for a 2-year postdoctoral fellowship in the laboratory of Howard Rundle at the University of Ottawa, Ontario, Canada.

Using various species of *Drosophila*, research in the laboratory investigates how natural and sexual selection interact during adaptation, and how both processes contribute to phenotypic divergence and speciation. In particular, we use experimental evolution and quantitative genetics to investigate the evolution of mate preferences within populations, their divergence among populations, and the population genetic consequences of the sexual selection they generate. For more information, consult the lab website at: <http://www.science.uottawa.ca/~hrund050>. Candidates with a background and interest in quantitative genetics are especially encouraged to apply.

Fellowships are open to Canadian and international candidates. The position is for two years and start date is quite flexible. The salary is CDN \$40,000 per year (tax free).

Applications should include a cover letter, a curriculum vitae, a short (~1 page) description of research interests, and the names and contact information (including e-mail) of three referees. All application materials should be submitted via email (preferably in pdf format) to Howard Rundle ([hrundle@uottawa.ca](mailto:hrundle@uottawa.ca)), to whom queries may also be addressed. Evaluation of applications will begin immediately and continue until the position is filled.

Located at the confluence of English and French Canada, Ottawa is a rich and vibrant national capital of approximately 1 million inhabitants (<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. Carleton University is only a few km away and research ties between the two Biology Departments are strong.

The Department of Biology has an active group of evolutionary biologists with diverse interests (<http://www.evolution.uottawa.ca>).

Howard Rundle Department of Biology, 30 Marie-Curie Priv. University of Ottawa, Ottawa, ON, K1S 0T1, CANADA Ph: +1 613-562-5800 x2835; Fax: +1 613-562-5486 Skype: howardddrundle <http://www.science.uottawa.ca/~hrund050> <http://www.evolution.uottawa.ca> hrundle@uottawa.ca hrundle@uottawa.ca

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## UToronto EvolutionaryBiology

The Department of Ecology and Evolutionary Biology at the University of Toronto < [www.eeb.utoronto.ca](http://www.eeb.utoronto.ca) > invites applications for Departmental Postdoctoral Fellowships in the areas of Ecology and Evolutionary Biology, broadly defined. One position is available this year, and we expect that another will become available next year through an ongoing EEB Post-Doctoral Fellowship Program. Positions may continue for two years, subject to review after one year, and can begin as early as July 1, 2010. The salary is \$40,000 Canadian per year, with research expenses covered by the Post-Doctoral Advisor.

The Fellow will be a fully participating member in the Department. Candidates must identify and communicate with a potential advisor (or advisors) in advance of the application process. All full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors (see < [www.eeb.utoronto.ca/postdoc](http://www.eeb.utoronto.ca/postdoc) > for a list of potential supervisors). Opportunities for teaching in an upper level course may be available.

To apply, applicants should first contact and obtain the agreement of a faculty advisor (or co-advisors). Afterwards, applicants should submit a cover letter clearly indicating the proposed faculty advisor(s), a curriculum vitae, copies of 2 publications, and a short (1-3 pages) description of past research accomplishments and future research plans. Applicants should include names and e-mail addresses for two potential referees. Applicants should also indicate the date they will be available

to begin the position. All application materials must be submitted as PDF's in a single email to: Elizabeth Rentzelos <[chairsec.eeb@utoronto.ca](mailto:chairsec.eeb@utoronto.ca)>.

For more information about the Department, contact your potential supervisor. Queries regarding the fellowship program should be directed to Demetrios Voudouris <[demetrios.voudouris@utoronto.ca](mailto:demetrios.voudouris@utoronto.ca)>. Review of applications will begin on March 12, 2010.

Toronto is a vibrant, multicultural city on the shore of Lake Ontario, with rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life. The EEB department is home to an interactive, collegial group of ecologists, geneticists, and evolutionary biologists, and currently supports a strong group of Post-Doctoral Fellows with diverse research interests.

John Stinchcombe Department of Ecology and Evolutionary Biology University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

<http://labs.eeb.utoronto.ca/stinchcombe/>  
john.stinchcombe@utoronto.ca

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## UUtah BioinformaticsGenomics

The Evan Johnson Lab at the Huntsman Cancer Institute and the University of Utah is currently searching for a motivated postdoctoral fellow with interest in applying computational/ statistical methods to high-throughput genomics. The fellow will be involved in the development of innovative methods for Next Generation sequencing technologies and will be interacting regularly with members of the Brad Cairns Lab on applied problems. The Huntsman Cancer Institute on the University of Utah campus is an excellent environment for genetic research and for collaborations with basic and translational research labs. Applicants should have strong programming skills and experience in statistics, bioinformatics, computer science or a related field. Interested applicants should send their CV and a brief research statement to: [johnsonlab@stat.byu.edu](mailto:johnsonlab@stat.byu.edu)

The University of Utah is an Affirmative Action/Equal Opportunity employer. Upon request, reasonable accommodations in the application process will be provided to individuals with disabilities. This position requires successful completion of a drug test and criminal

background check.

