EvolDir

June 1, 2009

Month in Review

Foreword

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

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

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

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Conferences

Adelboden Switzerland SocialEvolution Aug15-18

The use of vertebrate model systems to study social evolution 15 â 18 August 2009, Adelboden, Bernese Alps, Switzerland

Invited speakers: Prof. Nadia Aubin-Horth, UniversitÃ© de MontrÃ©al, Canada Prof. Sigal Balshine, McMaster University, Canada Prof. Tim Clutton-Brock, University of Cambridge, UK Prof. Jan Komdeur, Rijksuniversiteit Groningen, Netherlands Dr. David S. Richardson, University of East Anglia, UK

Summary: To understand the evolution of complex social organization (including structured groups, cooperation between group members, task sharing, individualized relationships, divergent social roles) we need suitable model systems that (1) dispose of the required complexity of social organization, (2) allow to observe and measure relevant traits and their fitness effects in the field, and (3) enable performance of crucial experiments to unravel underlying ultimate and proximate mechanisms of advanced sociality. Among vertebrates, there are a few model systems that fulfil these criteria, like meerkats, Seychelles warblers and Lake Tanganyika cichlids. The aim of this symposium is to provide state-of-the-art insight into the mechanisms underlying advanced social behaviour by bringing together experts studying respective model systems in mammals, birds and fishes.

Structure of the symposium: Invited speakers and other participants who wish to contribute to the theme of the symposium will present relevant results and overviews of the(ir) research on the respective model systems. In the discussion, we shall emphasize the involved ultimate and proximate mechanisms and attempt to compare them between different vertebrate taxa to understand the importance of intrinsic differences in their biology. We shall further discuss the pros and cons of the respective model systems to unravel general principles of social evolution. We expect that at the end of this symposium the participants will dispose of a good understanding of some of the most complex and best studied model systems of social evolution.

Where and when: The symposium will take place in Adelboden, an alpine village in the Bernese

Alps (http://www.adelboden.ch/en/navpage-SummerAB.html). The venue is the high-altitude holiday resort Crea (http://www.hotel-crea.ch/-adelboden/) that combines the convenience of a nice setting in a breathtaking landscape with the practical amenities of a well-proven seminar venue. It is within easy reach by public transport from any Swiss city. For all details of the meeting and registration please consult: http://behav.zoology.unibe.ch/-index.php?pp=56&pf Registration until 1 June 2008 at:marlis.gerteis@iee.unibe.ch

Credits:1-2 ECTS can be obtained, depending on the contribution of the participant Organizer: Michael Taborsky, University of Bern (michael.taborsky@iee.unibe.ch)

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Phone: +41 (31) 631 91 58

“von Kuerthy, Corinna” <corinna.vonkuerthy@iee.unibe.ch>

Berlin WildlifeGenetics Sep21-24

Dear Colleagues,

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

7th International Conference on Behaviour, Physiology and Genetics of Wildlife“ between 21st and 24th September 2009 in Berlin, Germany.

Please be reminded that THE DEADLINE FOR THE EARLY BIRD REGISTRATION AND ABSTRACT SUBMISSION ENDS ON 1st OF JUNE 2009 !

For those who have not registered yet, please do so: http://www.bayceer.uni-bayreuth.de/izw7/ The main topics of the conference are: - Life History & Maternal Effects (Pat Monaghan, Universtity of Glasgow, UK) - Stress & Disturbance (Marco Apollonio, Universita Sassari, Sardinien, Italy) - Reproduction Biology (David Wildt, Smithsonian National Zoological Park, USA) - Evolutionary Genomics in Conservation (Pierre Taberlet, Université Joseph Fourier, Grenoble, France) - Conservation Biology (Eric Dinerstein, Director of science WWF-USA, Washington, USA)

The Conference offers several workshops: 1. Evolutionary Genomics in Conservation (Pierre Taberlet, Université Joseph Fourier, Grenoble, France & Simone Sommer, IZW, Berlin, Germany)

2. Communication in Mammals and Birds (Francesco Bonnadonna, Centre d’Ecologie Fonctionnelle et Evolutive, Montpellier, France & Martin Dehnhard, IZW, Berlin, Germany)

3. Welfare and Conservation (Eric Dinerstein, senior scientist WWF-USA, Washington, USA & Marion East, IZW, Berlin, Germany)

4. Stable Isotopes, Nutrition and Energetics (Carlos Martinez del Rio, University of Wyoming, USA; Sylvia Ortmann, IZW, Berlin, Germany & Christian Voigt, IZW, Berlin, Germany)

5. Behavioural Rhythms (Serge Daan, University of Groningen, the Netherlands & Anne Berger, IZW, Berlin, Germany)

6. Research by, in, with and for zoos, aquaria and other ex situ-institutions (Kirstin Leus, EAZA & IUCN/SSC:CBSG Europe, Antwerpen, Belgium)

A practical training workshop on non-invasive monitoring of hormones will also take place at the IZW/Berlin during the week preceding the conference; Martin Dehnhard, IZW.

The conference dinner will take place at a beautiful setting in the city center overlooking the river ”Spree“.

You will find more information about the conference on our homepage at: http://www.izw-berlin.de/de/-flink/7thIZW-Conference.html Please do not hesitate to contact us if you require any further information: symposium@izw-berlin.de, IZW, Berlin, Germany.

We are looking forward to welcome you, Kind regards,

Simone Sommer

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

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

BrownU Genomics Jun8-11 2

The final Program of invited talks has been posted for The American Genetic Association Symposium on

"The Genetics and Genomics of Environmental Change"

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

Have a look at the program : http://www.brown.edu/Departments/EEB/aga/ The Symposium is open to all, and registration will remain open until the start of the meeting.

The deadline for Poster abstract submission will be open until Monday 25 May, so there is still time to contribute a paper at the meeting.

Speakers will address genetic and genomic approaches to the following topics:

Clinal variation and spatial scales of environmental change Paleontological scales of environmental change Life history evolution in response to temperature stress Adaptation to human environmental stressors Genotype x Environment Interactions

Hope to see you in Providence

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

Budapest RECOMB Comparative Genomics Sep27-29

Dear all,

Submission of papers is now open for the upcoming RECOMB Comparative Genomics (RECOMB-CG) meeting, which will take place in Budapest in September 27-29 2009. The deadline for paper submission is June 20, 2009.

DESCRIPTION OF THE CONFERENCE:

Comparison of related genomes offers enormous inferential power, revealing a wealth of knowledge about genome evolution itself and about genetic function and cellular processes. As the number of fully sequenced genomes grows, so do the opportunities and challenges for computational comparative genomics. This workshop brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and novel experimental results. The program will include a combination of keynote speakers and contributed talks. Topics of interest include, but are not limited to

* Algorithms in comparative genomics * Comparative study of orthologous genes * Gene finding using multiple genomes * Sequence homology * Genome rearrangements * Measures of evolutionary distance * Whole genome phylogeny reconstruction * Sequence assembly using sequence comparison * Multiple genome alignment * Gene and genome duplication * Identification of conserved and fast evolving sequences

CONFIRMED INVITED SPEAKERS:

- Richard Durbin (Welcome Trust Sanger institute) - Jotun Hein (University of Oxford, UK) - Laurence Hurst (University of Bath, UK) - Csaba Pál (Biological Research Center, Szeged, Hungary) - Lisa Stubbs (University of Illinois) - Jeroen Raes (EMBL Heidelberg)

MEETING WEBSITE: http://www.renyi.hu/conferences/recomb-cg2009/ CONTACT: rcg2009@renyi.hu

CONFERENCE CHAIRS:

István Miklós (Rényi Institute, Budapest) Francesca Ciccarelli (European Institute of Oncology IEO, Milan)

–

Francesca D. Ciccarelli, PhD Biocomputing IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303053 fax +39-0294375990 web: http://ciccarelli.group.ifom-ieo-campus.it/ francesca.ciccarelli@ifom-ieo-campus.it

Crete MediterraneanEvolution Sep21-25 DeadlineExtended

Dear colleague,

The published deadline for talk/poster presentations at the upcoming International Congress on the Zoogeography, Ecology and Evolution of Eastern Mediterranean

that will take place in Irakleio (Crete, Greece) between the 21^st and the 25^th of September (2009) (http://www.nhmc.uoc.gr/iczegar11/) is May 31st.

As several people have indicated that they need more time, we have decided to extend the deadline to *June 30*.

On behalf of the organizing committee, I thank you for registering promptly, as it makes all the difference is assembling the meeting schedule.

Poulakakis Nikos

– Assist. Prof. Nikos Poulakakis Department of Biology and Natural History Museum of Crete University of Crete Knossos Av., P.O.BOX 2208 Irakleio, Crete, GR-71409 Greece

Phone +302810324366, +302810393282 e-mail: poulakakis@nhmc.uoc.gr

Nikos Poulakakis <poulakakis@nhmc.uoc.gr>

Girona Spain SpongeEvolution Sep20-24

Dear Evoldir members

The next International Sponge Conference will be held in Catalonia, Spain

Dates: 20-24 September 2010

Venue: "Palau de Congressos" of the city of Girona:

http://www.auditorigirona.org/eng/pc.presentacio.php Girona is the capital of the province where our laboratory belongs. It is located some 100 Km North of Barcelona.

http://www.ajuntament.gi/web/eng/index.php The sponge conference is held every 4 years and gathers together people working on different aspects of sponge biology. Topics for the 8th edition will include:

Evolution and phylogeny Organismal biology Population biology Ecology Natural products Sponges and society Taxonomy

We are now setting up the web page and other details. We will post a second announcement once the webpage is working. In the meantime you can address any question to:

spongeconference2010@ceab.csic.es

With best wishes

M.J. Uriz, M.A. Becerro, M. Maldonado, X. Turon Organizing Committee 8th International Sponge Conference

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Xavier Turon Dept. of Aquatic Ecology Center for Advanced Studies of Blanes (CEAB, CSIC) Accés a la Cala S. Francesc 14 17300 Blanes (Girona) Spain

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KansasCity ArthropodGenomics Jun11-14

3rd ANNUAL ARTHROPOD GENOMICS SYMPOSIUM, June 11-14, 2009, Kansas City

ORGANISM GROUP MEETINGS:

We welcome the opportunity to facilitate meetings of the various organism groups during the Symposium. If you would like to organize a meeting of your organism group during the Symposium, please contact Doris Merrill, dmerrill@k-state.edu, for arrangements.

POSTER ABSTRACTS: If you would like to have your poster abstract considered for an oral presentation, the deadline for submission is Friday, May 15, 2009. Guidelines are available at http://www.k-state.edu/agc/abstracts/index.html.

REGISTRATION: The deadline for discounted registration fees is Friday, May 15. After May 15, we will continue to welcome your registration to attend the 3rd Annual Arthropod Genomics Symposium at a slightly higher cost.

Register online: http://www.k-state.edu/agc/symp2009/register.html and attend

Frontiers in Arthropod Genomics

June 11 - 14, 2009, Kansas City, USA

HOTEL < http://www.k-state.edu/agc/symp2009/hotel.html > RESERVATIONS: The deadline to reserve your hotel room at the conference site is Thursday, May 21, or until the room block is depleted.

SYMPOSIUM WEBSITE: www.k-state.edu/agc/symp2009

WORKSHOPS and SEMINARS:

- Pre-symposium workshop on Chado Databases and Integration with GMOD Tools, Scott Cain, Ontario Institute for Cancer Research

- Genomic Sequence Capture and Next-Gen Sequencing Seminar, sponsored by Roche NimbleGen

- BeeSpace demonstrations

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

SYMPOSIUM <file:///C:\Documents%20and%20Settings\Doris\My%20Documents\Arthropod\AGC%20 Comm-Symposium\2009%20Symposium\Schedule-Revised.pdf> PROGRAM: The symposium sessions will begin Thursday evening, June 11, and continue on Friday and Saturday, with additional events on Saturday evening and Sunday morning. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Workshops will be held Thursday prior to the Symposium and Friday evening. Activities will conclude by noon on Sunday, June 14.

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

KANSAS CITY JAZZ AND BBQ: Join the group in a fun-filled evening of Kansas City Jazz and Barbecue!!! Participants are invited to enjoy “Kansas City’s BEST BBQ” - Fiorella’s Jack Stack Barbecue at the Freight House location and the Kerry Strayer Jazz Trio on Saturday night. The separate charge for this optional activity is $50 ($25 for students). Transportation will be provided.

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

INFORMATION: Visit our website, www.k-state.edu/agc/symp2009, for complete details and brochure.

QUESTIONS: Contact us at (785) 532-3482 or dmerrill@ksu.edu. Please share this announcement with colleagues and students!

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

KEYNOTE SPEAKER:

*William M. Gelbart, Harvard University,

“Opportunities & Challenges for Arthropod Genomics and

Informatics in the NextGen World.”

FEATURED SPEAKERS:

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

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

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

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

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

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London E-Biosphere challenge Jun1

Dear All,

I would like to invite everyone attending e-Biosphere to join in a challenge entry that will i) illustrate the human sensor-net concept, and ii) be a collective demonstration of the semantic web in action. (To be fair, we should probably exclude ourselves from consideration during voting. But if we feel like we’ve won, I’ll buy beer for everybody.) There will be a number of ways to participate:

1. Post pictures of London wildlife during the conference, and encourage friends back home (or in other interesting parts of the world) to also post pictures. The metadata will be published in RDF, and integrated with background natural history data that is already in

RDF. This will enable us to pose and answer queries like “Show observations of species that are invasive where they were observed.”; “Show the Northernmost observation of the Asian Longhorned Beetle”; “Show observations of predators and prey of threatened species”; etc.

If requested, pictures will be sent to a crowdsourcing tool for species identification.

2. You can volunteer to help identify images.

3. You can specify queries that you would like to see supported. This is important for our demonstration, since part of the social/semantic web’s discrete charm is its flexibility in responding to ad-hoc queries. A wiki will collect user’s queries.

4. You can contribute RDF, and help assemble the glue (e.g., owl:sameAs statements, etc.) that will bind all the RDF together.

For reporting observations, you are welcome to use Spotter (http://spire.umbc.edu/spotter/), but can also simply submit data via spreadsheet or email.

Details on the other modes of participation will be forthcoming.

Here’s a brief description of the concept in the context of eco-blogging: http://ebiquity.umbc.edu/-blogger/2007/09/14/semantic-eco-blogging-spotter-10-released/ (For the challenge, photos need not be embedded in a blog. They simply need to exist somewhere on-line, e.g. on Flickr.)

Suggestions are most welcome.

I look forward to seeing what comes together - Joel.

Note: this message is duplicated at: http:/-/forum.e-biosphere09.org/viewforum.php?fe jsachs@csee.umbc.edu

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PortlandOR Ontologies Jul25

WORKSHOP on ONTOLOGIES FOR ICHTHYOLOGY & HERPETOLOGY

To be held in conjunction with the joint meeting of Ichtyologists and Herpetologists

Portland Oregon July 25, 2009

https://www.phenoscape.org/wiki/ASIH09_workshop WORKSHOP GOALS: Ontologies, controlled vocabularies with well-defined relations among terms, are a key tool in scientific data integration. By using ontologies, scientists from different disciplines can know when they are referring to the same entity by different names, and new discoveries are enabled by computer software being able to reason across disciplines and over large datasets. Already widely used in genomics, ontologies are of growing importance in systematics, ecology, behavior, genetics, morphology and physiology. This workshop aims to explore the utility of ontologies for ichthyology and herpetology, using the Teleost Anatomy Ontology and the Amphibian Anatomy Ontology as case studies of community resources that are being actively developed and used by members of ASIH. Participants will present examples of how these ontologies are being used to provide new ways of exploring data within morphological and phenotypic databases. Talks in the morning will be followed in the afternoon with ontology development workshops and hands-on demonstrations of Phenoscape and AmphibAnat tools.

DATE & TIME: Saturday, July 25, 2009 PLACE: Hilton Portland & Executive Tower

SPEAKERS: * Hilmar Lapp (National Evolutionary Synthesis Center) A gentle introduction to ontologies for biology * Monte Westerfield (Director, Zebrafish Information Network and Institute of Neuroscience, Eugene, OR) Linking animal models and human diseases * Paula Mabee (University of South Dakota) Phenoscape: Using ontologies to link comparative morphology to genes * Greg Riccardi (Florida State University) Why ontologies are important for understanding morphological images * Peter Vize (University of Calgary) The Xenopus ontology and database * Anne Maglia (Missouri University of Science and Technology) Development of an anatomical ontology for amphibians * Marc Robinson-Rechavi (Universite de Lausanne, France) Integrating ontology and homology for the study of gene expression evolution

SPONSORS & ORGANIZERS The workshop is jointly sponsored by the Phenoscape and AmphibAnat projects. Organizers include Paula Mabee, Anne Maglia, Professor, Todd Vision and Monte Westerfield.

tjv@bio.unc.edu tjv@bio.unc.edu

QueenslandU GenomicDataAnalysis Oct5-6

Dear colleagues,

You are cordially invited to attend The Australasian Conference on Statistical Methods for Genomic Data Analysis, to be held at The Queensland University of Technology Gardens Theatre on the 5th and 6th of October, 2009. The Conference is jointly organised by The Queensland University of Technology and the Queensland Institute of Medical Research.

Statistics applied to genetics and genomics is a growing field. There is significant expertise within Australia and New Zealand across a broad range of applications. The purpose of the conference is to bring researchers together to find out what is going on in local research and to facilitate collaboration, integration and resource sharing. This meeting will bring together experts in bioinformatics and statistical genetics from Australia, New Zealand and further afield to share recent groundbreaking discoveries and methods, and to facilitate new research partnerships, in a relaxed and friendly atmosphere. There will be sessions encompassing genome-wide association studies, genomic selection, sequence analysis, phylogenomics, QTL mapping, comparative and functional genomics, gene expression and network analysis.

Conference registration is free, but nevertheless please contact Zoe van Havre (zoe.vanhavre@qut.edu.au) before August 31 to register. Invited speakers have now been finalised, but a limited number of contributed talks are also sought. If you would like to present at the conference, please submit titles and short abstracts (up to 200 words) to Zoe van Havre at the above email address.

Further details of the conference are contained in the attached flyer and at the conference website (http://genepi.qimr.edu.au/genomics/ < http://genepi.qimr.edu.au/genomics/ >). A list of our internationally renowned invited speakers is available at the website, together with details of the venue. Please bookmark the website and keep an eye on it for future developments.

Regards, The Conference Organising Committee Allan McRae Beben Benyamin Carla Chen Jonathan Keith Kerrie Mengersen Naomi Wray Peter Visscher Zoe van Havre

Dr Beben Benyamin Queensland Statistical Genetics Queensland Institute of Medical Research 300 Herston Road,Brisbane 4029,Australia Tel: +61 7 3362 0169 Fax: +61 7 3361 0101 Email:bebenB@qimr.edu.au Web: http://genepi.qimr.edu.au/ Beben Benyamin <Beben.Benyamin@qimr.edu.au>

Regensburg GermanZoologicalSociety Sep25-28

The German Zoological Society, DZG, will hold its annual meeting for the Darwin Year 2009 in Regensburg, Germany, from Sept. 25 to Sept. 28, 2009.

Charles Darwin's theory of evolution provides the foundation of modern biology and its diverse subdisciplines. Therefore the organizers of this meeting have attempted to commemorate the 200th birthday of Darwin and the 150th anniversary of the publication of "The Origin of Species" through the selection of renowned main speakers, including Dorothy Cheney, Jim Goodson, Thomas Junker, Hubert Markl, Mark Martindale, Svante Pääbo, Massimo Pigliucci and Joan Strassmann.

Through your participation the meeting would reflect the entire breadth and meaning of modern zoology. Conference language is English. Please register at www.dzg2009.de before May 18.

Regensburg is a middle-sized town on Danube river. Its historical city center has recently obtained UNESCO World Heritage status and is certainly worth a visit. Regensburg can easily be reached from Munich (MUC) or Nuremberg (NUE) airports by train.