Keith A. Crandall, Ph.D. Professor & Chair,  
Department of Biology 401 Widtsoe Building  
Brigham Young University Provo, Utah 84602  
USA keith.crandall@byu.edu (801) 422-3495

kcrandallbyu@gmail.com

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## UWashington ComputationalBiology EvolutionarySystemsBiology

Postdoctoral positions in Computational Biology and Evolutionary Systems Biology at the University of Washington

Postdoctoral positions are available with Elhanan Borenstein's group in the Department of Genome Sciences at the University of Washington. Borenstein's group focuses on computational research in Evolutionary Systems Biology - an emerging field that examines the interplay between the evolutionary process and the organization of complex biological systems, with an eye to expanding fundamental theories in evolutionary dynamics, systems biology, and ecology.

Specific research themes include:

- Large scale computational analysis of biological networks and their evolution (with an emphasis on metabolic networks) - Metabolic interactions, community structure and systems biology of microbial communities (and specifically the human microbiome) and analysis of metagenomic data - Modularity, robustness, evolvability, and assembly rules of biological systems - Population genetics and evolutionary theory

Research in the group is multidisciplinary in nature and spans several levels of abstraction, ranging from state of the art computational analysis of complex networks and high-throughput data to theoretical studies of mathematical and computational models.

The University of Washington is consistently ranked as one of the top research universities in the country and is the largest university in the northwestern United States. The Department of Genome Sciences (<http://www.gs.washington.edu/>) addresses leading edge questions in biology and medicine by developing and applying genetic, genomic and computational approaches. The department faculty includes nine NAS members, five HHMI Investigators, and a 2001 Nobel laureate in Medicine. The department moved into the new, state

of the art Foege Building in 2006.

The Seattle area is home to many major academic institutes and hi-tech companies, forming a vibrant and exciting research community. Considered one of the nation's most beautiful and livable cities, Seattle boasts an array of cultural activities, parks, and restaurants, and serves as the gateway to National Parks and Forests, as well as boating, skiing and hiking areas.

The successful candidate is enthusiastic, creative, highly motivated, with a track record of research excellence in computational biology. Strong analytical, quantitative and computational/programming skills are essential as well as the ability to conduct independent cutting-edge research. Experience with complex biological networks, large-scale biological data, bioinformatics, and modeling is highly desirable. PhD in life sciences, computer science, mathematics, or bioinformatics is required. Candidates with a multidisciplinary background, spanning both life sciences and computer sciences are especially encouraged to apply.

Interested applicants should submit a CV, a brief (2-3 paragraphs) statement of her/his research interests and experience, and contact information of three references to Dr. Elhanan Borenstein ([elbo@u.washington.edu](mailto:elbo@u.washington.edu)).

[elbo@uw.edu](mailto:elbo@uw.edu) [elbo@uw.edu](mailto:elbo@uw.edu)

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## UZurich AlpineArabidopsis EvolutionaryGenomics

Postdoc position for evolutionary genomics of alpine Arabidopsis relatives at University of Zurich:

A two-year postdoc position will be supported by a new collaborative project of the Swiss National Science Foundation (SNF Sinergia), entitled "Adaptive genetic variation and plant adaptation to environmental heterogeneity (AVE)" starting in April 2010. The appointed postdoc is expected to analyze the genome-wide polymorphism data of six Brassicaceae species including Arabidopsis thaliana collected throughout the Swiss Alps. The goal is to identify adaptive genetic variation in extreme and diverse alpine environments. To exploit next-generation sequencers, the support from the Functional Genomics Center Zurich (<http://www.fgc.ethz.ch/>) and Genetic Diversity Center ETH (<http://www.gdc.ethz.ch/>) and a collaborative research environment including a bioinformatician and a technician are provided.

The postdoc is affiliated to the group of Evolutionary Functional Genomics at the University of Zurich (Prof. Dr. Kentaro Shimizu, University Research Priority Program of Systems Biology / Functional Genomics, <http://botserv1.uzh.ch/home/shimizu/index.html>), and the project is conducted in collaboration with the groups of Prof. Dr. Alex Widmer (Plant Ecological Genetics, ETH Zurich, <http://www.peg.ethz.ch/index.EN>) and of Prof. Dr. Rolf Holderegger (Ecological Genetics, Swiss Federal Institute for Forest, Snow and Landscape Research (WSL), <http://www.wsl.ch/forschung/forschungunits/genetik/index.EN>).

Remarks:

PhD in evolutionary genomics, evolutionary genetics, or bioinformatics would be preferred. Experiences in molecular biology and genetics are also appreciated. Please send your CV, 1-2 pages describing your past research, 1 page describing why you are interested in this project, and the names and the contact address of more than two references, preferably by E-mail to [shimizu@botinst.uzh.ch](mailto:shimizu@botinst.uzh.ch). The review of the applications will start in 10 February 2010, and continue until the position is filled.

Kentaro K. Shimizu, Assistant Professor Institute of Plant Biology University of Zurich Zollikerstrasse 107, CH-8008 Zurich Switzerland Phone +41-44-634-8247, 8270 FAX +41-44-634-8204 University Research Priority Program of Systems Biology / Functional Genomics Evolutionary Functional Genomics <http://botserv1.uzh.ch/home/shimizu/index.html> E-mail: [shimizu@botinst.uzh.ch](mailto:shimizu@botinst.uzh.ch)

[shimizu@botinst.uzh.ch](mailto:shimizu@botinst.uzh.ch) [shimizu@botinst.uzh.ch](mailto:shimizu@botinst.uzh.ch)

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**ZoolSoc London**  
**DiseaseMacroevolution**

Disease Macroecologist One Year Fixed-term Contract  
Initially Salary: £ 26,998 plus London Weighting £3554

A postdoctoral position is available from 1st March 2010 to build global spatial and temporal models of infectious disease emergence in humans. The work will build on previous publications (see Jones et al. Nature 451:990) to examine the roles of biodiversity, land-use change, climate change and other socio-economic, demographic and environmental drivers on disease emergence.

The position requires an independent, enthusiastic and innovative researcher with a PhD in a relevant discipline interested in applying comparative macroevolutionary and macroecological approaches to understanding disease emergence. Experience in environmental niche modelling, comparative phylogenetic analyses, disease modelling, using and compiling global biodiversity, environmental and socioeconomic datasets, and analysis of spatial data would be an advantage.

Informal enquires can be made to [kate.jones@ioz.ac.uk](mailto:kate.jones@ioz.ac.uk).

A Job Description can be requested from the email address below.

Please apply by CV and covering letter with contact details for three referees to: HR Dept., Zoological Society of London, Regent's Park, London, NW1 4RY or email [hr@zsl.org](mailto:hr@zsl.org)

Closing date for applications: 15th February 2010.

Registered Charity in England and Wales: 208728

Dr. Kate Jones Senior Research Fellow - Institute of Zoology Zoological Society of London Regent's Park London NW1 4RY tel: +44 (0)20 7449 6627 fax: +44 (0)20 7586 2870 [www.zsl.org/katejones](http://www.zsl.org/katejones)

ZOOLOGICAL SOCIETY OF LONDON LIVING CONSERVATION

Registered Charity in England and Wales: no. 208728

The Zoological Society of London is incorporated by Royal Charter Principal Office England. Company Number RC000749 Registered address: Regent's Park, London, England NW1 4RY Registered Charity in England and Wales no. 208728

Kate Jones <[Kate.Jones@ioz.ac.uk](mailto:Kate.Jones@ioz.ac.uk)>

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### Borneo AntEvolution Aug16-26

ANT COURSE 2010 <http://research.calacademy.org/ent/courses/ant> Danum Valley Field Centre, Sabah Borneo, August 16 - 26,

DEADLINE FOR APPLICATION: April 1, 2010 Application form: <http://spreadsheets.google.com/viewform?formkey=-3DdGNTcVh1ZzVGNjd1aVU5cnV1dWZNBVE6MA>

COURSE OBJECTIVES. - ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy and field research techniques. Emphasis is on the identification of the ant genera and species occurring in Southeast Asia. Lectures will include background information on the ecology, life histories and evolution of ants. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment/supply vendors, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. - Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the ant genera of tropical Asia; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the biological diversity of ants, and 4) experience keying to the species level.

SPONSORS. -California Academy of Sciences and Museum of Comparative Zoology.

BACKGROUND INFORMATION. - ANT COURSE will be taught from August 16 - 26, 2010 at the Danum Valley Field Centre, Sabah Borneo, (<http://www.etawau.com/PlacesInterest/>

[DanumValleyFieldCentre.htm](http://www.etawau.com/PlacesInterest/DanumValleyFieldCentre.htm) ). The Station is centered amid the richest ant fauna in Asia.

PARTICIPANT ACCEPTANCE CRITERIA. - ANT COURSE is open to all interested individuals. Priority will be given to those students for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology, genetics, and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 30 participants.

COSTS. - Tuition for the 10-day COURSE is \$475 for current students and \$675 for non-students. In addition, the Danum Valley station fees for this period, covering dormitory room and board, and flights from Kota Kinabalu to Lahad Datu and transfer to the station is \$750. Thus total costs for students is \$1225 and non-students \$1425. Transportation costs between home and Kota Kinabalu to be borne by all participants.