Looking forward to seeing you in Regensburg

Jürgen Heinze

Prof. Dr. Jürgen Heinze Biologie I Universität Regensburg D-93040 Regensburg Tel. –49 941 943 2475 Fax –49 941 943 3304 http://www.uni-regensburg.de/evolution

Juergen.Heinze@biologie.uni-regensburg.de

Roscoff France ViralEvolution Sep26-30

Understanding emergence of infectious diseases: focus on New Experimental and Theoretical Approaches to Virus Evolution

Roscoff (Brittany), France, September 26-30, 2009 http://www.cnrs.fr/insb/cjm/2009/elena_e.html (expended) deadline for application: May 15th, 2009

New viruses have been emerging during the last decades as a consequence of the climatic change and of the increasing introduction of human societies and its domestic animals and plants into virgin areas of the planet (HIV, SARS, Influenza, Ebola, etc). So far, and despite tremendous economical and manpower investments, efforts to control and eradicate viruses, with a few important exceptions (e.g., poliovirus), have been of quite limited success. Moreover, the perspective of future eradications will be overbalanced by the emergence of new viruses. This lack of success is a consequence of the great evolvability of viral populations owed to their large population size, short generation times and compacted genomes. This dynamic nature of viral populations has been largely ignored by pharmacological treatments. Owing to the failure of current approaches, new ones taking into consideration the evolvability of viral populations are thus very much needed. Understanding the ecological and genetic mechanisms behind the genesis, maintenance, and fate of viral diversity, and the interaction of heterogeneous viral populations with their standard and putative new hosts, became pivotal for the development of such new strategies.

In the recent years, comprehensive research programs have been conducted to gain insights into the mechanisms of emergence of plant and animal viruses. Not always paralleling these empirical progresses, theoreticians have been developing increasingly complex models to account for the peculiarities of viral populations with the aim of predicting their behavior.

The aim of this Jacques Monod Conference is to bring together empiricists and theoreticians working on virus evolution, whatever the host species (animal, plants, bacteria). The conference should then promote a cross-talk that will create the basis for reaching the dual goal of making more biologically realistic models and of designing new hypothesis-driven experiments. To achieve this goal, speakers will then be asked to present their work around one of the four following topics: (1) genesis and maintenance of viral diversity, (2) evolution of virulence and viral fitness, (3) genomic evolution, and (4) host-virus coevolution.

Invited speakers : (provisional titles)

BERKHOUT Ben (Amsterdam, The Netherlands) HIV-1 evolution: frustrating antiviral therapies, but disclosing molecular mechanisms

BLANC StÃ©phane (Montpellier, France) Multiple infection of individual host cells by genomes of a plant virus population

BONHOEFFER Sebastian (Zurich, Switzerland) Recombination in HIV-1

BRIONES Carlos (Madrid, Spain) Evolution of minority memory subpopulations within RNA virus quasispecies

BUCKLING Angus (Oxford, United Kingdom) Host-virus experimental coevolution

BURCH Christina L. (Chapel Hill, USA) Viral coinfection allows a test of Wright's physiological model of dominance

CHEVILLON Christine (Montpellier, France) Dengue virus type 2 evolution in French Guiana through 1993-2006: recombination, selection and migration patterns at light of full- length sequences

DESBIEZ CÃ©cile (Avignon, France) Emerging strains of Watermelon mosaic virus in France: evidence for limited spread but rapid local shift in populations

DOMINGO Esteban (Madrid, Spain) Molecular mechanisms of lethal mutagenesis of RNA viruses

ELENA Santiago F. (Valencia, Spain) Evolutionary Systems Biology approach to host-virus interaction

FROISSART RÃ©my (Montpellier, France) Host omic modifications due to virus adaptation

FROST Simon D.W. (San Diego, USA) Phylodynamics of simple epidemiological models of HIV and HCV transmission

GANDON Sylvain (Montpellier, France) Dynamics of mutation load in virus populations

GARCIA-ARENAL Fernando (Madrid, Spain) Arabidopsis thaliana as a tool to study virus-host coevolution

GOLDBERG Tony L. (Urbana, USA) Fine-scale ecological drivers of arbovirus evolution: the case of West Nile virus in Chicago, USA

HOLMES Edward C. (University Park, USA) The evolutionary genomics of RNA viruses

MALIM Michael (London, United Kingdom) APOBEC proteins and HIV-1 - lethal and beneficial editing?

MANRUBIA Suzanna (Madrid, Spain) Stochastic extinction of viral infectivity: the role of defectors

MICHALAKIS Yannis (Montpellier, France Effective population size and plant virus transmission

MOURY BenoÃ®t (Montfavet, France) Adaptation of viral populations to polygenic resistances in plants

ROOSSINCK Marilyn J. (Ardmore, USA) Plant virus metagenomics

SANJUÃN Rafael (Valencia, Spain) The role of robustness in evolution: experimental studies

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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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StonyBrook Evolution Nov4-8

Dear Colleagues:

Darwin 2009: 150 Years of Evolutionary Biology

On November 4-8 2009, the Department of Ecology & Evolution at Stony Brook University will celebrate the 150th anniversary of Darwins The Origin of Species by hosting a four-day meeting where leading evolutionary biologists will lecture and help lead discussions on the current status and future of the study evolutionary biology. We will have three stimulating days of keynote addresses, evening panels and discussion groups, and ample opportunity for communication on the important issues of the present and future of evolutionary biology. All lectures will be in modern and pleasant facilities at Stony Brook University, with available nearby lodging and convenient transportation to the meeting site.

To register, secure lodging, and get further information on transportation, our Advisory Board, and other matters, please visit our web site

http://darwin09.org Below is our schedule of events and speakers.

Wednesday, November 4

6:00 - 8:00 Welcoming Reception for Participants

Thursday, November 5

8:45 - 9:00 Welcome from Stony Brook University

9:00 - 9:40 Opening Keynote Address, Douglas J. Futuyma, Stony Brook University

9:40 - 10:00 Q&A

10:00 - 10:30 Coffee Break

10:30 - 11:10 History, Peter Bowler, Queens University, Belfast

11:10 - 11:30 Q&A

11:30 - 12:10 Natural Selection, Mark Kirkpatrick, University of Texas at Austin

12:10 - 12:30 Q&A

12:30 - 2:00 Lunch

2:00 - 2:40 Behavioral Ecology, Hanna Kokko, University of Helsinki

2:40 - 3:00 Q&A

3:00 - 3:40 Evolutionary Ecology, Anurag Agrawal, Cornell University

3:40 - 4:00 Q&A

4:00 - 4:30 Coffee Break

4:30 - 5:10 Organismal Adaptation, May R. Berenbaum, University of Illinois

5:10 - 5:30 Q&A

6:00 - 8:00 Dinner

8:00 - 10:00 Informal Discussions

Friday, November 6

8:45 - 9:00 Welcome and Announcements

9:00 - 9:40 Philosophy, Roberta L. Millstein, University of California, Davis

9:40 - 10:00 Q&A

10:00 - 10:30 Coffee Break

10:30 - 11:10 Evolutionary Genetics, Jianzhi George Zhang, University of Michigan

11:10 - 11:30 Q&A

11:30 - 12:10 Genetics of Population History, John Wakeley, Harvard University

12:10 - 12:30 Q&A

12:30 - 2:00 Lunch

2:00 - 2:40 Genomics, Doris Bachtrog, University of California, Berkeley

2:40 - 3:00 Q&A

3:00 - 3:40 Speciation, Richard G. Harrison, Cornell University

3:40 - 4:00 Q&A

4:00 - 4:30 Coffee Break

4:30 - 5:10 Evolvability, Gunter Wagner, Yale University

5:10 - 5:30 Q&A

6:00 - 8:00 Dinner

8:00 - 10:00 Informal Discussions

Saturday, November 7

8:45 - 9:00 Welcome and Announcements

9:00 - 9:40 Ancient Origins, Antonio Lazcano, Universidad Nacional Autunoma de Mexico

9:40 - 10:00 Q&A

10:00 - 10:30 Coffee Break

10:30 - 11:10 Tree of Life, David Hillis, University of Texas at Austin

11:10 - 11:30 Q&A

11:30 - 12:10 Evolution in the Fossil Record, to be determined

12:10 - 12:30 Q&A

12:30 - 2:00 Lunch

2:00 - 2:40 Evolutionary Developmental Biology, Gregory Wray, Duke University

2:40 - 3:00 Q&A

3:00 - 3:40 The Fossil Record of Diversity, Michael Foote, University of Chicago

3:40 - 4:00 Q&A

4:00 - 4:30 Coffee Break

4:30 - 5:10 Evolutionary Radiations, Jonathan B. Losos, Harvard University

5:10 - 5:30 Q&A

6:00 - 8:00 Dinner

8:00 - 10:00 Informal Discussions

Sunday, November 8

8:45 - 9:00 Welcome and Announcements

9:00 - 9:40 Human Origins, Tim D. White, University of California, Berkeley

9:40 - 10:00 Q&A

10:00 - 10:30 Coffee Break

10:30 - 11:10 Cultural Evolution, Peter J. Richerson, University of California, Davis

11:10 - 11:30 Q&A

11:30 - 2:30 Lunch

12:30 - 1:10 Applied Evolution, Joanne P. Webster, Imperial College London

1:10 - 1:30 Q&A

1:30 - 2:10 Closing Keynote Address, Hopi E. Hoekstra, Harvard University

Meeting web site address:

http://darwin09.org Jeffrey Levinton,

For the Organizing Committee

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

tel (631) 632 8602 fax (631) 632 7626 Marine Biology Web Page http://life.bio.sunysb.edu/marinebio/mbweb.html

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Tilton NewHampshire EvolutionaryGenomics Jul12-17

The Gordon Conference in Evolutionary and Ecological Genomics will be held from July 12-17 in beautiful Tilton, NH. The meeting is filling up fast, and we invite you to apply and register for what will be an extraordinary meeting of ecologists, genomicists and evolutionary biologists.

Meeting description: http://www.grc.org/programs.aspx?year=2009&program=evoeco To apply: http://www.grc.org/application.aspx If you haven't yet been to a Gordon conference, this would make a great entree - sessions are held in the mornings and evenings, with all afternoons available for relaxing and enjoying the company of your scientific colleagues in the beautiful setting of Tilton, NH. There will be access to kayaking, hiking and many other outdoor activities. The meeting will highlight the research of 22 internationally renowned scholars in the areas of global change genomics, plant ecological genomics, genomics of social insects, microbial genomics, human population genomics, and many other fields. You will have the opportunity to present your work in one of the poster sessions, which are attended by all at the meeting and provide a forum for getting the feedback of colleagues in a small but vibrant meeting. Apply now, and please contact Scott Edwards if you have any questions:

Scott Edwards Harvard University sedwards@fas.harvard.edu ph: 617-384-8082

sedwards@fas.harvard.edu sedwards@fas.harvard.edu

UBristol MathModelsInEcologyEvolution Sep10-11

Dear colleagues,

the University of Bristol will host Mathematical Models in Ecology and Evolution this year, from September 10th to 11th. MMEE 2009 will have a Darwinian flavour, in honour of the bicentenary of Darwin's birth, and 150 years since the publication of The Origin of Species. While not a mathematician himself, Darwin's ideas find natural expression in the form of mathematical models, allowing further development and refinement of the theory. This two-day meeting will showcase the latest developments of formal models in evolution and ecology, and will include keynote addresses on the mathematical modelling of Darwin's key theories and insights.

Keynote Speakers * Professor Rob Boyd, Department of Anthropology, University of California Los Angeles * Professor Alan Grafen, Department of Zoology, University of Oxford * Professor Hanna Kokko, Department of Biological and Environmental Science, University of Helsinki * Professor Franjo Weissing, Department of Biology, University of Groningen

Abstract Submission Abstract submission will close on June 12th 2009. Please visit the conference website for further details.

Registration Registration will close on July 10th 2009. Registration will cost 50 GBP for standard delegates, to include lunches, coffee breaks and conference reception. 40 free-registration places will be available for postgraduate student on a first-come-first-served basis.

Please visit the conference website for further details, and for a conference poster: www.cs.bris.ac.uk/-mmee2009 We hope to see you in Bristol in September.

Best wishes, James Marshall, John McNamara, Alasdair Houston

sean.rands@bristol.ac.uk sean.rands@bristol.ac.uk

UGuelph FrontiersEvolution May20-21 2

This is a friendly reminder that there is still space and time to register for the 'Frontiers in Evolution' colloquium at the University of Guelph, in sunny Guelph Ontario, May 20-21.

Invited speakers talking about research at the Frontiers of evolutionary biology include: Dr. David Sloan Wilson; levels of selection Dr. Ryan Gregory; genome evolution Dr. Richard Lenski; experimental evolution Dr. Belinda Chang; molecular evolution Dr. Craig Albertson; developmental evolution Dr. Hans Thewissen; paleontology and genetics

While there are no other speaking session except for the plenary, there is an opportunity to present posters during a social session on the evening of May 20.

For more information and to register, please see: http://www.uoguelph.ca/Ecologicalcolloquia/-Academic.html Faculty: 200$ Postdocs and Grads: 100$

Kind regards,

Beren W. Robinson Assoc. Prof. Dept. of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1, Canada

email: berenrob@uoguelph.ca Phone: 519-824-4120 x58968 Fax: 519-767-1656 Office location: Scie 2455 Lab location: Scie 2403

“Beren W. Robinson” <berenrob@uoguelph.ca>

UIdaho SSE2009 Jun12-16 reminder

Evolution 2009 is drawing close, and there are a few logistic updates. It will be possible to register to attend at any time, so walk-ins are fine. Meanwhile, if you plan to use conference bussing, on-campus housing, or to subscribe to a meal plan, please do so on or before May 24. Thanks, and we look forward to seeing you all in Moscow!

Olle Pellmyr Program chair, Evolution 2009

Olle Pellmyr <pellmyr@uidaho.edu>

UIdaho SSE PhotoPedagogy Jun12-16

Members of ASN, SSB, SSE:

I. Photo Contest

Please submit your photos of anything with an evolution theme to be shown at the annual joint meeting of our societies in Moscow, Idaho (6/12-6/16). Photos will be judged at the All-Society banquet and cash awards of 100, 50, and 25 US dollars or equivalent will be given to the top three entrants. The photos may contribute to the SSE web site. You do not need to attend the meeting or banquet, but you do need to be a member of one of the three societies.

Please submit one photo as a power point slide with a figure legend of 2-3 lines written in Ariel font (or similar) of font size 24, Black. Legend should begin with your name followed by a colon, e.g., Alice Smith: The LEGEND MUST BE IN BLACK FONT IN A WHITE TEXT BOX BELOW THE FIGURE (or will not be considered).

Please submit electronically by Monday noon June 8th to Charles B. Fenster, EVP SSE: cfenster@umd.edu

with subject header: Photo for Joint Meeting. In the text of your letter please indicate your society affiliation.

II. Pedagogy

Please submit an exercise or lecture aid that you use for a large lecture class to facilitate the explanation of an evolutionary concept or phenomenon., e.g., more clever than using dice to demonstrate probabilities, coin tossing to explain drift, a cryptically colored creature to demonstrate camouflage.

Please provide a power point slide to illustrate your teaching aid. Depending on time and entry number, contributions will be noted at the banquet. You do not need to attend the meeting or banquet, but you do need to be a member of one of the three societies.

Following review, all entries will be listed on the web site and contributors will be acknowledged.

Please submit electronically by Monday noon June 8th to Charles B. Fenster, EVP SSE: cfenster@umd.edu

with subject header: Pedagogy Joint Meeting. In the text of your letter please indicate your society affiliation.

Judy Stone <jstone@colby.edu>

UIdaho SSE UndergradDiversity 3

UNDERGRADUATE DIVERSITY AT SSE/SSB, CALL FOR MENTORS

Approximately 15 undergraduates will be participating in the NSF- and NESCent-supported Undergraduate Diversity at SSE/SSB program at Evolution 2009 in Moscow, ID. This program, which brings students to the annual Evolution meeting, has been running continuously since 2003.

An important component of the program is the mentoring that students receive from graduate students, postdocs and faculty. Duties will include meeting a pair of undergraduates in the program, attending and demystifying a day of talks with them, joining them for a meal, introducing them to colleagues, and in general befriending them in ways that show that evolutionary biology is a welcoming discipline. Based on surveys of participants, it is clear that they prefer to meet their mentors early in the meeting; therefore, mentors will be expected to meet their mentees at the opening reception. No costs for travel, housing or registration are covered.

If you are interested in serving as a mentor, please send an email to Rich Kliman (rmkliman@cedarcrest.edu), Scott Edwards (sedwards@fas.harvard.edu), or Jory Weintraub (jory@nescent.org). Please also indicate your broad field of interest, and we will do our best to pair you with students with overlapping interests. And please help spread the word about this very rewarding activity.

Thanks to those who have already volunteered!

Best regards, Rich Kliman

rmkliman@cedarcrest.edu rmkliman@cedarcrest.edu

UIowa SexRecombination May31-Jun3 2

Last call for abstracts for Evolution of Sex & Recombination: In Theory & In Practice May 31 to June 3, 2009.

http://ccg.biology.uiowa.edu/sexrec/ Sex & Rec is less than three weeks away. There is still plenty of room for additional attendees and poster-presenters.

Abstract submission deadline for inclusion in the program is May 18th.

For the scientific program, see: http://ccg.biology.uiowa.edu/sexrec/program.php Confirmed speakers (http://ccg.biology.uiowa.edu/sexrec/speakers.php) Aneil Agrawal Marco Archetti Irina Arkhipova Philip Awadalla Ricardo Azevedo Doris Bachtrog Graham Bell Bill Birky Antonio Bernardo Carvalho Adam Chippindale Josep Comeron Thomas D'Souza Lynda Delph Beth Dumont Ursula Goodenough Lilach Hadany Joseph Heitman Donal Hickey Tim James Vera Kaiser Alex Kondrashov Jennifer Kovacs Curt Lively Michael Lynch Bryant McAllister David Mark Welch Matthew Meselson Stephanie Meirmans Levi Morran Maurine Neiman Stephen Proulx Rosemary Redfield Denis Roze Tanja Schwander Rama Singh Ingo Schlupp Isa Schon Andrew Schurko David Soll Laurie Stevison Andrew Stewart Marcy Uyenoyama Melissa Wilson Clifford Zeyl

General Information follows:

“EVOLUTION OF SEX & RECOMBINATION: IN THEORY & IN PRACTICE”

May 31 - June 3, 2009 at the University of Iowa, Iowa City, USA

http://ccg.biology.uiowa.edu/sexrec The Roy J. Carver Center for Comparative Genomics and the Department of Biology at the University of Iowa announce an international conference on the evolution of sex & recombination taking place May 31 - June 3, 2009. The meeting will start on the evening of Sunday, May 31st with a reception and keynote talk (Graham Bell) and will conclude at ~1:00 pm on Wednesday, June 3rd.

This conference will immediately precede the 2009 Society for Molecular Biology and Evolution annual meeting (SMBE 2009: http://smbe2009.org), also located in Iowa City, on June 3-7, 2009. In order to integrate both meetings, an “overlap day” (June 3rd) will feature topics of clear interest to both sets of attendees.

The Sex & Recombination meeting was previously scheduled and fully organized for June 16-19, 2008, but was suddenly cancelled due to severe flooding in Iowa City. The organizers are pleased to note that a majority of the previously-scheduled attendees have committed to attend this meeting on the rescheduled dates.

Talks will be given by invited speakers at both the junior and senior level. There will also be some opportunities for contributed talks and posters to be given by conference attendees at all levels of seniority. A number of travel awards will be provided to deserving students and postdocs.

Topics will include: Advantages of sexual reproduction Experimental evolution of sex Estimating recombination rates Mating types & sex determination Linkage, selection & population size Sex chromosomes Sex & pathogenesis Sexual selection Sexual conflict

Sponsorship for this meeting includes generous support from the American Genetic Association, but we encourage additional sponsorship inquiries. A symposium issue to be published in Journal of Heredity is planned.

Check the website for up-to-date information on confirmed speakers, details regarding registration, accommodation, etc. Registration is $200 for grad students and postdocs and $300 for faculty. Registration includes the closing banquet (and keynote: Michael Lynch) to be held on the evening of June 2nd.

All enquiries are encouraged and should be directed to the organizers: sexrec@uiowa.edu.

Facebook users: Join our official meeting group.

On behalf of the organizing committee,

John Logsdon –

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

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

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

UIowa SMBE2009 Jun3-7 CallAbstracts

Last call for abstracts for SMBE 2009!

http://smbe2009.org SMBE 2009 is only three weeks away. There is still plenty of room for additional attendees and poster-presenters.

Abstract submission deadline for inclusion in the program is May 15th.

Some updates and reminders:

The scientific program of symposia and contributed sessions has been determined. See: http://ccg.biology.uiowa.edu/smbe/program.php Hotels are filling up fast. The cut-off date for the SMBE room blocks at the Marriott is May 19th. See http://ccg.biology.uiowa.edu/smbe/venue_accommodations.php for information on booking accommodation. Please remember to book as soon as possible; otherwise, finding lodging will become difficult.