FELLOWSHIPS. - Four fellowships are available. Two fellowships cover tuition fees and two fellowships cover station fees. Students may apply for additional fellowships to assist in travel. Those interested in attending the course should seek all possible avenues to secure funding for the course. You should only apply for an Ant Course fellowship if you cannot find other support and it is essential for your participation in the course. Beware that if you apply for an ant course fellowship it implies that fellowship funding is essential to your participation in the course. Thus, if you are not selected for a fellowship, you might not be accepted into the course. Please notify the course if your funding request status changes before the application due date.

COURSE APPLICATION. - Application and course information at <http://www.antweb.org>. The first step is to fill out a form at: <http://spreadsheets.google.com/viewform?formkey=-3DdGNTcVh1ZzVGNjd1aVU5cnV1dWZNBVE6MA> .



In addition, you must also submit a CV, personal statement, and letter of reference to AntCourse@gmail.com.

2010 POSSIBLE Instructors: Brian Fisher (Coordinator), Dept. of Entomology, California Academy of Sciences, San Francisco, CA, bfisher@calacademy.org Simon Robson (Coordinator), Department of Zoology, School of Tropical Biology, James Cook University, Townsville QLD 4811, Australia, Simon.Robson@jcu.edu.au Leeanne Alonso, Rapid Assessment Program, Conservation International, Washington, DC USA, L.alonso@conservation.org Chris Burwell, Curator (Entomology), Queensland Museum, Australia, chris.burwell@qm.qld.gov.au Arthur Chung, Forest Research, Centre, Sabah Forestry, Department, PO Box 1407, 90715 Sandakan, Sabah arthur.chung@sabah.gov.my Yoshiaki Hashimoto, Museum of Nature and Human Activities, Hyogo, 6chome Yayoigaoka Sanda Hyogo, Japan 669-1546, yoshiaki@hitohaku.jp

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## Montreal Population Genomics Jun1-4 2

Montreal Spring School of Population Genomics and Genetic Epidemiology

1st - 4th June 2010

Extended program

See [www.MontrealSpringSchool.ca](http://www.MontrealSpringSchool.ca) for details Instructional Program

Day 1 - June 1st Introductory Concepts in Human Populations and Medical Genomics Instructors: Philip Awadalla and Lluís Quintana-Murci Time: 8:00 - 17:00 Place: Room 1

Lecture will cover major modern concepts in population genetics. Models that describe genealogical histories underlying sampled chromosomes in natural populations are central to the analysis of such data. The lecture covers the derivation and properties of the basic model and its extension to include factors such as recombination, geographical structure.

o Mutation and recombination

o Recombination at pedigree level - concept of linkage disequilibrium (LD)

o Measures of LD and its decay

o Coalescence and population genealogies - demography  
Population mutation parameter, population recombination rate

The lab introduces methods of analysis using the statistical software package R.

Data resources

o 1000 genomes project

Demography of human populations. Inferences from uniparental and autosomal markers.

o This lecture will introduce the different models to explain human evolution. It will give an overview of the most recent genetic data explaining the human origins and migration patterns. It will concentrate on phylogeographic studies, mostly concerning uniparentally-inherited genomes.

o A rapid overview of the HapMap contribution to the better understanding of the demographic history of human population will be given.

o A new Human Genome Diversity Project (HGDP) resource

Day 2 - June 2nd Introductory Concepts in Genetic Epidemiology Instructors: Marie-Hélène Roy-Gagnon, Alexandre Bureau, Alexandre Alcaïs and Hélène Vézina Time: 8:00 - 17:00 Place: Room 1

We will first briefly introduce concepts and designs to study familial aggregation followed by basic principles of linkage and association analysis for qualitative traits. Topics covered will include designs and analytical methods used to study genetic linkage. Both parametric and non-parametric linkage analysis will be covered. Presentation of the concepts will be followed by a computer lab application using real data and currently available software such as MLB and MERLIN.

The second part of the lecture will cover designs and analytic methods for genetic association studies. Methods to investigate direct (candidate locus) and indirect (linkage disequilibrium mapping) associations with human disease will be introduced. Both family-based and population based designs will be presented.

Presentation of the concepts will be followed by a computer lab application using real data and currently available software such as FBAT.

Finally, a brief introduction to web resources will be presented, including databases useful in genetic epidemiology studies, an introduction to the BALSAC ge-

neological resource and presentation of existing tools for their analysis.

Day 3 -June 3rd (Concurrent Sessions - lectures and computer labs - followed by invited lecture)

Advanced Concepts in Population Genomics Instructors: Lluís Quintana-Murci and Luis B. Barreiro Time: 8:00 - 16:15 Place: Room 1

Simulation approaches (e.g. ABC, best-fitting) how we can infer demography from genetic data.