Banquet tickets are still available. If you did not purchase your ticket(s) at the time of your registration, you may log into the registration site (https://www.continuetolearn.uiowa.edu/conferencereg/login.aspx) and purchase them now for $50.00 each. We have booked a terrific band "The Diplomats of Solid Sound" to provide live music after the banquet.

If you have registered for the conference, but haven't submitted an abstract yet, don't forget! The abstract submission deadline is May 15th. Go to http://ccg.biology.uiowa.edu/smbe/subform.php to submit an abstract, using your unique five-digit registration number in your registration code. If you are not submitting an abstract, please fill out the abstract submission page with your information, selecting "None" for your presentation type.

To keep up on the latest information and updates, please visit the SMBE 2009 updates page at http://ccg.biology.uiowa.edu/smbe/updates.php General information on the meeting follows:

SMBE 2009, Iowa City "Darwin to the Next Generation "

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

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

The SMBE 2009 scientific program will include 4 plenary talks and 23 symposia. The program will feature ~240 talks; more than half will be contributed talks selected on a competitive basis from submitted abstracts. We anticipate ~300 poster contributions will be highlighted in two evening poster sessions.

SYMPOSIA (see website for detailed descriptions and confirmed speakers): * Biological networks from genes to populations * Epigenetics, environment & evolution * Evolution of networks * Genome evolution after polyploidy * Genomics of speciation & recent divergences * Historical roots of molecular evolution * Impacts of next generation sequencing on evolution * Insect evolutionary genomics * Molecular arms races * Molecular basis of speciation * Molecular evolution of biological complexity * Molecular evolution of functional noncoding sequences * Molecular evolution of plant:biotic interactions * Mutation accumulation in eukaryotic genomes * Origin & evolution of animal genomes * Population genomics: selection, demography & mutation * Population genomics: theory, computation & adaptation * Primate functional & comparative genomics * Reproductive protein function & evolution * Sex-specific demography using the X * Teaching molecular evolution * Types of molecular evolution * Vanishing genomes

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

–

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

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

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

UIowa SMBE2009 Jun3-7 MentoringProgram 2

SECOND CALL

MENTORS NEEDED SMBE UNDERGRADUATE DIVERSITY MENTORING PROGRAM AWARDS

2009 ANNUAL MEETING OF THE SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION

June 3-7, Iowa City

CONFERENCE WEBSITE

http://www.smbe2009.org PROGRAM OUTLINE

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

To achieve these goals, each recipient of an SMBE Undergraduate Diversity Mentoring Program Award will be paired with two mentors, one a senior graduate student and the other a postdoctoral fellow or faculty member (who may or may not be the students current advisor). WE ARE SEEKING INDIVIDUALS INTERESTED IN BEING A MENTOR. Specific activities will include:

Attending conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the goings-on at a multi-day scientific conference.

Interacting with the student during some mealtimes, coffee breaks and other social gatherings.

Introducing the student to other undergraduates, graduate students, postdoctoral fellows and faculty members as a way of facilitating connections with potential future graduate supervisors and colleagues.

Attending the poster session and SBME Undergraduate Diversity Program Award reception with the student in order to minimize/overcome the anxiety often felt by first-time conference attendees.

Serving as a contact point for the student to help resolve any issues surrounding conference registration, travel and accommodation.

CONFERENCE PARTICIPATION

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

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

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

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

Horace Freeland Judson, The Eighth Day of Creation

John Archibald <jmarchib@dal.ca>

UIowa SMBE2009 Jun3-7 updates

Some updates to SMBE 2009 follow:

1. All of the contributed talks and travel awards have been selected, Check the various symposia for participants. http://ccg.biology.uiowa.edu/smbe/-symposia.php 2. The program of symposia and contributed sessions has been determined. See: http://-/ccg.biology.uiowa.edu/smbe/program.php 3. There is plenty of room for additional attendees and poster-presenters. 4. Hotels are filling up and cut-off dates for hotel space are fast approaching. The cut-off date for the SMBE room blocks at the Sheraton and the Heartland Inn is May 3rd and the Marriot's is May 19th. See http://ccg.biology.uiowa.edu/smbe/-venue_accommodations.php for information on booking accommodation. Please remember to book as soon as possible; otherwise, finding lodging could become complicated. 5. We are currently seeking additional dormitory rooms. If you were interested in staying in the dorms, but have not yet registered to do so, please contact The Center for Conferences (conferences@uiowa.edu) and ask to be placed on a waiting list. You will need to include your requested dates, your gender and potential roommate names in any correspondence regarding dorms. 6. SMBE 2009 t-shirts are now available for pre-order! See the design at http://ccg.biology.uiowa.edu/smbe/tshirt.php . You may pre-order shirts in your requested size and style by logging into the registration site and clicking on "register now": (https://www.continuetolearn.uiowa.edu/-conferencereg/login.aspx) and adding it to your conference registration. The cost is $15.00 for shirts pre-ordered by May 19th; pre-ordered shirts will be provided to you upon arrival and registration. A limited number of shirts will also be available on-site at $20.00 each. 7. Banquet tickets are still available. If you did not purchase your ticket(s) at the time of your registration, you may log into the registration site (https://www.continuetolearn.uiowa.edu/-

conferencereg/login.aspx) and purchase them now for $50.00 each. 8. If you have registered for the conference, but haven't submitted your abstract yet, don't forget! The abstract submission deadline is May 15th for inclusion in the program. Go to http://ccg.biology.uiowa.edu/smbe/subform.php to submit an abstract, using your unique five-digit registration number in your registration code. If you are not submitting an abstract, please fill out the abstract submission page with your information, selecting "None" for your presentation type. 9. All registration and dormitory fees are required to be paid in full by May 15th. Please contact the Center for Conferences (conferences@uiowa.edu) to make your payment arrangements. Alternately, you may return to the Conferences website and pay your fees on-line. 10. To keep up on the latest information and updates, please visit the SMBE 2009 updates page at http://ccg.biology.uiowa.edu/smbe/updates.php General information on the meeting follows:

SMBE 2009, Iowa City "Darwin to the Next Generation "

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SYMPOSIA (see website for detailed descriptions and confirmed speakers):

* Biological networks from genes to populations * Epigenetics, environment & evolution * Evolution of networks * Genome evolution after polyploidy * Genomics of speciation & recent divergences * Historical roots of molecular evolution * Impacts of next generation sequencing on evolution * Insect evolutionary genomics * Molecular arms races * Molecular basis of speciation * Molecular evolution of biological complexity * Molecular evolution of functional noncoding sequences

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Uruguay Darwin200 Spe2-6

Dear Colleague,

150 years of Darwin's Evolutionary Theory: a South American celebration will gather internationally renowned evolutionary scientists in Punta del Este, Uruguay, on September 2-6, 2009. The meeting is the single Latin American scale of the Darwin200 Symposia, organized by The International Union of Biological Sciences (IUBS), and will include keynote lectures, several symposia and poster sessions.

Confirmed keynote speakers: Giorgio Bernardi, Daniel Dennett, Douglas Futuyma, Takashi Gojobori, Eviatar Nevo, Francisco Salzano, Emile Zuckerkandl

Symposia to be held: (chairs * and preliminary list of invited speakers) Evolutionary Genomics and Molecular Evolution (Fernando Álvarez*, Hugo Naya*, Giorgio Bernardi, Gastón Gonnet, Olivier Gascuel, Pablo Goloboff) Evolutionary Physiology (Francisco Bozinovic*, Ernesto Gianoli, Carlos Navas, Pablo Sabat, Ariovaldo P. Cruz-Neto, Enrique Caviedes-Vidal) Viral Evolution (Juan Cristina*, Raul Andino, Eckard Wimmer) Paleontology and Evolution (Richard Fariña*, Sergio Martínez*, Sergio Vizcaíno, Laura del Río) Human Evolution (Monica Sans*, Francisco Salzano, Héctor Puccarelli) Darwinism and Society (Alción Cheroni*, Daniel Dennett)

Abstract & Scholarship deadline: June 30th, 2009

150 Km horse back ride, following part of Darwin's path in Maldonado, will take place the two days before the meeting. For more information on Abstract submission, Fellowships for Students, Registration and Housing, please visit our web site www.darwin200.edu.uy You can also contact us by e-mail: darwin200@fcien.edu.uy

Fernando Alvarez On behalf of the Organizing Committee

Hector Romero <eletor@fcien.edu.uy>

USheffield InsectEvolution Jul15-17

Royal Entomological Society Symposium

focussing on insect evolution and ecology

Sheffield, UK , July 15-17 2009

Only one week left to register: deadline JUNE 1

Register online: http://www.royensoc.co.uk/register/-index.php Scientific sessions:

Evolution, Ecology and Mechanisms of nsect Infection and Immunity

Speakers include:

George Dimopoulos (John Hopkins Malaria Research Institute, USA)

Fotis Kafatos (Imperial College, UK)

Greg Hurst (University of Liverpool, UK)

Jean Luc Imler (Institut de Biologie Moléculaire et Cellulaire, Strasbourg, France)

Jacob Koella (Imperial College, UK)

Shelley Adamo (Dalhousie, Canada)

Brian Lazzaro (Cornell University, USA)

Paul Schmid-Hempel (ETH Zurich, CH)

Mike Siva-Jothy (University of Sheffield, UK)

Evolutionary Ecology of Predation

Invited speakers: Johanna Mappes (Jyväskylä, Finland) Robby Stoks (Leuven, Belgium)

Range Expansion Invited speakers: Jane Hill, York, UK Rosa Menendes, Lancaster, UK

Chemical Ecology

Stefano Turillazzi (University of Firenze)

Evening Plenary by Naomi Pierce, Harvard, USA: “Nabokov meets Darwin: origin and evolution of blue butterflies”

Register online

Register online: http://www.royensoc.co.uk/register/-index.php Student Travel Support:

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

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

Jens Rolff <JOR@sheffield.ac.uk>

UStAndrews ComparativeGenomics Aug18

Dear EvolDir,

I would like to draw your attention to these events in St Andrews this August:

- One day conference, “Comparative Genomics” - Summer school, “Bioinformatics and Comparative Genomics” - Workshop, “The Role of Behaviour in Speciation”

Details are below.

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Comparative Genomics one-day international conference

Date: 18th August 2009 Location: Bute Building, University of St Andrews, UK

****

The Scottish Bioinformatics Forum and the University of St Andrews are pleased to announce a one-day international conference, “Comparative Genomics”, with nine invited speakers and an open poster session.

Confirmed speakers:

- Prof MARK BLAXTER, University of Edinburgh. “Comparative nematode genomics”. - Prof GEOFF BARTON, University of Dundee. “A tale of three small RNAs”. - Prof DANNIE DURAND, Carnegie Mellon University. “The evolution of multidomain families”. - Prof NEIL HALL, University of Liverpool. “Fast forward genetics using second generation sequencing”. - Dr MATTHEW HEGARTY, Aberystwyth University. “Genomic mergers: the consequences of hybridisation and polyploidy in Senecio”. - Prof IAN KORF, University of California Davis Genome Center. “Intron mediated enhancement”. - Dr DAVID MARTIN, University of Dundee. “Predicting protein function”. - Dr ZEMIN NING, Wellcome Trust Sanger Institute. “Cancer genome assemblies and variation detection between normal and tumor human cells”. - Prof ZIHENG YANG FRS, University College London. “Population genomics and human-chimpanzee speciation”.

For more information on the conference, including registration and poster abstract submission, please see:

http://www.sbforum.org/events.php?e_idp

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Summer School - Bioinformatics and Comparative Genomics

Start Date: 15th August 2009, 9:00 am End Date: 18th August 2009 (including one-day conference) Location: University of St Andrews, UK
****

The Scottish Bioinformatics Forum and the University of St Andrews are pleased to announce the first Summer School on Bioinformatics and Comparative Genomics. The summer school will address practical bioinformatics for sequence analysis and comparative genomics, for use in biological and biomedical research.

The summer school will be held in St Andrews on 15th-17th August 2009. Registration for the summer school also includes attendance at the one-day conference on Comparative Genomics on 18 August (see above).

Confirmed tutors:

- Prof ZIHENG YANG FRS, University College London - Dr ZEMIN NING, Wellcome Trust Sanger Institute - Dr DAVID MARTIN, University of Dundee - Prof IAN KORF, University of California Davis Genome Center - Dr CHRIS JANSSEN, SBF and University of Glasgow - Prof NEIL HALL and Dr ALISTAIR DARBY, University of Liverpool - Dr DAVID FERRIER, University of St Andrews - Prof DANNIE DURAND, Carnegie Mellon University - Prof GEOFF BARTON and Dr JIM PROCTER, University of Dundee - Dr DANIEL BARKER, University of St Andrews

For more information on the summer school and registration details, please see:

http://www.genome-bioinformatics.org/index.html Workshop - The Role of Behaviour in Speciation

Start Date: 19th August 2009 End Date: 22nd August 2009 Location: University of St Andrews, UK

This is a separate workshop at St Andrews, arranged by the EU Marie Curie Initial Training Network "SPECIATION". Details of this workshop are available from Prof Mike Ritchie:

http://biology.st-andrews.ac.uk/staff/mgr.htm and will appear at:

http://speciation.group.shef.ac.uk Looking forward to seeing you in St Andrews!

Kind Regards

Daniel Barker

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

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

Utrecht EvolutionLanguage Apr14-17

Dear colleague,

Below is a conference announcement and call for papers for next year's Evolang; I would much appreciate it if you could distribute this announcement through the Evoldir mailinglist to researchers in evolutionary biology.

Many thanks, Willem Zuidema

***

EVOLANG8

The 8th International conference on the Evolution of Language (Evolang8), will be held 14-17 April, 2010 in the historic city of Utrecht, in the Netherlands. The conference again promises to be an exciting event. The following speakers have accepted an invitation for a plenary presentation: Stephen Anderson (Yale), Morten Cristiansen (Cornell), Terrence Deacon (Berkeley), Peter Gardenfors (Lund), Marc Hauser (Harvard), Wil Roebroeks (Leiden), Eors Szathmary (Budapest) and Maggie Tallerman (Newcastle). In addition, 12 experts in various contributing fields have been invited to present papers in an attempt to involve in the conference a larger number of pertinent areas and prominent participants. The full list of invited speakers, and lots of other information, is at our website: http://-evolang2010.nl CALL FOR PAPERS

The conference welcomes substantive contributions relating to the evolution of human language from any relevant discipline, including Anthropology, Genetics, Population Biology, Linguistics, Psychology, Primatology, Ethology, Paleontology, Archeology, Artificial Life and Mathematical Modelling. Normal standards of academic quality apply. Thus, submitted papers should aim to make clear their own substantive claim, relating this to relevant scientific literature, and briefly setting out the method by which the claim is substantiated, the nature of the relevant data, and/or the core of the theoretical argument concerned.

TYPES OF SUBMISSION

There are two possible types of submission: Full Papers, which can have a length of between 6 and 8 pages. Abstracts, which can be at most 2 pages long. All accepted submissions will be published in the proceedings of the conference. All papers or abstracts accepted will be allotted the same presentation length (probably 25 minutes plus 10 minutes discussion). Proceedings will be published by World Scientific. Formatting instructions (MS Word, Latex) are available through the website: http://evolang2010.nl SUBMISSION DEADLINE

Submissions due: 2 October 2009 Acceptance Notifications: 13 November 2009 Final versions due (provisional): 11 December 2009. All submissions are handled by our electronic submission system accessible through http://evolang2010.nl WORKSHOPS

Prior to the main conference, three full-day workshops are planned on Wednesday April 14th. Separate calls for papers for these workshops will be sent out in due time on the evolang mailing list – sign up for the mailing list on our website. The themes for these workshops are: - Human language & bird song - The evolution of semantics - Computational modelling of language evolution

LOCAL ORGANIZERS

The conference is hosted by the Utrecht Institute of Linguistics OTS (UiL OTS) of Utrecht University, the Netherlands. The Local Organizing Committee are taking various steps to ensure that Evolang 2010 will be a significant event from a scientific perspective. These include inviting, in addition to plenary speakers, a number of other leading scientists to present papers at the conference, extending the range of pertinent perspectives on language evolution to be included in the programme, revising the review procedure for submitted papers, and exploring the possibility of publishing, in addition to the proceedings, a selection of reworked/expanded papers with an publisher of high repute. All details are at http://evolang2010.nl . Jelle Zuidema <w.h.zuidema@uva.nl>

GradStudentPositions

ETH Zurich SexualSelection

PhD Position in Evolutionary Biology at the ETH Zurich

3-year PhD position funded through a Swiss National Science Foundation research grant. The student will be supervised by Dr. Oliver Martin and be part of the Experimental Ecology group (head: Prof. Paul Schmid-Hempel), Institute of Integrative Biology at the ETH Zurich (see: http://www.eco.ethz.ch/). The institute maintains close links with various local research groups at the ETH and University of Zurich and further afield providing opportunities for regular interactions with leading scientists working on related topics.

Project background: There is strong theoretical support for a role of sexual selection (especially sexual conflict) as a powerful engine driving speciation. Similarly, theoretical and comparative evidence indicates that sexual selection could cause extinction. A main focus of the PhD will be evaluating to what extent sexual selection is involved in shaping biodiversity. As part of this undertaking, the projects will assess impacts of sexual selection on individual and population fitness, the influence of environmental change & tradeoffs between reproductive and immune traits. Within this broad framework the student will have the opportunity to address a range of specific questions using rapidly breeding insect models (mainly Tribolium beetles). There is also plenty of scope for accommodating additional individual project ideas.

Starting date: Ideally the candidate will be able to start on the 1st of July 2009 or soon thereafter.

Salary details: Yearly salary: ca. CHF 39 000 p.a. in year 1 (then ca. CHF 42 000 in year 2 + ca. CHF 45 000 in year 3).

Application: Applicants must have a university degree (e.g. Diplom, M. Sc) required for entrance to the PhD program (preferably in evolutionary biology, ecology or molecular ecology). Previous experience with experimental evolution, behavioral observations, immune assays, insect rearing or molecular methods would all be advantageous. The working language in our multinational research group is English. Although not absolutely necessary, knowledge of German would certainly be practical for living in Zurich. Zurich is a very attractive international city set in beautiful surroundings. For information about studying at the ETH and Zurich see e.g.: http://www.ethz.ch/prospectives/index_EN http://www.zuerich.com/de/welcome.cfm Application procedure: Please email your application documents as a single pdf file to: oliver.martin@env.ethz.ch Documents should contain: cover letter stating motivation for pursuing scientific career and interest in this position, CV, summary of research interests and experience (ca. 1 page) and contact details for three people willing to provide references (additional pdfs of M. Sc or Diploma certificates, transcripts, theses or other documents are also welcome if relevant).

Closing date: Applications are welcome until the position is filled, evaluation of applications will begin immediately.

For further information: Dr. Oliver Y. Martin, Institute for Integrative Biology, Experimental Ecology, CHN K 14, Universitatstrasse 16, CH-8092 Zurich, Switzerland http://www.eco.ethz.ch/people/assistants/martioli oliver.martin@env.ethz.ch

Martin Oliver Yves <oliver.martin@env.ethz.ch>

INRA Rennes Ecotoxicology and evolution

PhD Position in ecotoxicology and evolution

A PhD position is available on the adaptive potential of molecular responses to stress, of a freshwater snail exposed to pesticides. Position is opened in the group of Ecotoxicology and quality of aquatic environments, UMR ESE 985, Rennes, of the French National Institute for Agricultural Research (INRA). The project is proposed in the context of population ecological risk assessment and pesticide use. Evolutionary processes are only recently incorporated as a relevant dimension into these research issues. Such processes are difficult to predict, due to the diversity of their potential determinants, among which: (i) activated mechanisms of physiological and molecular defence, (ii) interactions, (iii) relationship with other traits, including those related to fitness, (iv) potential cost, (v) population characteristics, including history of exposure, population size and level of genetic variability. Specific issues addressed in this project relate to the components of variation observed at the level of biochemical and molecular systems activated in response to pesticide stress, in a freshwater snail, /Lymnaea stagnalis/. We are specifically interested in estimating the adaptive potential of such systems (enzymatic activity, expression of genes involved in the antioxidant pathway and in less specific stress)*. The amount of genetic additive variation will be estimated using quantitative genetics (experimental lines), and adaptive divergence between populations will be searched for by comparing contrasted ecotypes, using common-garden experiments. Fitness-related traits will be jointly measured, in order to estimate possible costs and trade-offs. *depending on fundings obtained, the project may be extended to gene expression at a larger scale (transcriptomics)./

Salary: the project is currently submitted to several national / regional grant sources, including INRAs “Young Researcher Contract”, which includes both a 3 year PhD funding and a 2 year postdoc funding.

Expected start date is September 2009. If interested, please send (before June 1^st): CV, documentation of undergraduate grades, names and addresses of two referees and a statement describing the reason(s) for your interest in this research to: marie-agnes.coutellec@rennes.inra.fr <mailto:marie-agnes.coutellec@rennes.inra.fr>.

See also sujet n89 at: http://www.vas.univ-rennes1.fr/-themes/Concours_annuel/Profils/Autres/ –

Marie-Agnès Coutellec UMR INRA-Agrocampus Ouest 985 ESE Equipe Ecotoxicologie et Qualité des Milieux Aquatiques 65 rue de Saint-Brieuc - CS 84215 35042 Rennes cedex - FRANCE

tél.: +33(0)2 23 48 52 48 fax: +33(0)2 23 48 54 40

marie-agnes.coutellec@rennes.inra.fr

INRA Toulouse PopulationGenetics

We are seeking applications for a "Young Researcher Contract" in population / statistical genetics, which includes both a 3 year PhD funding and a 2 year postdoc funding. The PhD subject concerns the detection of loci under selection in livestock populations. The successful applicant will develop new detection methods that take into account the specificities of livestock populations (large number of breeds, small effective sizes, short divergence time ..). He will also analyse dense SNP genome-wide data arising from several projects on pig and sheep.

The PhD will take place at the Laboratory of Cellular Genetics in Toulouse (France), which is part of the French National Institute for Agricultural Research (INRA).

Interested applicants are invited to send a curriculum vitae to Magali San Cristobal msc@toulouse.inra.fr or Simon Boitard simon.boitard@toulouse.inra.fr before the 31th of May, and to contact them for further information. Strong statistical and programming skills, and a high interest in population genetics, will be required.

simon boitard <simon.boitard@toulouse.inra.fr>

KansasStateU GrassGenomics

PhD Assistantship Available: Ecological Genomics of Drought Stress in Prairie Grasses We have a position available for a PhD student to study the ecological genomics of drought stress. The project will include studies of the responses of native prairie grasses to variation in precipitation using the ecologically dominant prairie grass big bluestem as a model. The work is part of a project funded by the USDA Plant Biology Abiotic Stress program. The project will include common garden transplant experiments and genomic approaches to test for the signature of adaptive genetic differentiation among natural populations of big bluestem across the precipitation gradient of the Great Plains.

This collaborative research group assembles investigators with complementary expertise in Plant Ecological Genomics (Johnson www.ksu.edu/johnsonlab/, Garrett www.ksu.edu/pdecology), Genomics (Ahkunov eakhunov@ksu.edu), Evolutionary Genetics (Morgan(http://www.ksu.edu/morganlab/) and Restoration Ecology (Baer, SIU (www.plantbiology.siu.edu/-Faculty/Baer/index.html) to elucidate the response and adaptation of prairie grasses to abiotic stresses. This work will take place in the laboratories of Drs. Johnson, Akhunov, and Garrett, with close collaboration with Drs. Morgan and Baer. There will also be opportunities to interact with other researchers in the context of the Ecological Genomics Institute (www.ecogen.ksu.edu).

Applicants should have a demonstrated interest in ecological or evolutionary genomics. Preference will be given to individuals with experience in modern molecular approaches and genomics tools.

Review of applicants will begin June 1, and continue until the successful applicant is identified. The starting date is flexible. The position offers competitive salary of $25,000 and benefits.

Applications should include a cover letter with a statement of research interests and explanation of your motivation and suitability for the project, a CV, and names and contact information for three professional references who can document the applicant is self-motivated and can work independently. Please send your application through e-mail to Loretta Johnson (Johnson@ksu.edu). Please include the following in the subject of your e-mail: Application for Ecological Genomics Assistantship'.

Kansas State University is located in the college town of Manhattan (population ~45,000) in the Flint Hills of eastern Kansas, about 2 hours away from Kansas City. Kansas State University is an equal opportunity, affirmative action employer and actively seeks diversity among its employees.

johnson@ksu.edu johnson@ksu.edu

LavalU EvolutionarySystemsBiol

Graduate positions available in evolutionary systems biology

Chosen candidates will study the evolution of signaling networks using genomics, proteomics and bioinformatics tools. Projects will aim at understanding the evolution of protein-protein interactions among signaling molecules and the role of gene duplication in shaping these networks. The budding yeast Saccharomyces cerevisiae and its relatives will be used as models but other relevant species could also be used. We have tools to study protein-protein interactions on a genome-wide scale.

Our research is funded by the Canadian Institutes of Health Research (CIHR) and the Fonds de la Recherche en Sante du Quebec (FRSQ). Research will be conducted at the Laval University Institut de Biologie Intégrative et des Systèmes (IBIS), in Québec City, Canada. IBIS hosts more than 30 researchers working in genetics, genomics and proteomics as well as organismic biology. Laval University is one of the oldest universities in North America and is a major research institution in Canada. Quebec city is a magnificent and vibrant city.

Competitive stipend + bonus for students who can obtain external fellowships.

Starting date: September 2009 or January 2010

Requirements: The ideal candidate is highly motivated, has experience or training in molecular biology, biochemistry or microbiology, is interested in evolution and has basic skills in bioinformatics.

Pertinent references: How perfect can protein interactomes be? Science Signaling 2009.

Weak functional constraints on phosphoproteomes. Trends in Genetics 2009.

Systems biology spins off a new model for the study of canalization. Trends in Ecology and Evolution 2009.

An in vivo map of the yeast protein interactome. Science 2008.

Genetic properties influencing the evolvability of gene expression. Science 2007.

Systems-level analysis and evolution of the phototransduction network in Drosophila. PNAS 2007.

Interested candidates should send an application with a complete CV, academic transcripts and a short statement of interest by email and have three letters of references sent to:

clandry@post.harvard.edu

Letters of recommendation from these references should be sent separately.

Informal inquiries are welcome,

Christian Landry, PhD Département de Biochimie Faculté de Médecine Université de Montreal C.P. 6128, Succ. Centre-Ville Montreal, Quebec, Canada H3C 3J7

Christian Landry <clandry@post.harvard.edu>

Munich EvolutionaryBiology

Dear all,

With this e-mail I would like to encourage students who are interested in doing a PhD in the field of evolution, ecology and systematics to consider coming to the University of Munich. Munich has a very lively community of researchers working on a wide range of topics in evolution, ecology and systematics. We have Master and PhD students from all over the world. See http://www.eeslmu.de/eeswiki There are currently two possible routes to become a PhD student in the EES (Evolution, Ecology and Systematics) program in Munich:

1) apply to the newly established Graduate School Life Science Munich (http://www.lsm.bio.lmu.de/). You can apply to this school with a BSc or with an MSc degree. If you hold an MSc degree, you can apply for the three year PhD program. Students in this program are paid by the individual research groups (usually about 1000 Euro per month). The LSM graduate school offers additional training and services. The LSM also accepts students with a Bachelor's degree. For these students there is the possibility to obtain a Master's degree before starting with the PhD, or to do a two or three semester preparatory program and enter the PhD without obtaining a Master's degree. The LSM will only accept a very limited number of outstanding applicants with a Bachelor's degree. Students in the fast-track path will get a scholarship of 643 Euro per month during two or three semesters for living expenses. The deadline for the LSM is the 30th of June 2009.

2) if you have an idea for a research project which you would like to do in Munich and which has an evolutionary focus, there is the possibility to apply for a research grant at the Volkswagen Foundation. This foundation funds PhD and Postdoc projects. The next deadline is the 15th of October 2009 (see http://www.volkswagenstiftung.de/funding/thematic-impetus/evolutionary-biology.html?L=1)

If you are interested in either of these two possibilities, please have a look at the EES website http://www.eeslmu.de/eeswiki/EES_people and contact the person you would like to work with. Alternatively, you can contact me first (Pleuni Pennings, pennings@lmu.de).

Best wishes, Pleuni Pennings

–

Pleuni S. Pennings

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

* Postdoc in theoretical evolutionary biology

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

Tel: 0049 89 2180 74 234 http://www.eeslmu.de/eeswiki/Pleuni_Pennings pennings@lmu.de

pennings@zi.biologie.uni-muenchen.de

NorthCarolinaStateU InsectPhylogeny

North Carolina State University Department of Entomology Insect Museum

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

Opportunity A: Student will study molecular phylogenetics and diversification in empidine dance flies (Empididae) as part of an NSF- funded project on the evolution of dance fly mating systems, behavior, and morphology. (Advised by: Dr. Brian Wiegmann)

Opportunity B: Student will address biodiversity and evolutionary questions concerning Hymenoptera (Advised by: Dr. Andy Deans)

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

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

How to apply: North Carolina State University hosts a top-rated Entomology program, and as a vertex of North Carolina's Research Triangle, we benefit from close proximity to a large community of evolutionary biologists and our affiliation with the National Evolutionary Synthesis Center (NESCent; http://www.nescent.org/) <http://www.nescent.org/ >.

Interested students must apply to the NCSU Department of Entomology: http://www.cals.ncsu.edu/entomology/students/how-do-i-apply More details and contact information available here: http://entomology.ncsu.edu/ /AA/EOE. ADA Accommodations: Drs. Andrew R. Deans andy_deans@ncsu.edu or Brian Wiegmann brian_wiegmann@ncsu.edu, 919-515-2833.// NC State welcomes all persons without regard to sexual orientation./

Brian M. Wiegmann Department of Entomology North Carolina State University http://www4.ncsu.edu/unity/users/b/bwiegman/public_html/labweb/
Andrew R. Deans Department of Entomology North Carolina State University http://deanslab.org/
brian_wiegmann@ncsu.edu brian_wiegmann@ncsu.edu

SimonFraserU SharkExtinctionRisk

Readvertised

* *

Extinction risk, life histories and demography and in sharks and rays

Funded PhD project available at Simon Fraser University, Vancouver; starting 2009

Sharks and rays are among the most threatened vertebrates because they have slow life histories1,2 and they are subject to high mortality due to unregulated bycatch in trawl and longline fisheries3,4. The aim of this project is to use the existing knowledge to develop predictive models of extinction risk grounded in life histories and demography.

This funded PhD project will provide the student with broad training in phylogenetic comparative analysis and statistical modeling of large complex datasets. The student will be expected to collaborate with and work alongside other students and will gain a wider training in the links among life histories, population dynamics and conservation biology of fishes. The student will be based at the vibrant and expanding Earth to Ocean research group at the Department of Biological Sciences, Simon Fraser University, Burnaby, Vancouver, BC Canada.

To apply for this project please send a CV with details of three referees, a 1-page research proposal (including context, hypotheses and approach) and a cover letter to the contact supervisor (Nick Dulvy: nkd3@sfu.ca with the subject heading $B!H(BPhD competition B$B!I(B) before June 31st2009. It is strongly encouraged that the candidate read the references provided below prior to building the conceptual framework of their own proposal. An understanding of life histories and population dynamics is desirable. Ideal candidates should have good organizational skills and be comfortable working autonomously, as needed. We are keen to consider candidates without prior experience of fish or fisheries. Financial support will be CAD$20,000 per year. International students considering graduate studies at Simon Fraser University should obtain current immigration requirements from a Canadian Embassy or consulate.

1. MG Frisk, TJ Miller, MJ Fogarty (2001). Estimation of biological parameters in elasmobranch fishes: a comparative life history study. *Canadian Journal of Fisheries and Aquatic Sciences* *58*, 969.

2. MK McAllister, EK Pikitch, EA Babcock (2001). Using demographic methods to construct Bayesian priors for the intrinsic rate of increase in the Schaefer model and implications for stock rebuilding. *Canadian Journal of Fisheries and Aquatic Sciences* *58*, 1871.

3. JK Baum, RA Myers, DG Kehler, B Worm, SJ Harley, PA Doherty (2003). Collapse and conservation of shark populations in the northwest Atlantic. * Science* *299*, 389.

4. SC Clarke, MK McAllister, EJ Milner-Gulland, GP Kirkwood, CGJ Michielsens, DJ Agnew, EK Pikitch, H Nakano, MS Shivji (2006). Global estimates of shark catches using trade records from commercial markets. *Ecology Letters* *9*, 1115.

Dr Nick Dulvy

Canada Research Chair in Marine Biodiversity and Conservation

Biological Sciences Simon Fraser University Burnaby, BC V5A 1S6 Canada

e-mail: nick_dulvy@sfu.ca tel: +1-778-782-4124 (direct), 782-4475 (secretary) fax: +1-778-782-3496 skype: nick.dulvy http://www.dulvy.com Why not submit a paper to Conservation Letters! www.blackwellpublishing.com/conl Why not submit a paper to Journal of Applied Ecology! http://www.blackwellpublishing.com/jpe Why not submit a paper to Fish and Fisheries! http://fishandfisheries.googlepages.com Nick Dulvy <nick_dulvy@sfu.ca>

Spain Biodiversity

SUBJECT: New edition of the Master's Degree Program "Biodiversity in Tropical Areas and its conservation"

MAIN TEXT: ANNOUNCEMENT of the new edition of the Master's Degree Program in "Biodiversity in Tropical Areas and its conservation"

As the previous edition, the Master's Degree Program in "Biodiversity in Tropical Areas and its conservation" is a one-year MSc program (75 ECTS) offered jointly by the International University Menendez Pelayo (UIMP, Ministry of Education, Spain), the Spanish National Research Council (CSIC, Ministry of Science, Spain), and the Universidad Central del Ecuador (UCE, Ecuador). The program is fully funded by the CSIC, with a strong emphasis on fellowships for Latinamerican students; the title is an official European MSc degree conceded by the UIMP; and the program will be taught in Ecuador, with an emphasis on practical studies in natural reserves. The program is international, with a minimum of 15 and a maximum of 30 students.

ROUTE TO PHD DEGREE.- Excellent graduates from the MBATC program have the possibility to continue their PhD studies in CSIC Departments (Real Jardin Botanico, Museo Nacional de Ciencias Naturales, etc.) through separate application calls opened each year. They can also apply to other programs in the Spanish science system, or to any European or American university, as this MSc title is an official European degree.

WHAT DO I NEED TO APPLY TO THE PROGRAM?.- You are eligible to apply to the program if you hold a Bachelor's degree in any suitable field, especially on biosciences: biology, forestry, or agriculture, but also in geography, for example. You must be proficient in Spanish language.

FINANCIAL SUPPORT.- The CSIC offers 5 full scholarships (6300 euros/student) and 5 for registration fees (1300 euros/student). The program finances additional full scholarships for Latin American applicants.

HOW TO APPLY?.- The application period for studies starting in September 2008 begins 4-May-2009 and closes 3-July-2009. You can find all the information and detailed instructions on how to apply at

http://www.masterenbiodiversidad.org/ –

Jesús Muñoz e-mail: jmunoz@rjb.csic.es Real Jardín Botánico (CSIC) Plaza de Murillo 2 tlf. +34 91 420 3017 E-28014 Madrid fax. +34 91 420 0157 ESPAÑA (Spain)

http://www.masterenbiodiversidad.org http://www.rjb.csic.es/jardinbotanico/jardin/contenido.php?Pag=413&tipo=cientifico&codf KRAKEN research group (environmental modelling, data processing & analysis): http://www.unex.es/unex/grupos/grupos/kraken SYNTHESYS: EU funds short visits to our institution: http://www.synthesys.info/index.htm Jesús Muñoz <jmunoz@rjb.csic.es>

Switzerland NicheEvolution

Sorry for any cross postings.

Ph.D. Positions in Ecology and Evolution

The goal of the interdisciplinary project SPatially Explicit Evolution of Diversity (SPEED) is to understand how evolutionary history and the potential for rapid evolution can influence the response to climate change by species, biotic communities, and regional patterns of biological diversity. The project focuses on species in the Restionaceae, a family of grass-like monocots that are primarily found in the fynbos of South Africa. The project employs the tools of molecular phylogenetics, evolutionary modeling across phylogenies, field experimentation, plant physiology, community phylogenetics and niche modeling. Collaborating institutions include the University of Lausanne, the University of Zurich and the Swiss Federal Research Institute WSL. SPEED is funded by the Sinergia program of the Swiss National Fund for Science (SNF). There are three open positions, each with funding for three years. Here are the two Ph.D. student positions:

Ph.D. in evolutionary modeling and phylogenetics. This position will focus on models of niche evolution through the development of Bayesian models to estimate how niche parameters of species are evolving through time and lineages. The project will also generate molecular data to complement actual Restionaceae phylogenetic trees. This students primary location will be in the Salamin lab at the University of Lausanne (http://www.unil.ch/phylo).

Ph.D. in population genetics and ecological niche variability. This position will focus on the relationship between geographical range and niche and genetic variation, and explore the patterns of inheritance of the niche and genetic attributes of selected species. This students primary location will be in the Linder lab at the University of Zurich.

Applications MUST be received no later than Sunday, May 31, 2009. Interviews to be held fourth week in June. Start date in September, 2009. For further information about the SPEED project:

http://www.wsl.ch/projects/SPEED Please contact Peter B. Pearman or the relevant person linked to your interest. The SPEED project proposal is available to interested applicants upon request.

To apply, send the following materials, as separate PDF files: 1. PDF of cover letter, addressed to The SPEED Search Committee, indicating –position applied for –your career goals –your research interests in context of the SPEED project –a detail of how the previous experience and skills shown in your CV prepare you specifically for the position for which you are applying 2. PDF of CV, complete, showing contact information, title of thesis and dissertation, date, universities, research experience, notable skills, advanced courses, publication list, posters and talks presented, awards, service, etc 3. PDF of the abstract of your Masters thesis or Ph.D. dissertation research 4. PDF of university report of coursework, showing grades and degrees earned (must be in English) 5+. PDF's of published papers and papers in-press.

Send application as e-mail with attachments, with the following subject line

SPEED Project (and insert position applied for: evolutionary modeling or population genetics)

Send a separate e-mail, cover letter (PDF), and other PDF documents for each position applied for (if more than one) to:

sibylle.hauser@wsl.ch

Dont forget the deadline!

– Peter B. Pearman, Ph.D. Land Use Dynamics Federal Research Institute WSL Zürcherstrasse 111 8903 Birmensdorf Switzerland

pearman@wsl.ch Tel. ++41 (0)44 739 2524 Fax ++41 (0)44 739 2215

pearman@wsl.ch pearman@wsl.ch

TexasAMIntlU 2 CichlidEvolution

There is an opening this fall for 2 Masters students in the lab of Dr. Michael Kidd in the Department of Biology and Chemistry at Texas A&M International at Laredo. There are number of potential projects concerning the labs primary interest of understanding the molecular basis of complex behaviors, which includes work on an exciting NSF funded project studying the molecular basis of mate choice in cichlid fishes. Students in my lab will have the opportunity to learn a wide variety of techniques, including; how to quantify behavior, perform hormone assays and manipulations, in situ hybridization, quantitative PCR, and the statistical analysis of microarray data. Research assistanceships (RA) are available.

Applicants should have a B.S. or B.A. in biology, genetics, or a related field. Although preference will be given to students with some field or lab experience, particularly in molecular genetics, endocrinology or behavior, the only requirement is an interest and enthusiasm for animal behavior, evolution, and genetics. Please send me a copy of your CV with coursework, description of research experience, and the names and contact information for the people you will ask for letters of reference.

Prospective students should contact me directly:

Dr. Michael R. Kidd University of Texas at Austin Section of Integrative Biology 1 University Station, #C0930 Austin, Texas 78712

Phone: 512-475-7318 Fax 512-471-3878 Email: mrkidd@mail.utexas.edu

mckidd@earthlink.net

Trondheim PopulationBiology

PhD position in population ecology, Trondheim, Norway One PhD position in population ecology with particular focus on the interaction between parasites and host populations is available at the Department of Biology, NTNU. The fellowship is for three years with the possibility of a fourth year including 25 % teaching duties to the Department of Biology. The aim of the PhD project is to quantitatively investigate the coevolutionary dynamics between parasites and hosts, with particular emphasis on the impact of the infracommunity of parasites on host population dynamics in a metapopulation consisting of 18 insular populations of house sparrows (Passer domesticus) in northern Norway. *Application deadline: May 22 2009. *

You can find the official job announcement in the following link: https://secure.jobbnorge.no/-visstilling2.aspx?stillid=57656 ** Thor Harald Ringsby, Associate Professor (PhD) Centre for Conservation Biology (CCB) Department of Biology Norwegian University of Science and Technology NO-7491 Trondheim Norway

Office: +47 73596277 Fax: +47 73596100 Mobile: +47 91897032

E-mail: Thor.Harald.Ringsby@bio.ntnu.no Website Department of Biology: http://www.ntnu.no/biologi/-english Website CCB: http://www.ntnu.no/ccb Website personal: http://www.bio.ntnu.no/users/thorr/ thorhr <thor.ringsby@bio.ntnu.no>

UBasel BehaviouralEvolution

PhD-POSITION IN BEHAVIOURAL EVOLUTION. We are looking for a highly motivated graduate student interested in behavioral/social evolution. The research of our group focuses on the early evolution of family interactions by cooperation, conflict and coadaptation. Our research is carried out using a (sub-)social insect species, the common earwig Forficula auricularia (Dermaptera). Earwig females provide food to their early instar nymphs and protect them against predation. The nymphs interact with their mothers to influence food provisioning, and they compete among each other for resources. Earwigs are an ideal system to help us better understand the functional context in which the early evolution of family life took place, because nymphs are not fully dependent on maternal care. One aspect our previous work showed, which we will investigate further, is that insect progeny solicit from their caring parents by chemical signalling (pheromones). The details of the project will be developed together with the successful candidate also depending on her/his skills and interest.