Methods in population genetics and hands-on lab

- o Quality control of the data (e.g. test for HW equilibrium)

- o Haplotype reconstruction using Phase o Methods to detect selection from molecular data

- o Description of interspecies neutrality tests (e.g. dn/ds)

- o Sequence-based neutrality tests

- o Population differentiation methods (i.e. Fst approaches)

- o LD-based methods

Advanced Concepts in Genetic Epidemiology and Statistical Genetics Instructors: Marie-Hélène Roy-Gagnon, Alexandre Bureau and Alexandre Alcaïs Time: 8:00 - 16:15 Place: Room 2

Data quality control (pedigree and genotyping error checks)

Introduction to quantitative genetics theory and linkage and association analysis for quantitative traits I

Introduction to quantitative genetics theory and linkage and association analysis for quantitative traits II

Haplotype analysis

Invited Lecture Speaker: to be determined Time: 16:15 - 17:00 Place: Room 1

Day 4 -June 4th (Concurrent Sessions - lectures and computer labs)

Advanced Concepts in Population Genomics Instructors: Lluís Quintana-Murci, Luis B. Barreiro, Philip Awadalla, Nicolas Lartillot Time: 8:00 - 17:00 Place: Room 1

Analysis of signatures of selection in genomic data - applications

- o Analysis of real data on which students will perform all different types of neutrality tests

- o Practical examples of natural selection in humans, and its utility in epidemiology o Extensions of The Co-

alescent in Population Genetics

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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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## NESCent GMOD 2010 SummerSchool May6-9

I am pleased to announce that we are now accepting applications for:

2010 GMOD Summer School - Americas 6-9 May 2010 NESCent, Durham, NC, USA [http://gmod.org/wiki/2010\\_GMOD\\_Summer\\_School\\_-\\_Americas](http://gmod.org/wiki/2010_GMOD_Summer_School_-_Americas) This will be a hands-on multi-day course aimed at teaching new GMOD users/administrators how to get GMOD Components up and running. The course will introduce participants to the GMOD project and then focus on installation, configuration and integration of popular GMOD Components.

GMOD (<http://gmod.org/>) is a collection of open-source and interoperable software components for visualizing, annotating, and managing biological, especially genomic, data. GMOD is also a community of users and developers addressing common challenges with their data.

The course will be held May 6-9, at the US National Evolutionary Synthesis Center (NESCent) in Durham, NC. These GMOD components will be covered: \* Apollo - genome annotation editor \* Chado - a modular and extensible database schema \* Galaxy - workflow system \* GBrowse - the Generic Genome Browser \* GBrowse\_syn - A generic synteny browser \* JBrowse - genome browser \* MAKER - genome annotation pipeline \* Tripal - web front end for Chado

The deadline for applying is the end of Friday, February 22. Admission is competitive and is based on the strength of the application (especially the statement of interest). In 2009 there were over 50 applications for the 25 slots. Any applications received after the deadline will be placed on the waiting list.

See the course page for details and an application link: [http://gmod.org/wiki/2010\\_GMOD\\_Summer\\_School\\_-\\_Americas](http://gmod.org/wiki/2010_GMOD_Summer_School_-_Americas) Thanks,

Dave Clements GMOD Help Desk

PS: We are also investigating holding a GMOD course in the Asia/Pacific region, sometime this fall. Watch the GMOD mailing lists and the GMOD News page/RSS feed for updates. – [http://gmod.org/wiki/2010\\_GMOD\\_Summer\\_School\\_-\\_Americas](http://gmod.org/wiki/2010_GMOD_Summer_School_-_Americas) [http://gmod.org/wiki/GMOD\\_News](http://gmod.org/wiki/GMOD_News)  
clementsnescent@gmail.com

## Netherlands ResourceInteractions Jan31-Feb4

Postgraduate Course Consumer - Resource Interactions: Danger, Disease and Density-Dependence

31 January - 4 February 2010

De Bergse Bossen, Driebergen, the Netherlands

All organisms require inputs of energy and/or materials in order to grow and reproduce. Consumer-resource interactions in all its variations (i.e. plant-nutrient, plant-herbivore, predator-prey, host-parasitoid, and host-parasite) are central to ecological and evolutionary research. However, consumer-resource interactions are also the basis of exploitative competition (two or more consumers share resources), facilitation (one consumer increases resources for another) and many mutualisms (species trade 'resources'). Most organisms function as both consumers and resources in a food web.

The functional and numerical responses of the consumer and a function describing resource population growth are essential components of any consumer-resource interaction. Understanding these responses often requires that we understand the adaptive processes V evolution, behaviour, and phenotypic plasticity V that shape these interactions on both short and long time-scales.

**SCOPE OF THE COURSE** This one-week course will illustrate how adopting a consumer-resource approach can change our understanding of interactions, and how adaptive processes can be important in understanding both academic and applied problems in ecology. The course will focus on three selected topics within the broad field of consumer-resource interactions: Danger, Disease and Density-dependence.

These topics will be introduced by world leading experts, with a focus on the latest developments and ongoing research efforts.

The introductions will provide the starting point for

practical work by the participants to make the acquired knowledge operational. To this end, sub-groups are challenged to develop ideas for their own research: analyzing their own data, writing a proposal, planning an experiment, developing a model or writing a paper.

The experts and organisers will be available to all groups during the practical work, allowing participants intensive interaction with them. The main goal of the course will be achieved if the participants acquire novel ideas and techniques for their own research.

**LECTURERS** Peter Abrams (University of Toronto) Joel Brown (University of Illinois at Chicago) Bob Holt (University of Florida) Don DeAngelis (University of Miami) Han Olf (Groningen University) Theunis Piersma (Groningen University, Royal Netherlands Institute for Sea Research)

**COURSE SET-UP** On Sunday evening, we start with guest lectures by Han Olf and Theunis Piersma. On Monday, the basics of consumer-resource interactions and the topics will be introduced. Then groups will be formed. During the following days, there will be three one-hour lectures on specific topics, followed by discussion. The rest of the day will be spent on the practical work, under the supervision of the experts and the organisers. On the last day, the groups present their practical work to all participants.

**LOCATION** Hotel & Conference Centre De Bergse Bossen Traaij 229, Driebergen The Netherlands [www.debergsebossen.nl](http://www.debergsebossen.nl)  
<file://www.debergsebossen.nl>

**REGISTRATION** You can register online via: [www.pe-rc.nl](http://www.pe-rc.nl) <file://www.pe-rc.nl> , (under Courses and activities) or send an email to PE&RC: [pe-office@wur.nl](mailto:pe-office@wur.nl)

**FEE** (Includes B&B, coffee, tea, lunches, dinners and course materials): - PE&RC, SENSE, RSEE and NIOO PhD candidates with an approved Education Plan (TSP) £á 400,- - All other PhD participants £á 700,- - External participants £á 1.200,-

**ORGANISERS** Wolf Mooij (Netherlands Institute of Ecology, [w.mooij@nioo.knaw.nl](mailto:w.mooij@nioo.knaw.nl)) Bart Nolet (Netherlands Institute of Ecology, [b.nolet@nioo.knaw.nl](mailto:b.nolet@nioo.knaw.nl)) Frank van Langevelde (Wageningen University, [frank.vanlangevelde@wur.nl](mailto:frank.vanlangevelde@wur.nl)) Jan van Gils (Royal Netherlands Institute for Sea Research, [jan.van.gils@nioz.nl](mailto:jan.van.gils@nioz.nl)) Claudius van de Vijver (Graduate School for Production Ecology and Resource Conservation, [claudius.vandevijver@wur.nl](mailto:claudius.vandevijver@wur.nl))

**FURTHER INFORMATION** See: [www.pe-rc.nl](http://www.pe-rc.nl) <file://www.pe-rc.nl> under courses and activities For information on the content of the course please contact

one of the organizers For information on registration, fees and logistical matters please contact PE&RC (pe-office@wur.nl).

“Mooij, Wolf” <W.Mooij@nioo.knaw.nl>

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## Portal Arizona Phylogeography Apr4-9

Course Advertisement: Statistical Phylogeography course at the AMNH Southwestern Research Station near Portal, Arizona.

This course will cover several advanced topics in model-based approaches to the analysis of phylogeographic data, including those based on Monte Carlo simulations and parametric bootstrapping, approximate Bayesian computation, various power analyses, species delimitation, and hypothesis testing. Participants will be asked to bring their own data to the course, and the design and implementation of analyses for individual data sets will be emphasized. To facilitate these analyses, students will learn some basics of UNIX and R.

Course requirements: participants must bring a laptop computer running either Mac OSX or Linux operating systems. We suggest that participants install R and PERL prior to arrival, as well as several other open source programs (ms, seq-gen, msBayes, popABC, DIYABC, STEM, Mesquite, ). Participants will have access to wireless internet at the SWRS, and will be encouraged to conduct analyses remotely on servers at their universities.

Prospective students should send a brief letter and a CV by January 20, 2009 to swrs.statistical.phylogeography<at>gmail.com . In the letter, please indicate how model-based phylogeography would enhance your research program and describe the data that you would like to analyze. We prioritize participants with data from empirical systems that can be analyzed during the workshop.

Instructors: Bryan Carstens, Assistant Professor, Louisiana State University <http://www.lsu.edu/faculty/carstens/> Mike Hickerson, Assistant Professor, Queens College, City University of New York <http://qcpages.qc.cuny.edu/Biology/Hickerlab/index.html> Naoki Takebayashi, Associate Professor, University of Alaska Fairbanks <http://www.faculty.uaf.edu/ffnt/>

Course Dates: Participants will arrive at the SWRS on Sunday, April 4th. There will be a brief reception Sun-

day evening, and the first classroom session will begin on Monday, April 5th. The workshop will end at noon on Friday, April 9th. Course Fees: (including room & board at the SWRS) will be \$950

Bryan Carstens

SWRS Statistical Phylogeography  
<swrs.statistical.phylogeography@gmail.com>

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## Portugal MolecularEvol Feb15-19

Dear mailing list member,

Registration is now open for

MEPA10 - Molecular Evolution, Phylogenetics and Adaptation

Please visit the GTPB website for details:

<http://gtpb.igc.gulbenkian.pt> This course is likely to be very competitive for seats. Our maximum capacity is 20 seats. Early application is recommended!