BACKGROUND. Applicants should have a MSc degree (or equivalent) in a relevant field, and a strong background and keen interest in behavioural and/or chemical ecology. Previous experience with behavioral observation and quantification is an advantage, and an interest in learning GC/MS techniques is required.

RESEARCH GROUP AND INSTITUTE. Our research group is part of the Zoological Institute at the University of Basel, which hosts various groups sharing a common interest in evolutionary biology (see www.evolution.unibas.ch for more information).

POSITION AND APPLICATION. The PhD-position is funded through a Swiss National Science Foundation (SNF) research grant for the duration of three years. Starting date is negotiable, but should ideally be between 1st July and 1st October 2009. Please send your application documents (CV, list of publication, short summary of your current research, a statement on your reasons to pursue a PhD, contact details for two referees) by e-mail and as single pdf to:

Dr. Mathias Kolliker (Ass Prof SNF), University of Basel, Zoological Institute, Evolutionary Biology, Vesalgasse 1, 4051 Basel. E-mail: mathias.koelliker@unibas.ch; internet:www.evolution.unibas.ch/koelliker . Applications received before **31. May 2009** will be given full consideration.

Mathias.Koelliker@unibas.ch Mathias.Koelliker@unibas.ch

ULausanne SocialEvolution

PhD POSITION, SOCIAL EVOLUTION AND ANTI-PARASITE DEFENCES, LAUSANNE

Applications are invited for a PhD position in the research group of Michel Chapuisat (Department of Ecology and Evolution, University of Lausanne). We study social evolution, social conflicts and collective defences against parasites in ants. Please look at http://www.unil.ch/ dee/page7000.html for information and references.

The project will focus on (1) the impact of entomopathogenic fungi on ant societies of various degrees of complexity and (2) the collective defences of ants against fungi. The main model system will be the socially polymorphic ant Formica selysi and several of its naturally occurring fungal pathogens. The precise questions and methods will be developed together with the successful candidate, depending on his skills and interests. We seek candidates with a strong motivation to pursue a scientific career, good knowledge in evolutionary biology, and some specific expertise in fields that are relevant for the project (e.g. behavioural ecology, parasitology, molecular ecology, chemical ecology).

The position will be funded by the University of Lausanne and the Swiss National Science Foundation. It is available for three to four years, and involves some teaching. The gross salary starts at 46'662 CHF per annum. Starting date is negotiable, but September 2009 would be ideal. The Department of Ecology and Evolution provides an excellent training environment for PhD students (see http:// www.unil.ch/dee/, http://www.unil.ch/ee and http://www.unil.ch/fbm/ page2334_en.html).

Informal enquiries and applications should be sent to Michel.Chapuisat@unil.ch. Applications should include a cover letter, complete CV with publication list, and contact details of three referees, preferentially embedded in a single pdf file.

I will review the applications on 22 June 2009, but will continue to consider incoming applications until the position is filled.

Michel Chapuisat <Michel.Chapuisat@unil.ch>

Michel Chapuisat

Department of Ecology and Evolution Biophore, Quartier Sorge University of Lausanne CH-1015 Lausanne (Switzerland)

Ph: +4121 6924178 http://www.unil.ch/dee/page7642.html Michel Chapuisat <Michel.Chapuisat@unil.ch>

ULaval ModellingForestGeneIntrogression

Modelling gene introgression in native Populus of western Canada

A PhD position in evolutionary genomics and ecological modelling is available with Université Laval and the Canadian Forest Service (Laurentian Research Center; CFS). Full funding is provided by the Canadian Regulatory System for Biotechnology in the context of wider projects on the genomics of Canadian forest tree species. The research problem is this: Over the last century, several exotic Populus hybrids were widely introduced over the prairie and parkland regions of western Canada. CFS researchers have developed diagnostic markers for the detection of exotic genes and documented their spread within native populations of P. balsamifera. The research opportunity is to develop spatial- temporal models to explain observed patterns of introgression and project them into the future while accounting for the ecological consequences of the introduction of novel traits. Most of the necessary data has been assembled, including extensive historical records of the time and location of specific introductions across the region.

The successful applicant will develop advanced skills in spatial simulation, multi-level statistical modelling and management of large complex databases. Some experience with programming and with R will be significant advantage. A working knowledge of GIS would also be an asset, although technical support will be available. Otherwise, the main qualifications for this position are strong quantitative skills and an interest in molecular ecology, spatial simulation and ecological modelling, regardless of disciplinary background. The position is funded for 3yr at $21,500/yr. Holders of their own scholarships will be eligible for a top-up of $7,000/yr over the period of their grant. The position may commence in September 2009. The student will be part of an active and growing "meta-lab" on spatial simulation, statistical ecology and conservation biology, and will be a member of the Centre d'étude de la forêt < http://www.cef-cfr.ca/ > . Québec is a world heritage site with a rich cultural environment and many opportunities for outdoor recreation. It is also presents an excellent opportunity to acquire or master the French language. Note that although the language of instruction at Université Laval is French, one's thesis is expected to be written in English. Applicants should submit a one-page statement of interest, a current CV, and the names of three references to any of the undersigned, who may be contacted for further information.

Steve Cumming Chaire de Recherche du Canada-Boreal Ecosystems Modelling Centre for Forest Research Département des sciences du bois et de la forêt Université Laval stevec@sbf.ulaval.ca

Eliot McIntire Canada Research Chair-Conservation Biology Centre for Forest Research Université Laval eliot.mcintire@sbf.ulaval.com

Nathalie Isabel Ressources naturelles Canada, Service canadien des forêts, Centre de foresterie des Laurentides Chaire de recherche du Canada en génomique forestière et environnementale, Université Laval Nathalie.Isabel@RNCan- NRCan.gc.ca

"Lamothe, Manuel" <Manuel.Lamothe@RNCan-NRCan.gc.ca>

UMontpellier ExperimentalCoevolution

University of Montpellier

Institute of Evolutionary Sciences

PhD dissertation fellowship: Experimental coevolution

Applications are invited for a 3-year PhD fellowship to study antagonistic coevolution between phage pathogens and their bacteria hosts in spatially heterogeneous environments. The thesis is funded by the French Agence Nationale de la Recherche, and will by supervised by Dr. Michael Hochberg.

The project will address the dynamics of genetic and phenotypic adaptation in Pseudomonas fluorescens and its lytic bacteriophages. Specifically, the student will conduct experiments and develop mathematical models to understand how space and environment influence trait evolution in both antagonists. In addition to experimental and mathematical (or programming) techniques, the thesis will involve molecular assays and sophisticated statistical analysis.

We seek candidates holding the equivalent of a Masters Degree or equivalent in evolutionary biology. Experience in experimenting with microbes is strongly preferred.

Additional information about our lab including reprints, can be found at http://mike.hochberg.free.fr/-, or by email by writing to Dr. Hochberg at mhochber@univ-montp2.fr .

The thesis will be conducted in our laboratories at the Université de Montpellier II, France. Interested candidates should send a detailed CV, a letter of motivation, and the names and contact details of three potential referees to Dr. Hochberg on or before the 30th of June.

Michael Hochberg <mhochber@univ-montp2.fr>

UNeuchatel PlantEvolution

How do plants adapt to environmental change? - This is the main question addressed by a SNF-funded project on the genetics and ecology of drought adaptation in Arabidopsis lyrata. A three-year graduate/PhD position is available to join this project, supervised by Yvonne Willi at the Institute of Biology, University of NeuchÃtel, Switzerland.

The causes and mechanisms of adaptation to environmental change are relevant to many fields of biology, and we will tackle them from multiple sides: An experimental evolution study on drought resistance, a study of phenotypic change in morphological and physiological characters, and tracking allele frequency shifts at candidate genes. We will also work on drought resistance in natural populations across environmental gradients.

The Institute of Biology at NeuchÃtel consists of a dozen groups working in diverse fields of ecology, evolution, physiology and molecular and cell biology. For more information, contact Yvonne Willi (yvonne.willi@agrl.ethz.ch) or see http://www2.unine.ch/biol/ Neuchatel is a University town in the French-speaking part of Switzerland, situated between the Jura Mountains and a 40km long lake. The town is well connected with larger centers such as Lausanne, Geneva or Berne by public transportation.

Applicants must have a university degree in the natural sciences (ideally evolutionary biology, molecular ecology and/or plant physiology) that allows entrance to a PhD program, and very good organizational, analytical and writing skills. Motivated applicants should submit (1) a one-page letter that summarizes interests and relevant experience, (2) a CV, (3) copies of undergraduate and masters/diploma transcripts, and (4) contact information for 3 references (all as PDFs) to: yvonne.willi@agrl.ethz.ch

Yearly salary: CHF 38â000 - 44â000.

Closing date: Applications are welcome until the position is filled. Earliest evaluation of applications is on June 15, 2009.

Yvonne Willi <yvonne.willi@agrl.ethz.ch>

UPorto Portugal EvolutionaryBiology

PhD Students Proposals

Selection of candidates for a PhD grant proposal to submit to the Portuguese Foundation for Science and Technology

We accept applicants for a PhD grant proposal to be submitted to the Portuguese Foundation for the Science and Technology under the following topics:

1. “A genome-wide sequencing study to characterize genes responsible for the development and adaptation in Vertebrates”. Major phenotypic changes in vertebrates (from mammals to fish), occurred by the evolution of various gene products over the last half billion years. Understanding the genetic basis of the diversification of development genes in vertebrates can provide fundamental biological insight about species evolution, ecological fitness, and genetic diseases.

2. “A molecular genomic approach to unravel the evolution of natural toxins”. Gene families, which encode toxins, are found in many marine animals (from deadly poisoning jellyfishes to sea snakes), yet there is limited understanding of their evolution at the nucleotide level and the evolutionary significance of their protein mutations. Understanding the evolution of ecological specialization is important for making inferences about the origins of natural toxins biodiversity.

3. “Global phylogeny and biogeography of cyanobacteria species”. It is much debated whether microorganisms are easily dispersed globally or whether they, like many macro-organisms, have historical biogeographies. Recent findings using faster evolving genetic markers in protozoa species revealed considerable genetic structure

and suggested that protest biodiversity may be significantly higher than previously thought.

4. "Genomic diversity of proto-eukaryotes symbiosis". Harvesting light to produce energy and oxygen (photosynthesis) is the signature of all land plants. This ability was co-opted from a precocious and ancient form of life known as cyanobacteria. The most widespread cyanobacterial symbiosis is that of plastids in eukaryotes that happened more than 2 billion years ago. However, much more recent episodes of symbioses occurred between cyanobacteria and eukaryotic hosts, both non-photosynthetic (from marine sponges to ascidians) and photosynthetic (from diatoms to the flowering plants) hosts. Characterizing the evolutionary mechanism underlying such genetic cooperation is fundamental to understanding the origin of genomic symbiosis.

5. "Genomic research on the chimerical origin of Eukaryotic genomes". Eukaryotic genomes are replete with genes of eubacterial ancestry, namely from the Cyanobacteria, the Proteobacteria, and the Thermoplasmatales. These signals correspond to distinct symbiotic partners involved in eukaryote evolution: plastids, mitochondria, and the elusive host lineage. Evaluating the evolutionary relationships between such ancient relationships is important for making inferences about the origins and diversification of life.

The granted candidates will have a monthly salary of 980 euros and will develop their work at CIMAR, University of Porto, Portugal (http://www.cimar.org/). The candidates should have a B.S. or Graduation in Biology, Biochemistry or other related fields with a competitive score (16 out of 20, or 15 plus a Master degree) and should have a strong interest in developing research in Molecular Evolution, Genomics and Population Genetics.

The candidates should include:

- Detailed curriculum vitae; - Scanned copy of the Graduation title (and Master title if applicable). Preference will be given to European (EU) citizens but other applicants will also be considered.

The applications should be submitted till 21 May 2009 by email to Dr Agostinho Antunes (aantunes@ncifcrf.gov)

Dr. Agostinho Antunes Geneticist Laboratory of Genomic Diversity - National Cancer Institute, Frederick, Maryland 21702-1201, USA; Tel: 301-846-1299 Fax: 301-846-6327 e-mail: aantunes@ncifcrf.gov

In Portugal: CIMAR, University of Porto Rua dos Bragas, 177; 4050-123 Porto, Portugal; Tel: (351) 22 3401 813 Fax: (351) 22 3390 608

Agostinho Antunes <aantunes@ncifcrf.gov>

USouthernMississippi ConservGenetics

A graduate student (M.S.) position in fisheries conservation genetics is available in the Department of Coastal Sciences at the University of Southern Mississippi. The project will involve developing molecular markers and studying population genetics of Gray Triggerfish in U.S. waters. Interest in fisheries conservation genetics is suitable and experience with molecular techniques is an asset. The successful applicant will be provided a 12-month full-time Research Assistantship and a tuition waiver. The position is available with an anticipated start date in fall 2009 and is contingent upon acceptance to the Department of Coastal Sciences graduate program. The Department of Coastal Sciences is located at the Gulf Coast Research Laboratory (http://www.usm.edu/gcrl) in Ocean Springs, Mississippi, on the Gulf of Mexico coast.

Interested individuals should send CV, unofficial transcripts, GRE test scores and letter of interest to: Eric Saillant, Assistant Professor, The University of Southern Mississippi Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39564, E-mail: eric.saillant@usm.edu

AA/EO

Eric.Saillant@usm.edu Eric.Saillant@usm.edu

UVermont InvasivenessEvolution

PhD Assistantship available evolution of invasiveness at the Department of Plant Biology, University of Vermont. PhD position in population and evolutionary ecology with particular focus on the evolution of invasiveness is available in the Department of Plant Biology, University of Vermont. We seek one highly motivated PhD student to work on the evolution of invasiveness in one of several model experimental systems being used in the lab. Students interested in projects that focus on how the genetic changes influence invasive success are encouraged to apply. The PhD student should have an excellent background in evolution. Students with master?s degrees are strongly preferred. Support in the form of a teaching or research fellowship will be guaranteed throughout the degree. Applications will be accepted until June 15th . Interested applications should send their CV, a summary of their transcript, their GRE scores, the names of 3 letters of recommendations and a brief statement of interest. Students who are being considered will need to fill out an official application to the Department of Plant Biology, University of Vermont. More information about the department and the project can be found on the website www.uvm.edu/~plantbio and www.uvm.edu/~plantbio/~jmolofsk.

Jane Molofsky, Professor Department of Plant Biology University of Vermont Burlington, Vermont 05405 Email: Jane.Molofsky@uvm.edu Fax:802-656-0440

Jane Molofsky <jmolofsk@uvm.edu>

UWesternOntario EvolutionaryPhysiology

MSc/PhD Studentship: Evolutionary Physiology/ Evolutionary Ecology of Insect Cold Tolerance

The Sinclair lab at the University of Western Ontario seeks a creative, motivated and evolutionary-minded MSc or PhD student to start in 2010. Research will fall within the general theme of insect cold tolerance, preferably with a strong evolutionary slant. Projects could be largely physiological or ecological (or a combination thereof), and may include insects from the wild or a multi-species Drosophila system we have established in the lab.

The Sinclair lab (http://publish.uwo.ca/~bsincla7/) is medium-sized, vibrant and social, and we aim to perform excellent science while having fun. The lab is exceptionally well-resourced for insect low temperature biology in an evolutionary/ecological context thanks to recent CFI infrastructure grants, uses techniques from molecular to macroecological, and has active collaborations with researchers in France, the UK, the USA, South Africa and New Zealand, with potential for lab or field work in those countries. The Biology Department at the University of Western Ontario is a research-intensive department with over 150 students in the graduate programme. The University's picturesque campus is located in London, Ontario (pop. 370,000), close to both large cities and rural areas. UWO provides competitive bursaries and Teaching Assistantships to both Canadian and non-Canadian students.

This position will suit students with a background in ecology, physiology, evolutionary biology or entomology (and preferably an interest in all four!). Please email Dr Brent Sinclair (bsincla7@uwo.ca) to initiate informal discussions.

Brent J. Sinclair, PhD

Assistant Professor of Invertebrate Biology Department of Biology Room 2078, Biological & Geological Sciences Building 1151 Richmond Street North The University of Western Ontario London, ON N6A 5B7 Canada

Tel: + 1-519-661-2111 ext 83138 Fax: + 1-519-661-3935 bsincla7@uwo.ca http://www.uwo.ca/biology/Faculty/sinclair/index.htm

Brent Sinclair <bsincla7@uwo.ca>

UWesternOntario Phylogenetics Sociogenomics

Two graduate positions available at The University of Western Ontario, Canada.

1) Graduate position in insect sociogenomics. I have an opening for an MSc or PhD student with an interest in insect genomics as it relates to the study of social behaviour. The project will focus on the honey bee, Apis meliffera, and employ newly available oligo arrays and on- line bioinformatic resources to screen for genes important to social living (reproduction, immunity, division of labour, etc).

The suitable candidate will have experience in nucleic acid quantitation, and have interests in animal behaviour, molecular biology and evolution. For more context and information about our general research theme, please see our lab web site: http://tinyurl.com/ce87eo .

The University of Western Ontario has a large and vibrant Department of Biology (http://www.uwo.ca/biology/), and has strong links to the London Regional Genomics Centre (LRGC) and SHARCNET computing facilities, as well as the Bee Lab at the nearby University of Guelph.

Candidates must meet the entry requirements for Graduate Studies at Western: http://www.uwo.ca/biology/graduate/graduate.htm. To inquire, submit (via email) a cover letter with a brief summary of your research interests and a CV to: graham.thompson@uwo.ca - Graham Thompson Department of Biology, University of Western Ontario, London Ontario. The anticipated start date is September 2009 or January 2010. The deadline for September admission is June 15, 2009.

2) Graduate position in molecular phylogenetics. I have an opening for an MSc or PhD student with an interest in computational biology and its application to the evolution of insect social behaviour. The project will focus on the analysis of large amounts of nucleotide sequence data within a phylogenetic context. The ultimate goal is to develop a statistically well-founded phylogeny of termites (Isoptera) and use this phylogeny to develop and test alternative hypotheses regarding the evolution of insect social behaviour (and other character sets). Prospective students should have an interest in computational biology (bioinformatics, in silico analyses, evolutionary algorithms) or evolutionary biology (molecular evolution, phylogenetics, sociobiology, insect biodiversity). For more context and information about our general research theme, please see our lab web site: http://tinyurl.com/ce87eo The University of Western Ontario is located in London, Ontario, Canada. It has a large and vibrant Department of Biology (http://www.uwo.ca/biology/) and hosts the SHARCNET high-performance research computing facility (http://www.sharcnet.ca/). Southern Ontario also hosts a large invasive subterranean termite population, suitable for experimental work.

Candidates must meet the entry requirements for Graduate Studies at Western: http://www.uwo.ca/biology/graduate/graduate.htm. To inquire, submit (via email) a cover letter with a brief summary of your research interests and a CV to: graham.thompson@uwo.ca - Graham Thompson Department of Biology, University of Western Ontario, London Ontario. The anticipated start date is September 2009 or January 2010. The deadline for September admission is June 15, 2009.

Graham Thompson Assistant Professor Department of Biology University of Western Ontario 1151 Richmond Street North London, Ontario N6A 5B7 CANADA

519 661 2111 (ext 86570) 519 615 6066 (cell) graham.thompson@uwo.ca http://www.uwo.ca/biology/Faculty/thompson Graham Thompson <graham.thompson@uwo.ca>

Zurich InvasionBiology

The Swiss Federal Research Institute Agroscope Reckenholz-Tänikon ART, located in Zürich, is looking for a highly motivated PhD student to join the biosafety group. This group is responsible for all aspects in research and implementation of biosafety issues related to organisms used in biological control, to genetically modified plants and to invasive arthropods. The incumbent will work on a project funded by the Swiss Federal office for the Environment (http://www.bafu.admin.ch/) in collaboration with the University of Fribourg (http://www.unifr.ch/biol/ecology/).