Instructors: Hernan Dopazo, François Serra Duration: 5 days Course Fee: Eur 400

Course description: More than 30 years ago, Theodosius Dobzhansky claimed: “Nothing in Biology makes sense except in the light of evolution” Currently, the simplest Bioinformatics analysis uses species comparisons in order to hypothesise the function of a novel biological sequence. Moreover, in most Molecular Biology labs, evolutionary and phylogenetic concepts are constantly being used with more or less formality: homology, similarity, evolutionary rates, long branch attraction, rooted and unrooted trees, monophyletic group, molecular clock, adaptation, lineage effects, neutralism, cladograms, phylograms, etc. The course covers these and other major concepts in Evolutionary Biology and Phylogenetics. Attendees will acquire specific skills in using the methodology in Comparative and Evolutionary Biology problems. The course is designed to be a mixture of theoretical and practical sessions developed in 5 days, where both classic and recently introduced methods for phylogenetic reconstruction will be covered. As outcome of the more recent developments, the course dedicates a day to the analysis of adaptation at a molecular level. The software resources that will be used in the practical sessions include: Phym1, Phylip, MEGA, TreePuzzle, Mr-Bayes, PAML, Modeltest-Protest, and the Phylemon web server.

Please feel free to pass this information to colleagues in your community.

Pedro Fernandes – Pedro Fernandes GTPB coordinator Instituto Gulbenkian de Ciência Apartado 14 2781 OEIRAS PORTUGAL

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## Portugal MolecularEvol Feb15-19 2

“Great lectures, really well organized and, most importantly, great balance between lectures and practicals. Met my expectations in 100%” - statement by an attendee of the MEPA course in 2009

REMINDER ===== DEADLINE FOR APPLICATIONS: JAN 30th 2010

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Please feel free to pass this information to colleagues in your community.

Pedro Fernandes – Pedro Fernandes GTPB coordinator Instituto Gulbenkian de Ciência Apartado 14 2781 OEIRAS PORTUGAL

Pedro Fernandes <pfern@igc.gulbenkian.pt>

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## Roscoff France MarineEvolutionaryGenomics May24-Jun4

MGE Summer Course Marine Evolutionary & Ecological Genomics May 24th à June 4th, 2010 Station Biologique de Roscoff, France <http://www.sb-roscoff.fr>

Aims: to introduce genetic and genomic approaches for the analysis of biological diversity, evolution and adaptation at the species and population level in the ocean

Target group:

PhD students (at least in their second year) and post-docs with a solid knowledge in phylogenetics and/or population genetics.

Topics:

The course will consist of lectures, tutorials and computer based exercises in the following subjects.

\* Phylogeny & tree of life- sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies \* Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies \* Population genetics à structure, connectivity and gene flow, assignment, effective size and population dynamics, case studies \* Functional genomics à database searching, genome structure, molecular evolution at the functional level \* Comparative genomics - whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, transposable elements in marine species, co-evolution \* Environmental and functional genomics - methods for detecting adaptive variation; detecting diversity; EST libraries: why and how; case studies.

Confirmed teachers:



Sandie Baldauf, U. Uppsala, SE Jonas Coll  n, U Paris 6, FR Simon Creer, U Bangor, UK Yves Desdevises, CNRS Banyuls, FR Michael Hansen, U Aarhus, DK Galice Hoarau, U Bodo, NO Jeanine Olsen, Univ Groningen, NL Fr  d  ric Partensky, SB-Roscoff, FR Heroen Verbruggen, U Gent, BE Fr  d  rique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE Mathias Wegner, ETH Zurich, SW

Organizing committee:

Claudie Perron, SB-Roscoff, FR Jeanine Olsen, Univ Groningen, NL Jonas Coll  n, SB-Roscoff, FR Fr  d  rique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

Costs, course, accommodation and meals:

\* The course fee is paid by the MGE Network and includes a welcome reception, excursion (incl. lunch) and farewell dinner. \* On site accommodation at the SBR guesthouse is included. \* All participants pay their own travel and board (self catering is possible)

The guesthouse offers lunch and supper at 5.50   perpersonandmeal.

Application and contact:

To apply please fill in the application form and send to Jonas Coll  n (collen@sb-roscoff.fr) together with a 2-page CV

before March 26th 2010.

16 participants will be selected on 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 with different research backgrounds; probably not more than one person per institute will be considered. We will also aim at an equal gender distribution.