Rationale Invasive alien species are regarded as one of the major threats to biodiversity. Invasion is a process involving several steps. The routes followed by invaders and processes enabling their survival and reproduction after arrival have received little attention. Sound knowledge on the initial dispersal stage is particularly important as early detection and eradication is considered the most cost-effective approach to reduce the negative impact of invasive species.

Ever-growing human travel, tourism and trade erased barriers between previously isolated geographical regions and facilitate the movement of animals and plants across biogeographic regions. The worldwide airline transportation network contributes to unwanted species movement by providing frequent transportation, mostly of small organisms such as insects, along numerous routes. Climate, especially temperature has a strong and direct influence on insect development, reproduction and survival. A fundamental requirement for the establishment of any species outside its home range is that the potential invaded range must have suitable climatic conditions for the invader. Like invasive species, climate change is thought to represent a major threat to ecological equilibrium. Predicted climatic changes are expected to increase / decrease the geographical range, affect phenology, and influence the growth rate and development time of several species. Surprisingly, invasive species and climate change have largely been studied independently. The proposed project aims to identify pests and pathways (cargo type and origin) that are posing a high risk to European agriculture and ecosystems under current and future climates. This knowledge could be used to tailor inspection schemes and monitoring plans at and around airports for early detection, and to develop action plans for eradication campaigns for the most likely pest organisms. The project will be conducted in close collaboration with a research group at the University of Fribourg (Sven Bacher) as well as different international partners.

Requirements Applicants for the PhD position should hold a masters degree in Biology or Agronomy. Knowledge or expertise in applied entomology, statistical multivariate analyses, climate-matching tools (e.g. CLIMEX), large database management and interest in independent research and team work would be relevant. Good oral and written communication skills in English are expected.

Conditions Total duration of the project is 3 years. The doctoral thesis will be done as a series of English manuscripts. The working place will be the Agroscope ART research station close to Zurich (http://-www.art.admin.ch).

Start of the project To be discussed

Applications If you are interested, please send your CV, certificates, and the names (with E-mail address) of potential referees per E-mail to Dr. Alexandre Aebi, Agroscope ART, Reckenholzstr. 191, 8046 Zurich, Switzerland, E-mail: alexandre.aebi@art.admin.ch.

The deadline for application is June 30, 2009.

For further information, please contact Dr. Alexandre Aebi via E-mail or phone (+41-44-3777669).

alexandre.aebi@art.admin.ch

Zurich MaleReproductiveTactics

PhD position

Evolution, Hormones, Metabolism and Behavior: Interactions and Causal Relationships

We are looking for a PhD candidate to study causal influences of hormones on alternative male reproductive tactics in the African striped mouse (Rhabdomys pumilio). The main aim of our research group is to understand the evolved physiological mechanisms that allow animals to behave adaptively in a changing environment. In the proposed study we want to test for a causal influence of hormones on social behavior while taking into account interactions between the different hormones and resting metabolic rate. The study will be based at the University of Zurich and experiments will be conducted with a captive colony. The study will use methods of hormone manipulations via implants, hormone measurements, measurements of oxygen consumption (RMR) and behavioral observations. A summary of the proposed PhD project can be found below.

We are seeking a highly-motivated, independent candidate with excellent organizational skills. The ideal candidate has a background in animal behavior, behavioral endocrinology, physiology or ecology and evolution, some experience with animal handling, lab work, and experience in experimental design and statistical analysis of data. A degree equivalent to a diploma or MSc in Biology is required. Good knowledge of written and spoken English is essential. The working language in our group is English. Some knowledge of German would be beneficial for living in Switzerland but is not necessary.

The student will be supervised by Dr. Carsten Schradin and be part of the research group studying striped mice (see www.stripedmouse.com). The student will be based at the Department of Animal Behavior at the Zoological Institute of the University of Zurich (www.zool.uzh.ch). Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities (http://www.zuerich.com)

The position is funded for two years, and the salary follows the Swiss National Science Foundation scale (CHF 39 600 for the first year, CHF 42 600 for the second year). The student is expected to apply for funding for a third year from other foundations, for example from the Forschungskredit, a foundation based at the University of Zurich (http://www.researchers.uzh.ch/-promotion/forschungskredit.html). The student will get full support from Dr. Carsten Schradin when applying for additional grants.

The earliest starting date is July 2009, but can be negotiated.

Deadline for application is the 20th of May, and interviews will take place at the end of May. If not enough suitable applicants applied by this deadline, a second call will be released and interviews will then take place at the start of July.

Please send your application including a CV (as PDF), PDFs of publications (published, in press or in preparation), PDF of your diploma or master thesis, a letter outlining your past research and particular motivation for this position (max. 2 pages), as well as contact details of 2 referees to carsten.schradin@zool.uzh.ch.

PD Dr. Carsten Schradin Research Associate, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486 Fax: +41 - (0)44 635 5490 (Tel. secretary: +41 - (0)44 635 5271) Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Succulent Karoo Research Station, Goegap Nature Reserve, Private Bag X1, 8240 Springbok, South Africa.

visit http://www.stripedmouse.com Summary

The newly established field of endocrine ecology has increased our knowledge about how physiological mechanisms enable animals to be successful and survive in challenging environments. However, so far most studies are correlative, especially in mammals. If experiments are conducted, interactions between hormones are normally not taken into account, nor are the possible effects of hormones on other important physiological parameters such as metabolic rate. Since 2001 we have conducted field studies on the African striped mouse (Rhabdomys pumilio) in the Succulent Karoo desert. The striped mouse is now one of the best studied mammal species in the field of endocrine ecology, enabling the planning of experiments under controlled laboratory conditions. It is a useful example to study the influence of hormones on social behavior because it shows extraordinary social flexibility. Males have three different social tactics that differ physiologically: (i) philopatric group-living males have low testosterone and prolactin levels, high corticosterone levels and high resting metabolic rate (RMR), (ii)

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Jobs

AfricanWildlifeFoundation GIS Modeler

*GIS/STATISTICAL MODELER CONTRACTOR SOUGHT *

/Geographic Information System Analyst/

//Terms: Part time, independent contract position working with EcoAdapt and the African Wildlife Foundation

*Salary: TBD. Tasks will be completed subject to deadlines of subcomponents of the project following a schedule determined by the consultant and EcoAdapt/AWF. Upon inquiry, and submission of a cv or resume, suitable candidates will receive a detailed scope of work. We will request a bid along with a 1-2 page proposal of methods that will be used to complete the scope of work from qualified candidates. *

*Duration: Immediate to **31 July, 2010** *

Location: Can work from your home base, with some travel expected

GENERAL DESCRIPTION

The GIS Analyst will play an important role within the African Wildlife Foundation-EcoAdapt project "The Implications of Global Climate Change for Mountain Gorilla Conservation in the Albertine Rift." The foundation of this project is a multi-stakeholder assessment of the implications of global climate change to mountain gorilla conservation in the Albertine Rift, East Africa. The GIS Analyst (Analyst) will work closely with the project team to create and maintain a georeferenced database of numerous gorilla, forest, protected area, and regional environmental condition parameters, and perform customized statistical (spatial and temporal) analyses including creating models of relevant scenarios, and informative, easy-to-read data presentation tools.

SOME ESSENTIAL and DESIRED SKILLS AND BACKGROUND:

* Demonstrable command of appropriate GIS (ESRI ArcGIS preferred) and relevant statistical software, proven GIS data management skills, solid database skills, and experience with relational database systems. * Familiarity with general environmental, ecological, geological, and biological processes. Experience working with environmental and GIS issues in the Albertine Rift region is a plus. * Experienced and inventive with mathematical and statistical spatial analyses of complex data sets in GIS unique to the field of landscape ecology, and possess sufficient programming skills to create the necessary customized mathematical algorithms. * Masters or PhD degree in either biology, ecology, environmental science, conservation biology, forestry, or similar, with training in GIS and at least 4 years' experience applying these combined skills.

Please send cover letter and curriculum vitae or resume to Tasha Belfiore at careers@ecoadapt.org. Inquiries will be considered as they are received, but not later than June 22, 2009.

Natalia Belfiore <nmb@berkeley.edu>

Barcelona CRG GroupLeader

Group Leader in Bioinformatics & Genomics Ref. GL-BG-0509

The Bioinformatics and Genomics Programme of the CRG, coordinated by Roderic Guigó, comprises 4 groups: Bioinformatics and Genomics (Roderic Guigó), Comparative Bioinformatics (Cedric Notredame), Comparative Genomics (Toni Gabaldón) and Evolutionary Genomics (Fyodor Kondrashov). The programme has strong links with the IMIM-UPF Research Group of Biomedical Informatics (GRIB, http:www.imim.es/grib). Within the framework of the partnership with the EMBL, the Bioinformatics and Genomics Programme has established a specific collaboration with the European Bioinformatics Institute (EBI). The CRG is now looking for group leaders from all areas of bioinformatics, such as algorithms, molecular evolution, comparative genomics, transcriptome analysis, epigenomics, etc, but priority will be given to outstanding candidates with expertise in image bioinformatics, medical bioinformatics, or algorithms for next generation sequencing. Candidates combining computational and experimental approaches are encouraged to apply. Candidates should have an MD, PhD, or equivalent degree.

Each group leader position comes with funds for one postdoctoral position, one graduate student, and one technician, an equipped laboratory for up to 7 people, as well as funding for consumables and equipment. The initial contract is for 5 years, renewable up to 9 years upon review by an external scientific committee.

The Centre for Genomic Regulation (CRG, www.crg.cat), located at the Parc de Recerca Biomèdica de Barcelona (PRBB, www.prbb.org), is a leading Institute in Genomics Research. The CRG includes 6 research programmes: Gene Regulation, Differentiation and Cancer, Cell & Development Biology, Systems Biology, Genes and Disease, and Bioinformatics and Genomics, and has a partnership with the EMBL through the Systems Biology Programme. The PRBB regroups 3 other institutions: the department of Life Sciences of the University Pompeu Fabra (CEXS/UPF, www.upf.edu/cexs), the Municipal Institute of Medical Research (IMIM, www.imim.es), and the Centre for Regenerative Medicine (CMRB, www.cmrbarcelona.org), in a scientific international environment, prone to collaborations. Scientists have access to state-of-the-art core facilities including genomics and next generation sequencing instruments, proteomics, advanced optical microscopy, FACS and a modern animal house.

Fyodor Kondrashov

fyodor.kondrashov@crg.es

BrownU OneSemesterTeaching EvolutionaryBiol

Teaching Position: Evolutionary Biology at Brown University

Applications are being sought for a one-semester sabbatical replacement position to teach the introductory evolutionary biology course at Brown University in Providence, RI (www.brown.edu). The course will be offered from September - December 2009 and involves three 50-minute lectures per week, with additional discussion sections lead by graduate students. Enrollment will be approximately 50-60 students. The instructor will be responsible for the overall organization of the course, giving the lectures, writing problem sets and exams, and contributing to the correcting of problem sets and exams.

A complete set of course notes, prepared lectures, and old tests are available for the successful candidate, if needed.

Please send a CV, a brief statement of teaching and research interests, and the names and email addresses of three (3) people who can serve as a reference, to

Trina_Pappadia@brown.edu

David M. Rand Professor of Biology Department of Ecology and Evolutionary Biology Box G-W, 80 Waterman Street Brown University Providence, RI 02912 Voice: (401) 863-2890 (Office - Walter Hall 202) (401) 863-1063 (Lab - BioMed Center 516-518) Fax: (401) 863-2166 email: David_Rand@brown.edu web pages: http://www.brown.edu/Departments/EEB/rand/index.htm http://research.brown.edu/research/profile.php?id=3D1100924991&r=3D1 david_rand@brown.edu

Denver OneYearResTech MolPopBiol

A full time research technician is needed to perform molecular biological procedures for a study of Indiana Bats at the Rocky Mountain Center for Conservation Genetics and Systematics in Denver, Colorado. This position is a one year temporary position with the US Geological survey that may be extended if funding is available. The position requires experience in molecular biological techniques including PCR, DNA sequencing and electrophoresis, DNA extraction, and microsatellite characterization. Candidates with experience in primer design, genetic studies of populations, and use of related software analytical tools wanted. The successful candidate would be joining the Rocky Mountain Center for Conservation Genetics and Systematics, which is staffed by both university and government researchers. For more information and to apply go to www.usajobs.gov< http://www.usajobs.gov > using announcement number CR-2009-0345. This position closes on May 26, 2009.

tom.quinn@du.edu tom.quinn@du.edu

KansasStateU ResTech QuantGenet

Research Technician, Division of Biology, Kansas State University

A position is available for a Research Technician in our lab in Division of Biology at Kansas State University. We are seeking an enthusiastic person interested in science to manage day-to-day lab activities and participate in our molecular quantitative genetic research. Our lab studies the genetics and evolution of environmental- stress-response phenotypes in Drosophila (see http://www.ksu.edu/morganlab for more info). Job responsibilities will include maintaining Drosophila stocks, performing basic molecular biology techniques, and participating in large scale phenotypic assays. Additional opportunities for independent research projects may exist, depending on the experience and interest of the successful candidate. Minimum required qualifications: B.S. degree in biology or a related field and a minimum of 1-2 years experience in genetics or molecular biology. This should include experience with DNA/RNA extraction, PCR, and DNA sequencing. Preferred: M.S. degree in biology or related field. The successful candidate should be motivated, have good organizational skills, and be able to work independently. Salary will be commensurate with experience and will include benefits.

Kansas State University has a very active community within the life sciences, thus creating numerous opportunities for stimulating academic interaction.

These include the large and diverse Division of Biology (www.ksu.edu/biology), as well as the interdepartmental programs of the Ecological Genomics Institute (ecogen.ksu.edu) and the Arthropod Genomics Center (www.ksu.edu/agc).

Kansas State University is located in the city of Manhattan (www.ci.manhattan.ks.us), a pleasant community of about 50,000 located in the scenic Flint Hills of north central Kansas, about 2 hours west of Kansas City. For more information on life in Manhattan see www.ksu.edu/morganlab . Review of applications will begin on June 8, 2009, and continue until the position is filled. For further information, please contact Ted Morgan at (785)532-6126. To apply, send an electronic copy of a cover letter, CV, and contact information for three professional references to: Ted Morgan, Division of Biology, Kansas State University, 116 Ackert Hall, Manhattan, KS 66506; email: tjmorgan@ksu.edu. KSU is an Equal Opportunity Employer, and actively seeks diversity among its employees. Background check required.

Theodore Morgan Division of Biology Kansas State University 116 Ackert Hall Manhattan, KS 66506 office: 785.532.6126 lab: 785.532.6074 fax: 785.532.6653 Email: tjmorgan@ksu.edu www.ksu.edu/morganlab tjmorgan@ksu.edu tjmorgan@ksu.edu

LeesMcRaeCollege Teaching

Job: Asst Prof Biology at Lees-McRae College

I would like to bring the following teaching position to the attention of the Evoldir community. The position is for a full-time junior faculty position to teach Anat&Phys and PreHealth Biology related courses, as well as core curriculum science courses. The college focuses on teaching but is interested in faculty-guided student research as well. Applications received after May 26th will be considered. Please feel free to direct questions regarding the position to Chrissy Spencer (spencerc@lmc.edu).

Banner Elk, NC is situated in the Blue Ridge Mountains of southern Appalachia, with area skiing, hiking, and cycling, and nearby access to the Blue Ridge Parkway and the Appalachian trail. The town is 30 minutes from Boone, NC and Appalachian State University.

Job ad posted in the Chronicle: Position: Assistant Professor or Instructor of Biology Institution: Lees-McRae College Location: North Carolina Date posted: 5/12/2009

Position: Lees-McRae College invites applications for a full-time assistant professor or instructor of Biology, beginning in August 2009. This is a one-year appointment with the possibility of renewal. The College is seeking a caring, energetic, and highly motivated individual with traits such as a sense of humor, a commitment to a liberal arts education, flexibility, creativity, and a sense of daring.

Qualifications: Potential candidates must possess a doctorate in biology, though master's or ABD candidates will be considered for an instructor's position. Teaching duties may include introductory biology courses for majors and non-majors, anatomy & physiology, biomechanics, elective courses to support a pre-health program, and senior research. Other responsibilities include advising of pre-health biology students, scholarship, and service to the College and profession. Preference is given to candidates with a commitment to service learning, a desire to conduct faculty/student research projects, and an interest in interdisciplinary curriculum.

Submission: Review of applications will begin May 26, 2009. Interested individuals should electronically submit a letter of application describing teaching experience and philosophy, vita, all college transcript copies, and names of three references with contact information to the Biology Faculty Search Committee at franklin@lmc.edu.

Lees-McRae College, a four-year, co-educational liberal arts college affiliated with the Presbyterian Church, USA, is located in the scenic Blue Ridge Mountains of northwestern North Carolina. Being a year-round tourist destination, the area provides the best of a vibrant college community coupled with natural beauty and a rich history. Please see www.lmc.edu for more information. Lees-McRae is an AA/EO employer committed to increasing the diversity of its faculty.

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Chrissy Spencer PO Box 1962 Banner Elk, NC 28604 USA

email: chrissy.c.spencer@gmail.com cell: 828 789 9089 work: 828 898 8764 website: web.me.com/chrissy.spencer

Chrissy Spencer <chrissy.c.spencer@gmail.com>

rose@zi.biologie.uni-muenchen.de

LudwigMaximilianU StatisticalGenetics

An Assistant Professor position (Akademischer Rat/Akademische Rätin, A13, auf Zeit) is available in the group of Statistical Genetics at the Ludwig-Maximilians University in Munich, Germany.

The assistant will be involved in the research projects in our group, such as the development of mathematical models and statistical methods for population genetic analyses. He or she will be responsible for teaching undergraduate and graduate courses for a total of five hours per week.

A prerequisite for this position is a doctoral degree in Mathematics, Statistics, Biology or a related field. Applicants should demonstrate expertise in some of the following areas: theoretical population genetics, stochastic processes, modern methods of multivariate statistics, evolutionary bioinformatics, quantitative genetics, MCMC and other methods of computational Bayesian statistics. Of advantage is experience teaching in English and German, in the analysis of biological data (preferably in R), in developing interdisciplinary projects, in programming (preferably in C/C++), and in grant applications.

The position is available starting in October 2009 initially for three years, with the possibility of extension for an additional three years.

The University of Munich is interested in increasing the number of female employees and encourages women to apply. The university is an equal opportunity employer and handicapped candidates with equal qualifications will be given preference.

The application should include: a full CV, names and contact information of three referees, and a statement of research interests. If you submit your application electronically, please include all documents in a single pdf file.

Please submit your application by May 25, 2009 to:

Prof. Dr. Dirk Metzler Biozentrum der LMU Department Biologie II Großhaderner Str. 2 82152 Planegg-Martinsried

metzler@bio.lmu.de

http://www.zi.biologie.uni-muenchen.de/evol/StatGen.html rose@zi.biologie.uni-muenchen.de

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ManchesterU FieldAssist EcuadorianAmazon

Field Assistant Position

We are looking for a field assistant to accompany a PhD student for a field season (August - November 2009) in the Ecuadorian Amazon. The research project is an interdisciplinary study examining the link between socioeconomic variables and environmental impacts in indigenous Kichwa communities. Field-work for the project will include a series of interviews and focus groups in indigenous communities and households as well as a series of biodiversity surveys using standard techniques (Transects, Quadrats) and indicators (Amphibians, Ferns, Dung-Beetles).

This is a unique opportunity to live along-side indigenous communities in the Amazon basin, gain extensive hands-on experience of biological and sociological research tools and receive authorship on any relevant publications. Successful applicants will also experience some of the last remote and untouched rainforests in one the world's biodiversity hotspots.

Living conditions will be basic (often with no running water or electricity) and the work is very physically demanding. Interested applicants should be prepared to walk long distances (up to 15km per day) and work long hours (sampling during the day and night). Conditions are also psychologically challenging since one is often out of regular communication for long periods of time and with little privacy since living quarters will most likely be shared

This post would suit budding researchers with an interest in social anthropology and/or conservation biology. Previous fieldwork experience and good working knowledge of Spanish are essential.

Please send enquiries to Johan Oldekop (johan.oldekop-2@postgrad.manchester.ac.uk) or Richard Preziosi (preziosi@manchester.ac.uk)

JOHAN OLDEKOP

PREZIOSI LAB Faculty of Life Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT England

T: +44 7984 771405

E: johan.oldekop-2@postgrad.manchester.ac.uk

W: http://www.preziosilab.org Johan.Oldekop-2@postgrad.manchester.ac.uk Johan.Oldekop-2@postgrad.manchester.ac.uk

NatHistMus London BotanicalDiversity

Research Scientists in Botanical Diversity

The Natural History Museum is one of the world's leading museums, internationally recognised for its dual role as a centre of excellence in scientific research and as a leading exponent in the presentation of natural history to the general public through exhibitions, public programmes and the web.

The Department of Botany houses over six million specimen collections of immense value and international importance and is a world-class centre of excellence for collections-based studies, inspiring research that reflects the remarkable variety of botanical life in the natural world. Researchers make a significant contribution to the scientific future of the department and museum.

You will have a proven research record and interests in one or more of the preferred research areas below. Consideration will be given to interests in other areas, providing they address the Museum's and Department's priority research foci.

* Global Plant Diversity Specialist * Plant Monographer

* Research Bryologist * Research Lichenologist

Closing date: Thursday 11 June 2009.

At the Natural History Museum we value the diversity of our employees and the unique perspectives they bring to our business.

Emilie

Human Resources Officer

Tel: 020 7942 5865

Emilie Tunstall <e.tunstall@nhm.ac.uk>

OhioStateU AnimalEvolutionaryBiol

Visiting Assistant Professor Animal Evolutionary Biology Department of Evolution, Ecology, and Organismal Biology The Ohio State University

We seek an individual to fill a one-year, non-tenure track position in animal evolutionary biology. The successful candidate will teach or co-teach three courses: Introductory Biology (Autumn Quarter), Organismal Diversity (Winter Quarter), and Extinction (Spring Quarter). Supervision of Graduate Teaching Associates is required for each course. Laboratory space also is available for research activities. A Ph.D. in animal evolutionary biology or the equivalent is required. Instructor of record experience teaching college-level biology courses is desirable. Position start date is September 1, 2009 and salary is $60,000 per year. More information about the EEOB department can be found at eeob.osu.edu < http://eeob.osu.edu/ > and about the city of Columbus, Ohio at www.osu.edu/visitors/-columbus.php.

To apply, submit electronically a cover letter, your current CV with the names of three professional references, and a statement of teaching and research interests to: Ms. Faith Haleem, Haleem.2@osu.edu (phone contact: 614-292-8280). To build a diverse workforce Ohio State encourages applications from individuals with disabilities, minorities, veterans, and women. EEO/AA employer. To assure full consideration you must apply by June 28, 2009.

Thanks very much,

PS Curtis

Peter S. Curtis Professor and Chair Dept. of Evolution, Ecology, and Organismal Biology The Ohio State University 318 W. 12th Ave. Columbus, OH 43210-1293 614-292-8280 curtis.7@osu.edu http://www.biosci.ohio-state.edu/~pcurtis/

"Curtis, Peter" <Curtis.7@osu.edu>

Phoenix DesertPlantConservation

Program Director Conservation of Threatened Species and Habitats Desert Botanical Garden, Phoenix, Arizona

One of the world's major botanical gardens specializing in desert plants seeks an individual to direct an expanded and enhanced conservation program. The successful applicant will have (1) training in botany and the ecology of rare species, (2) knowledge of conservation policy issues and governmental regulatory frameworks and (3) experience in implementing conservation measures. The Program Director will be a member of the Research Department and report to the Director of Research. Responsibilities include program development and management, collaboration with other conservation organizations and governmental agencies, and seeking extramural funding for program initiatives. Ph.D. and strong supervisory skills are required. Send C.V., a 1-page description of your philosophical approach to conservation issues, and names and contact information of three references to Ms. Mary Catellier, Director of Human Resources, Desert Botanical Garden, 1201 N. Galvin Pkwy., Phoenix, AZ 85008

Review of applications will begin June 15, 2009 and applications will be accepted until position is filled. An Equal Opportunity Employer.

sfehlberg@dbg.org

ResAssist DrosophilaMitochondrialEvolution

Research Assistant Position: Drosophila mitochondrial genetics at Brown University

A research assistant position is available to work on nuclear- mitochondrial fitness interactions in the laboratory of David Rand and Brown University. The general theme of this NIH funded project is to study the epistatic interactions among nuclear and mitochondrial genotypes that modulate fitness, physiological and biochemical traits in Drosophila. Mitochondrial genotypes from different strains and species of the melanogaster subgroup are placed on various nuclear chromosomal genetic backgrounds to dissect the genetic basis of life history traits. The project involves molecular and quantitative genetic assays of Drosophila strains, genetic mapping experiments, microarray and biochemical assays of specific genotypes, and inferences from molecular population genetics and evolution.

Applicants must have completed a B. A in Biology before starting the position, and have some combination of experience with molecular genetic techniques, Drosophila genetics, quantitative genetics, biochemical assays, molecular evolution, computational analysis, and an interest in evolution or genetics. Salary will depend on previous experience.

Applications can be filed through the Human Resources link on the Brown web page: www.brown.edu Search for job posting M02141

The start date is spring or summer 2009. Applications will be reviewed until the position is filled. To apply please send 1) a CV, 2) a short statement of research interests and experience, including a paragraph on how your previous experience makes you well qualified for this position, and 3) contact information for three references to:

David Rand email: David_Rand@brown.edu

Department of Ecology and Evolutionary Biology Box G-W, 80 Waterman Street Brown University Providence, RI 02912 Voice: (401) 863-2890 (Office) (401) 863-1063 (Lab) Fax: (401) 863-2166 web pages: http://research.brown.edu/research/profile.php?id=1100924991&r=1 http://www.brown.edu/Departments/EEB/rand/index.htm The Department of Ecology and Evolutionary Biology at Brown is an interactive group with strengths that span genomics, evolutionary biology, functional morphology, ecology, and environmental science. There are close ties to the Department of Molecular and Cellular Biology, and the Center for Computational Molecular Biology, as well as the Marine Biological Laboratory in Woods Hole

http://www.brown.edu/Departments/EEB/index.html http://www.brown.edu/Departments/Molecular_Biology/ http://www.brown.edu/Research/CCMB/ http://www.mbl.edu http://jbpc.mbl.edu/ http://ecosystems.mbl.edu/ Information on postdoctoral studies at Brown can be found here: http://biomed.brown.edu/grad-postdoc/ Providence is widely recognized (by Rhode Islanders) as the Venice of New England and is wonderful place to live.

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

SantaClaraU OneYearTeach EvolutionaryBiol

Position Title: Lecturer V Ecology and Evolution Department:Biology Status: Annual Year Lecturer (AYL)

Overview The Department of Biology at Santa Clara University, A Catholic, Jesuit comprehensive university located in the Silicon Valley, is seeking applicants for a one-year Lecturer position for the 2009-2010 academic year to teach undergraduate courses in Ecology, Evolution, Conservation Biology, and Biostatistics. The Biology Department is focused on undergraduate education. The selected candidate will be required to teach the equivalent of seven quarter-long courses per year.

Qualifications: Ph.D. in Biology or related field, and demonstrated excellence teaching relevant courses at the college level.

Rank and salary: Academic year lecturer, $48,300 to $51,100, depending on experience

Starting date: Sept. 1, 2009

Deadline: May 27, 2009

Responsibilities: Duties include but are not limited to teaching 1) a laboratory course in ecology/evolution as part of our introductory series for majors; 2) an upper division course in conservation biology, and 3) an upper division course in Biostatistics.

Application Procedure: Applications should include the following 1. Letter of interest outlining qualifications, teaching experience (including a statement describing experience working with people of diverse cultures and identities), and teaching philosophy. 2. Curriculum vitae 3. Names and contact information for three references

Applications may be submitted electronically to Biology@SCU.edu, (mailto:Biology@SCU.edu,) or by regular mail to Biology Department, Santa Clara University, 500 El Camino Real, Santa Clara, CA 95053. Please state Lecturer in Biostatistics, Ecology and Evolutionary Biology in the subject line.

Janice Edgerly-Rooks, PhD Chair, Biology, Santa Clara University Santa Clara, CA 95053 tel. (408) 554-4149

Janice Edgerly-Rooks <jedgerlyrooks@scu.edu>

UArizona ResTech DesertMiceEvolution

Research Technician / Research Specialist, University of Arizona

A research position is available in the laboratory of Dr. Michael Nachman in the Department of Ecology and Evolutionary Biology at The University of Arizona. The successful candidate will be the primary lab manager in a laboratory of population and evolutionary genetics. The responsibilities include conducting evolutionary studies using molecular techniques, breeding experiments with mice, occasional field work in the Sonoran Desert, analysis of data, ordering lab supplies, assistance in preparing manuscripts for publication, supervision and training of undergraduates in the lab, and travel to national meetings to present research results. Details of the research can be found at http://eebweb.arizona.edu/faculty/nachman/. Qualifications: bachelor's degree in biology or a related field and some laboratory research experience as well as some computational experience. Knowledge of evolutionary genetics, genomics, bioinformatics, and molecular biological techniques preferred. To apply, please send a letter describing your interests and qualifications, a CV, and contact information for three references to: Dr. Michael Nachman (nachman@u.arizona.edu). The University of Arizona is an Affirmative Action / Equal Opportunity Employer.

Ming Beckwith Program Coordinator IGERT Program in Genomics Biosciences West, Room 328 University of Arizona Tucson, AZ 85721

Phone: 520.626.0988 Fax: 520.621.9190 genomics@email.arizona.edu

UIowa ResTech MolecularPrimatology

The Ting Laboratory for Molecular Anthropology at the University of Iowa seeks a full time research laboratory technician to aid in various projects that investigate the impact of human hunting and habitat fragmentation on African primate communities. The technician will be responsible for collection and organization of molecular data as well as general laboratory administration. This one-year position will begin in August 2009 and is extendable dependant on funding. It would serve as an excellent opportunity for a recent graduate who is seeking further experience prior to graduate school. Please visit http://www.biology.uiowa.edu/ting/ for more information about the Ting Lab.

The successful candidate will have a BA/BS in Biology, Anthropology, or related field and at least 1-2 years of laboratory experience in genetics. In particular, the candidate must be organized, detail oriented, and experienced in one or more of the following methods: DNA isolation, PCR, microsatellite genotyping, and sequencing. Motivated candidates may have the opportunity to conduct fieldwork and have greater involvement in data analysis, write up, and publication. Salary will range from 25-30K depending on experience.

Interested applicants should send a letter of interest, CV, and names and contact information of three references to Dr. Nelson Ting (nelson-ting@uiowa.edu). The subject of the email must read ResLabTech for consideration. Applications will be reviewed as they are received and the position will remain open until filled.

Nelson Ting, Ph.D. Assistant Professor Department of Anthropology Macbride Hall 114 University of Iowa Iowa City, IA 52242-1322 Office: (319) 335-2891 Fax: (319) 335-0653 http://www.biology.uiowa.edu/ting/
nelson ting <nelson-ting@uiowa.edu>

UMichigan OneYear EvolutionaryBiology

Lecturer, Department of Ecology and Evolutionary Biology University of Michigan

The Department of Ecology and Evolutionary Biology invites applications for a Lecturer III position to begin September 1, 2009. This is a full-time, one year position with the possibility of reappointment. Responsibilities include serving as course coordinator for Biology 171 (Introductory Biology: Ecology and Evolution). Attend all class lectures, teach honors discussion sections, evaluate and design section exercises, conduct and coordinate workshops that provide training for first-time Graduate Student Instructors (GSIs) in Biology, run course prep sessions, and fill in for GSI absences in discussion sections. Duties also include scheduling makeup exams, coordinating grading, and responding to student emails regarding the course. Other teaching duties are included as appropriate to the expertise of the successful candidate. Courses of potential interest include core courses in vertebrate anatomy, animal physiology, animal diversity, ecology, and evolution, and courses in any relevant area for non-majors.

Terms and conditions of employment for this position are subject to the provisions of a collective bargaining agreement between the University of Michigan and the Lecturers' Employment Organization.

To apply, please send an application letter explaining your qualifications and teaching philosophy, a current CV, evidence of teaching excellence, and the names of two references to:

Barry OConnor Associate Chair for Curriculum Department of Ecology and Evolutionary Biology 2019 Kraus Natural Science Building 830 N. University Ann Arbor, MI 48109-1048

Or by email to: bsonja@umich.edu

Requirements include a PhD in Biology, Ecology, Evolutionary or Organismal Biology, Botany, Zoology, or related field. Prior teaching experience at a university level is required, with experience teaching or coordinating a large-enrollment undergraduate course highly preferred.

"Oconnor, Barry" <bmoc@umich.edu>

UniversidaddelosAndes Bioinformatics

The Department of Biological Sciences at the Universidad de los Andes (Bogotá, Colombia) seeks to fill a position for a full time assistant or associate professor with formal training and research experience in computational biology or bioinformatics. Applicants must have a Ph.D. degree, preferably with postdoctoral research and teaching experience. Researchers with experience in the analysis of molecular data in the context of evolutionary or genomic studies are especially welcome.

The successful candidate is expected to teach an introductory course in biology and the Genomics and Bioinformatics course, to supervise undergraduate and graduate students, and to promote and conduct research projects in the proposed field.

Send curriculum vitae, copies of recent publications, a research program, and two letters of recommendation by July 31th, 2009

Faculty Search Committee Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-10 P.O. Box 4976 Bogotá, Colombia ccontbio@uniandes.edu.co

– Carlos Daniel Cadena Profesor Asociado Departamento de Ciencias Biológicas Universidad de los Andes Apartado Aéreo 4976 Bogotá, Colombia Tel: (57-1) 3394949 Ext. 2072

http://evolvert.uniandes.edu.co http://evodiversidad.blogspot.com/ Co-Editor Ornitología Colombiana www.ornitologiacolombiana.org/revista.htm Carlos Daniel Cadena Ordonez <ccadena@uniandes.edu.co>

UniversidaddelosAndes VisitingProf

UNIVERSIDAD DE LOS ANDES

The Department of Biological Sciences (DCB) at Universidad de los Andes (Bogotá, Colombia) seeks a visiting professor in the area of Ecology (for undergraduate non-biology majors) for the 2009 fall semester. Applicants must have a Ph.D. degree and be fluent in Spanish. Researchers with a potential interest in joining one of the labs at the DCB as postdoctoral fellows are especially encouraged to apply (see http://cienciasbiologicas.uniandes.edu.co/centros.htm). This message is sent to evolutionary biologists because the course involves teaching basic principles of evolutionary theory in an ecological context, and because research interests in labs at the DCB cross bridges between ecology and evolutionary biology.

Send curriculum vitae and two letters of recommendation by June 30, 2009 to:

Faculty Search Committee Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-10 Apartado Aéreo 4976 Bogotá, Colombia ccontbio@uniandes.edu.co

– Carlos Daniel Cadena Profesor Asociado Departamento de Ciencias Biológicas Universidad de los Andes Apartado Aéreo 4976 Bogotá, Colombia Tel: (57-1) 3394949 Ext. 2072

http://evolvert.uniandes.edu.co http://evodiversidad.blogspot.com/ Co-Editor Ornitología Colombiana www.ornitologiacolombiana.org/revista.htm Carlos Daniel Cadena Ordonez <ccadena@uniandes.edu.co>

UOulu PopGenetics

A professorship in evolutionary/or population genetics/genomics will be open at the University of Oulu, Finland. The biology department at the University of Oulu has en emphasis on evolution/ecology, with many active groups in this area, see http://cc.oulu.fi/~biolwww/english/genetics_research.html . The Finnish National Graduate School for Population Genetics is coordinated by the Univ. of Oulu. Teaching can be in English or Finnish. Population genetics and bioinformatics related work at the University also takes place within Biocenter Oulu (http://www.biocenter.oulu.fi/).

For further information about the position, please see http://www.lutk.oulu.fi/english/index_english.htm and/or get it touch with Outi.Savolainen@oulu.fi or Pertti.Tikkanen@oulu.fi.

Outi Savolainen Department of Biology PO Box 3000 FIN-90014 University of Oulu Finland

Outi Savolainen <Outi.Savolainen@oulu.fi>

UPerpignan ResAssist MolBiolEvolution

Job: Research Assistant in Molecular Biology and Evolution Institution: University of Perpignan, France Location: University of Perpignan - UMR5244 CNRS-EPHE-UPVD, Perpignan, France Start date: 1st of July 2009

A Research Assistant position is available starting the 1st of July 2009 in a molecular evolution laboratory supervised by Dr. Serge Planes in the Centre de Biologie et Ecologie Tropicale et Méditerranéenne at the University of Perpignan, France (< http://cbetm.univ-perp.fr/ephe/personnel/planes.htm > http://cbetm.univ-perp.fr/ephe/personnel/planes.htm). The successful candidate for this position will assist with ongoing research projects, with primary responsibilities to include extraction of DNA, PCRs, sequencing, and genotyping microsatellites (including the set up of protocols), and some laboratory management duties including occasional training and supervision of laboratory personnel. Requires a bachelor of science degree in the biological sciences (biology, biochemistry, molecular biology or related area) and a master of science degree (or equivalent experience) in biological sciences (or related fields). Must have laboratory skills in working with DNA and microsatellites (including screening). Salary is 1350 euros net per month (including social security benefits). Screening of applicants to begin immediately and continue until position is filled. To apply, email a cover letter briefly describing your experience, interest in the job, and career goals, along with your resume, and contact information for three references to Dr. Serge Planes at planes@univ-perp.fr (place "Research Assistant position" in subject line). This is a non-tenure track, fixed-term appointment funded for six months from date of hire with a possibility of re-funding for another 12 months.

– Ce message a été vérifié par MailScanner pour des virus ou des polluriels et rien de suspect n'a été trouvé. CRI UPVD http://www.univ-perp.fr Cecile Fauvelot <cecile.fauvelot@univ-perp.fr>

UUmea WildPopulations

Assistant Professor in Terrestrial Animal Ecology

The Department of Wildlife, Fish and Environmental Studies at SLU, Umea in Sweden, invites applications for a 4-year full-time Assistant Professorship. Job description: Our department studies the ecology of populations, typically combining fundamental and applied aspects in our ambition to improve our understanding and capacity to manage wild populations and the ecosystems they inhabit. We are now looking to strengthen our competence in terrestrial systems, particularly in the field of animal ecology. The successful candidate will be expected to develop and maintain an active, independent research program in this area. Qualifications: We are looking for a highly motivated candidate with a PhD in biology, interested in terrestrial small animal ecology, and with an ambition to address both applied and fundamental research questions. A record of innovative and productive research combining multiple analytical approaches and data types (e.g. behavioral, physiological, and epidemiological) will be a strong merit. Proficiency in theoretical/modeling and quantitative approaches to ecology will also be evaluated favorably. Eligibility: Applicants should have a PhD or the equivalent. Priority will be given to applicants who have been awarded their PhD within five years of the application deadline. Salary is negotiated on an individual basis.

For further information please see http://-personal.slu.se//LEDANS/2009-1212eng.pdf Goran.Spong@vfm.slu.se Goran.Spong@vfm.slu.se

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WesleyanU Visiting IntroEvolBiol

Dear Brian, thank you very much for the info. We would be delighted to hire an evolutionary biologist, since we think the kind of interdisciplinary breadth we seek is more likely in someone trained in evolutionary bio than a more reductionist discipine. So I do think Evoldir is a good place to post the listing.

Here it is, in plain text– the heading can be something like "Visiting position at Wesleyan" if thats not too long.

thank you again

Sonia

Visiting Assistant Professor Biology/Molecular Biology & Biochemistry Departments Wesleyan University

A Visiting Assistant Professor is sought for the 2009-2010 academic year. The initial appointment will be for two years with the possibility of renewal for a further two years. The Visitor will teach and coordinate teaching assistants for the undergraduate laboratory component of Introductory Evolutionary Biology in the fall and spring semesters, and will also teach a section of the Introductory Evolutionary Biology lecture course in the fall (32 students), and an elective course in the area of his/her expertise in the spring. Applicants must possess a Ph.D. degree and be broadly trained in the biological sciences; prior teaching experience is preferred, and commitment to teaching excellence is essential. Interested applicants should submit a curriculum vitae and a teaching statement, and have three letters of reference sent via e-mail to our administrative assistant, Ms. Deborah Alexson (dalexson@wesleyan.edu), or by mail to Search Committee, Department of Molecular Biology and Biochemistry, Wesleyan University, Middletown, CT 06459-0175. Applications must be received by June 15. See www.wesleyan.edu/mbb/ for more information about this position.