The selected persons will be notified at the end of April and have to confirm within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Contacts:

Jonas Coll  n (collen@sb-roscoff.fr) Fr  d  rique Viard (viard@sb-roscoff.fr) Station Biologique de Roscoff BP 74, 29680 ROSCOFF CEDEX France Phone: (33)2 98 29 23 23 Fax: (33)2 98 29 23 24

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

## Switzerland EvolutionaryBiol Jun20-26

\*Evolutionary Biology Workshop in the Alps\*

20 - 26 June, Arolla, Switzerland

\*Faculty\*: David Haig (Harvard University) John Pannell (University of Oxford) Jerome Goudet (University of Lausanne) Tadeusz Kawecki (University of Lausanne)

\*Target participants\*: PhD students, advanced master students

This workshop, based on a concept developed by Steve Stearns and John Maynard Smith, takes place in a small Alpine village (Arolla), which will allow you to focus while being able to enjoy the landscape and the Alpine flora. The main goals of this course are to develop the following skills: - developing your scientific ideas through discussions in groups - thinking critically and expressing oneself clearly - turning a general idea into a research project - writing a research proposal and defending it It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your ideas. You, as a group, will decide what the important questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer your questions, provide coaching and give you feedback on your projects, but they will generally take the back seat. Additionally, the faculty will give informal talks about their research and be available for discussion with individual students. At the end you will present your projects to other participants, and we will party.

\*Costs\*: CHF 420.- for room and board.

More information under <http://www.unil.ch/ee/-page73344.html> \*To apply,\* send a single file (pdf or rtf) containing a short motivation letter, a cv and the name of your scientific advisor to tadeusz.kawecki@unil.ch.

\*Deadline\* for application: March 1, 2010

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lausanne, Switzerland tadeusz.kawecki@unil.ch

tadeusz.kawecki@unil.ch tadeusz.kawecki@unil.ch

## ULiverpool Coevolution Apr14-15

The MMEMS network is holding a two day workshop “Coevolution: Models and microbial model systems” at the University of Liverpool on the 14-15th of April 2010. The workshop is intended to encourage dialogue and closer collaboration between theoreticians and empiricists studying coevolution.

Confirmed speakers: Akira Sasaki (SOKENDAI); Mike Boots (Sheffield); Angus Buckling (Oxford); Sylvain Gandon (CNRS, Montpellier); Eva Kisdi (Helsinki); Britt Koskella (Santa Cruz); Oliver Kaltz (Montpellier II); Andy Fenton (Liverpool)

Registration fee: £50 (covers refreshments, lunch and wine reception) Optional dinner on Wednesday evening: £25 Registration Deadline: 26th March 2010 Participants should book their own accommodation

Scientific enquiries: Dr. Mike Brockhurst (michael.brockhurst@liverpool.ac.uk)

Admin enquiries: Ann Linfield (masadl@maths.bath.ac.uk)

For more details, and to register please go to: [http://www.mmems.org/index.php?id\\_pag=115](http://www.mmems.org/index.php?id_pag=115) Michael.Brockhurst@liverpool.ac.uk Michael.Brockhurst@liverpool.ac.uk

## WoodsHole MolecularEvol Jul25-Aug6

Workshop on Molecular Evolution, Woods Hole

<http://www.molecularevolution.org/workshop> 25 July - 6 August 2010, individual research session 6 - 13 August 2010

Application Deadline 1 March 2010

Michael P. Cummings, Director

The Workshop on Molecular Evolution has been the finest course on the subject since first offered in 1988 in Woods Hole, USA. The Workshop consists of a series of lectures, demonstrations and computer labora-

tories that cover various aspects of molecular evolution. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in molecular evolution. Included among the faculty are developers and other experts in the use of computer programs and packages such as BLAST, BEAST, Clustal W and Clustal X, FASTA, FigTree, GARLI, Genealogical Sorting Index, LAMARC, MAFFT, MrBayes, PAML, PAUP\*, and SeaView who provide demonstrations and consultations. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students with prior experience in molecular evolution and related fields. Scientists with strong interests in molecular evolution, phylogenetics, population genetics, and related fields are encouraged to apply for admission. 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. Participants find the individual research session to be especially useful.

Topics to be covered include:

- Databases and sequence matching: database searching; protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches
- Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis; hypothesis testing
- Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters
- Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conservation
- Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution
- Comparative genomics: genome content; genome structure; genome evolution
- Molecular evolution integrated at lower levels: biochemistry; cell biology; physiology; relationship of genotype to phenotype

2009 Fees: \$2650 (room and board at no additional charge), plus an additional \$1000 for the individual research session.

More information is available at <http://www.molecularevolution.org/workshop> The direct link to application information is <http://gosnold.mbl.edu/StudentApp/StudentApp.asp?CourseID=3DMOLE>

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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. 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.