Wesleyan University is proud of its record of commitment to diversity, and encourages applications from women and persons of color. Wesleyan University is an Equal Opportunity/Affirmative Action Employer

– Sonia E. Sultan Professor of Biology Department of Biology Wesleyan University Middletown, CT 06459-0170 USA

Phone: 860.685.3493

Fax: 860.685.3279

http://www.wesleyan.edu/bio/sultan/sultan.html Sonia Sultan <sesultan@wesleyan.edu>

Other

AFLP problems

Dear EvolDir Members,

I am contacting you regarding some peculiar AFLP results (bright white smears) a few of us have been experiencing in the last few months.

Background: We use the AFLP protocol adapted from Ajmone-Marsan (1997) which involves a Taq and EcoRI enzyme digestion. We have used this protocol for some years now and it has always worked fine.

Problem: 3 months ago unusual bright white smears were seen in pre-amplification checking gels, sometimes starting from the wells and other times slightly extended smears, but always exceptionally bright (the pre-amp was carried out using a ligation mix that had previously given good profiles). This was repeated numerous times but always gave the bright smears, sometimes in the negative as well and sometimes not. Soon after all PCR reagents were changed and the bright smears disappeared from the pre-amps. I thought it was as simple as that, but when I carried out the selective PCR and sent to fragment analyse there were no peaks (sometimes just one or two at around 50-80bp but nothing like the profiles I am used to getting with >100 peaks). We ran these selective products on a gel and saw the same bright white smears in everything (sometimes in the negative as well and sometimes not, sometimes there are also faint bands in the gel, but often not).

Since this we have tried new reagents (multiple times), other peoples reagents, new primers, new enzymes, different PCR machines, different samples, new low TE buffer for the dilutions and all of this has been tried twice independently by myself and a colleague. We are running out of ideas. The most frustrating thing is that we have no idea what the bright white smears could be (contamination or the result of two or more reagents reacting adversely?). Also, we occasionally get a good selective PCR profile but often using the same reagents that haven't worked previously?

Apologies for the lengthy e-mail but we are now clutching at straws, so to speak. I would be very grateful if you have any suggestions as to what may be happening to cause these smears or what we could try next...

Much obliged, Jo Bluemel and colleagues BluemelJK1@cardiff.ac.uk

Joanna Bluemel PhD student Cardiff School of Biosciences, Biomedical Sciences Building, Cardiff University, Cardiff, CF10 3AX, UK

02920 875073

sbijkb@groupwise.cf.ac.uk sbijkb@groupwise.cf.ac.uk

AGARst software

Dear evoldir members,

I have been searching on the web for the software AGARst (Harley 2002) with no success: Harley EH (2002) AGARst. A program for calculating allele frequencies, GST and RST from microsatellite data plus a number of other population genetic estimates and outputting files formatted for various other population genetic programs. Available at http://web.uct.ac.za/Departments/chempath/genetic.htm . The above link doesn't work anymore. I have also tried an alternate link I found in a recent paper, but again, it is not working:

http://www.web.uct.ac.za/depts/chempath/genetic.htm I'll be very grateful if somebody can either send me (1) a copy of the program, (2) the correct link, or (3) Prof. Eric H Harley's current email address so I can contact him directly.

Thank you in advance, Daniel

Dr Daniel Gomez-Uchida Visiting Postdoctoral Fellow for Parks Canada Department of Biology, Life Sciences Centre Dalhousie University 1355 Oxford Street Halifax, Nova Scotia Canada B3H 4J1 Phone: (902) 494 1688 Fax : (902) 494 3736 Email : daniel.gomez-uchida@dal.ca

daniel.gomez-uchida@dal.ca daniel.gomez-uchida@dal.ca

Automated flow cytometer

Dear all,

My name is Andreas v. Bohl and at the moment I'm doing my bachelor thesis in the Work group of Gisep Rauch in the institute for evolution and biodiversity in the University of Münster in Germany. My research project, for my bachelor thesis, is to establish a parallel and automated method for counting *Paramecium tetraurelia* and its bacterial parasites with a flow cytometer (BD Facscanto II). The problem is that the cells (100μm long and 30μm broad) are too big for the flow cytometer and that they block the capillary.

Does anybody have experience working with *Paramecium* using a flow cytometer? Has anybody an idea how to solve the problem of blocking the flow cytometer capillary? Has anybody already established an automated counting routine for *Paramecium* using an alternative technique?

I would be very thankful for any advice. Andreas

andreas.v.bohl@googlemail.com

Andreas v. Bohl

Institute for Evolution and Biodiversity Westfälische Wilhelms-Universität Hüfferstrasse 1, D48149 Münster, Germany

andreas.v.bohl@googlemail.com

Beauveria primers

Dear Evoldir members,

I would like to know about any specific primer that only amplifies Beauveria. The idea is to seggregate Beauveria from other isolates from my collection without being sequenced. Please reply me.

Johny – Johny Shajahan 4120, Department of Biological Sciences Illinois State University Normal, IL-61790-4120, USA Ph:(309) 438-7799

“Shajahan, Johny” <jshajah@ilstu.edu>

Brehmmer supports

Dear community,

I’d like to aknowledge all the people who have sent me “how to” in order to obtain decay indexes. Thank you so much and feel free to contact me for anything. Cheers,

– Prof. Dr. Rodrigo A Torres Laboratório de Genômica Evolutiva e Ambiental Departamento de Zoologia Centro de Ciências Biológicas Universidade Federal de Pernambuco Av. Prof. Moraes Rego s/n Cidade Universitária Recife, PE 50670-420 +55(81) 2126-8353 +55(81) 9692-9547

“Rodrigo A. Torres” <rodrigotorres@ufpe.br>

Bremmer support PAUP

Dear community,

Does anyone know a “how to protocoll” to generate Bremmer supports at PAUP* ?

Thanks a lot and best regards.

Prof. Dr. Rodrigo A Torres Laboratório de Genômica Evolutiva e Ambiental Departamento de Zoologia Centro de Ciências Biológicas Universidade Federal de Pernambuco Av. Prof. Moraes Rego s/n Cidade Universitária Recife, PE 50670-420 +55(81) 2126-8353 +55(81) 9692-9547

“Rodrigo A. Torres” <rodrigotorres@ufpe.br>

Brits Appointments to BBSRC

Dear all,

It would be very beneficial for the community to get some interested evolutionary biologists to apply for these positions on the BBSRC panels and committees. It is hard work but very rewarding in many ways.

Sincerely

Max Telford (apologies for cross posting)

Appointments to BBSRC Strategy Panels, Research Committees and Pool of Experts

The Biotechnology and Biological Sciences Research Council (BBSRC) funds basic and strategic biological research, supports postgraduate training, promotes knowledge transfer and public engagement with science.

We are looking to appoint high calibre, committed individuals from academic and industrial sectors to fill a number of vacancies on our Strategy Panels and Committees.

The Panels play leading roles in the development and implementation of the Council’s policies and priorities. The Committees play key roles in delivering BBSRC’s Mission by carrying out peer review of research grant proposals, the awarding of studentships and fellowships and assessing final reports on funded proposals.

This year applications are also encouraged from individuals who wish to join the BBSRC Pool of Experts to assist BBSRC with its many other activities, such as the Research Committee Pool of Experts, scientific reviews, initiative panels or advisory groups.

Appointments will commence in January 2010 for one year initially, with anticipated extension for a further two years.

Further details, including role of the Panels, Committees and Pool of Experts, Person Specification and Expression of Interest Form can be found on the BBSRC website at http://www.bbsrc.ac.uk/media/news/-2009/090420_appointments_panels_commit tees.html

The closing date for applications is Friday 9 June 2009.

The BBSRC welcomes applications from all sections of the community irrespective of race, age, transgender, ethnicity, religion, sexual orientation, disability or gender.

m.telford@ucl.ac.uk

Celegans strain

Hi,

Can anyone tell me whether the exact location of the ccIs4251 transgene (containing GFP coding sequence) in the PD4251 strain has been described? I need to know the sequence of the genomic regions flanking this transgene but all I found so far is that it maps to the center of chromosome I...

Thanks!

Sara Carvalho Instituto Gulbenkian de Ciência Portugal

saranlcarvalho@gmail.com

CitizenScienceChallenge Instructions

Greetings everyone,

Here are instructions for participating in the “citizen science on the semantic web” challenge. Please circulate to anyone (anywhere) who you think will want to contribute.

For those in London, here’s a preliminary list of places to mini-blitz: http://spire.umbc.edu/ebio/-Main/London If you know London, please feel free to add more. (Email me for the edit password.)

See you all soon - Joel.

joel sachs <jsachs@csee.umbc.edu>

Class data sets

Dear friends,

I am teaching Biostatistics for Biology students and I would like to use measurements of hominids skulls and dinosaurs body, skulls, etc. To teach about graphs and analysis.

I am trying to obtain data from articles or in websites but nothing until now!

If you have some published data or indication of websites for students with data like that please send me!!!

Thanks for any help!!!

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamiferos (ECOMAM) UNITAU, Depto. Biologia, Taubate, SP. 12030-010. * Grupo de pesquisa ECOMAM: http://jcvoltol.sites.uol.com.br/ * Fotos de projetos e cursos: http://jcvoltol.fotoblog.uol.com.br/- * Exemplo de um curso de ecologia de campo: http://trabiju.blogspot.com/ * Fotos artisticas: http:/-/voltolini.fotos.net.br/texturas jcvoltol@uol.com.br

Computer time

Dear evoldir members,

I’m looking for somewhere I can run a few computer simulations remotely, on a computer system that’s at least 10 times faster than my 2.2 GHz MacBook Pro. My university doesn’t have any central facility where I can do this, just a ’grid’ of computers that are individually too slow to be useful. I don’t mind paying a modest charge.

The simulation is written in Perl (about 1000 lines of code). It doesn’t do anything fancy so I think it should run on any unix system. The runs are very computationally intensive; the MacBook Pro takes about a day to run 10,000 evolutionary cycles on a 20kb genome, and I’d like to get data for a few runs of 100,000 or more cycles on a 200 kb genome.

Given the widespread availability of web sites where we can run sophisticated DNA sequence analyses for free, I'm thinking that somebody somewhere must have a site where I can upload my program and run it, perhaps paying for cpu with my credit card or PayPal.

Any suggestions?

Thanks,

Rosie

Dr. Rosemary J. Redfield redfield@interchange.ubc.ca

Department of Zoology Office: (604) 822-3744 Univ. of British Columbia Lab: (604) 822-6323 Vancouver, B.C. V6T 1Z4 Fax: (604) 822-2416 Canada

We're now in the Life Sciences Centre (RJR office 2551, lab 2520; email us for directions)

Web site: http://www.zoology.ubc.ca/ ˜ redfield Research blog: http://rrresearch.blogspot.com redfield@zoology.ubc.ca redfield@zoology.ubc.ca

Conserved proteins

Hi,

I am trying to find protein alignments for gene families that are very well conserved, and so can encompass both eukaryotes and prokaryotes, like basic enzymes and transporters. Anyone?

I work for Ensembl, so www.ensemblgenomes.org doesn't count.

Thanks,

Albert.

avilella@ebi.ac.uk avilella@ebi.ac.uk

Copy of paper

Dear all,

thank you very much for all those who sent me a copy of Smocovitis 1992 paper. I received almost 20 messages with the requested file. And it was fun also, because two evoldir members conditionally requested to me the same file !

Thank you for your kindness.

Aldo

Aldo <aldomel@portoweb.com.br>

Couterselect Bac Modification Kit Genebridges

Dear kollegues,

I am trying to get the Couterselect Bac modification kit, a recombineering kit working with a high copy plasmid construct. Problems with bacterial resistance occured, esp concerning streptomycin. Does anyone of you have any experience with this kit and could give some hints how to get it working.

Thanks.

Sincerely,

Dorothea Baranyai.

dorothea.baranyai@arcor.de

Daphnia DNA extractions answers

Dear all

A few days ago I posted a request concerning efficient DNA extractions in plates. Below you find my original e-mail:

> I like to do DNA extractions from single Daphnia using the chelex > method for economical reasons. As I have to proceed a high quantity of > samples, I would like to do the extractions directly in > 96-well-plates. Does anyone have any experiance if this works and do > you have found a good systems for grinding the animals directly in the > plate?

Please find below a selection of the answers I received.

Many thanks for all your help and the useful information!

Best regards, Barbara Barbara Walser University of Fribourg E-mail: barbara.walser@unifr.ch

From: Ben Longdon (b.longdon@ed.ac.uk) We do Drosophila chelex extractions using heavy duty 96 well plates with deep wells, putting ball bearings in the wells, then shaking the flies on a homemade device which consists of a sheet sander, which we've adapted to strap the plates to. Can then transfer the DNA to a standard 96 well plate for ease of use.

From: Brant Faircloth (brant@ucla.edu)

you may wish to look into the use of steel beads (1-2 per well; BioSpec Products, Inc. SKU 11079132c; you may prefer stainless beads, however) along with a paint-shaker or reciprocating saw to do your tissue disruptions (i can send PDFs if you don't have access):

1) reciprocating saw methodology - http://www3.interscience.wiley.com/journal/118523651/abstract 2) paint shaker - see http://www.springerlink.com/content/d70250873105gq05/ once the tissues are disrupted, you can chelex normally. The stainless beads are less likely to introduce nasties to your samples, but they are more expensive and non-disposable (treat with 10% bleach and a few ultra-pure water washes prior to re-use).

if you wish to separate the solution from the chelex (it is hard to remove supernatant from chelex extracted samples in plates and chelex can cause problems with some tips/needles in liquid handlers), you can filter it out using Millipore plates (MAHVN4510) or similar suspended over inexpensive skirted plates + centrifugation at 900 G for 5 m.

Use filtrate from the plates normally in downstream applications (PCR, etc.).

From: Lena Bayer-Wilfert [lb445@cam.ac.uk] for single Drosophila flies, we grind the flies in a deep 96 well plate with the help of ball bearings and a home-made contraption using a sander and some bits of wood. Not sure whether that would grind single Daphnia well enough. I guess that you'll get some more useful feedback from the Daphnia community, but if not let me know and I can try to get you a better description of what we do.

Tom Little [tlittle1@staffmail.ed.ac.uk]

We use the CTAB method, which is very reliable. Chelex used to cause some trouble (I think especially if the samples were to be stored, probably Chelex is fine if you use the DNA right away). John Colbourne at Indiana would be a good source of update information.

From: Africa Gomez [A.Gomez@hull.ac.uk] May I suggest that you consider an alternative method to Chelex which we have shown to work on Daphnia and allows for easy high-throughput (and can be carried out in 96-well plates)? Paper freely available at: http://www.aslo.org/lomethods/free/2008/0218.pdf From: Michael Monaghan [monaghan@igb-berlin.de]

I have used 96-well plates extensively for DNA extraction, mostly with insects but also with Daphnia. The animals can be placed in lysis buffer + protK in a 96-deep-well plate overnight in a water bath. there is no need to grind them. i use the deep well plate available from VWR (cat. nr. 732-0585) and cover it with plastic film or a PCR plate cover to minimize evaporation.

From: Joaquin Munoz [quini@ebd.csic.es]

I have no experience making DNA extraction with Chelex in 96-well plates, but I suggest to read our recent paper describing a new cheaper method which use HotSHOT protocol in resting eggs and pieces of adults from Daphnia, Artemia, Rotifers....

From: natassa [natassa_g_2000@yahoo.com] I used Chelex a long time ago for the same economic reasons, and I just wanted to say that I am not convinced it is worth it. I was screening a lot of transformants to find mutants, and I realized a long time later that I had far more than i estimated (due to poor DNA quality). It all depends on your goal... I used heat shock for lysing cels, but well, it is far easier in the fungus I was working on rather than in Daphnia I suppose. From: Alice Dennis [alicebdennis@gmail.com] I use Chelex for extractions in the snail's I'm working on, but I use 8-well strip tubes because they have a cap that snaps tighter than anything I've found for a 96-well plate. This makes vortexing and

— / —

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

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DNA from parasitic wasp larvae

Hi

I am working with small parasitic wasp larvae (around 1 mm), and I am only getting small amounts of DNA from it. A colleague mentioned that I should try the GenomiPhi V2 DNA amplification Kit (from GE Healthcare) and I would like to know if anyone ever used this before. If you did, can you please tell me if it was successfull and if you changed any thing in the protocol?

Many thanks,

Ana Santos

"Santos, Ana" <a.santos05@imperial.ac.uk>

Drosophila difference database

Dear all,

David Stern and I compiled more than 150 morphological, physiological and behavioral traits that have been reported to differ between at least two species of the D. melanogaster subgroup (D. melanogaster, D. simulans, D. sechellia, D. mauritiana, D. yakuba, D. santomea, D. teissieri, D. erecta and D. orena). Our compilation is available online at www.normalesup.org/~vorgogoz/FlyPhenomics . This database may be useful for Drosophila researchers who aim to identify the mutations underlying phenotypic variation and for biologists in general who want to get a picture of the amount of phenotypic variation between closely-related species.

All comments and suggestions are welcome.

With best wishes,

Virginie – Virginie Orgogozo CNRS - Université Pierre et Marie Curie UMR7622 - case 24 9 quai Saint Bernard 75005 Paris France (33) 1 44 27 22 59 www.virginie.orgogozo.org vorgogoz@snv.jussieu.fr vorgogoz@snv.jussieu.fr

FarmingHumanPathogens

Farming Human Pathogens: Ecological Resilience and Evolutionary Process by R Wallace et al., Springer (http://www.springer.com/computer/computational+biology+and+bioinformatics/book/978-0-387-92212-6).

Dear Colleagues,

Farming Human Pathogens: Ecological Resilience and Evolutionary Process has just been published by Springer under its computational biology and bioinformatics line.

The book introduces a cutting-edge formalism based on the asymptotic limit theorems of information theory to describe how punctuated shifts in mesoscale ecosystems imposed by human intervention can entrain patterns of gene expression and organismal evolution. The development is applied to several infectious diseases, including HIV and influenza. The book also presents a related treatment of Eigen's Paradox and the RNA 'error catastrophe' that bedevils models of the origins of viruses and of biological life itself.

More information about the book can be found at the book's blog at http://.farmingpathogens.wordpress.com . Sincerely,

Rob Wallace Department of Geography University of Minnesota

rwallace24@gmail.com

– Robert G. Wallace, Ph.D. Visiting Assistant Professor Department of Geography University of Minnesota 414 Social Sciences Building 267 19th Avenue South Minneapolis, MN 55455, U.S.A. walla353@umn.edu

Finding Pedigree Software

Dear all,

I am experiencing some troubles trying to access the link I have for Pedigree Software by Smith et al 2001 (Genetics, 158, 1329â1338).ÂÂDoes anyone knows if it has been moved?

Thank you very much Sincerely,

Carolina I. MiÃ±o, MSc. Doctoral Student LaboratÃ³rio de GenÃ©tica de Aves Departamento de GenÃ©tica e EvoluÃ§Ã£o Universidade Federal de SÃ£o Carlos Rodovia Washington Luis km 235 SP-310 CEP: 13565-905 Monjolinho. SÃ£o Carlos,SP, Brazil. Phone number: +55 16 3351 8391 (Work) Fax: +55 16 3351 8377 Mobile: +55 16 91190380

Carolina Minio <carolinaianido@yahoo.com.ar>

Fst question

Hello,

I am looking for software that will allow me to estimate PAIRWISE Fst for EACH LOCUS separately. I have only been able to find programs that will calculate locus-specific Fst globally.

Also, is there a program that uses jackknifing or bootstrapping to get confidence intervals for Fst?

Thanks for your help, Erika

Erika Crispo, PhD candidate McGill University, Department of Biology http://www.biology.mcgill.ca/grad/erika/index.htm Erika Crispo <erika.crispo@mail.mcgill.ca>

Juniperus seed DNA

Dear Evoldir members,

We are working with Juniperus cedrus (crupessaceae) in population genetics. We have tried to extrac DNA from seed (endocarp tissue) using different protocols and comercials kits. However, we havent obtain DNA enough . Juniperus seeds are small and very hard. So, there are anybody that have extracted DNA from similar seeds or woody tissues successfully?

Thank in advance,

Beatriz Rumeu

brumeu@ipna.csic.es

canariensis750@hotmail.com

Lepidopteran housekeeping primers

Dear all,

Can anyone recommend a primer set for a general insect or Lepidopteran-specific housekeeping gene? I have been trying to amplify CO1 (see Lunt et al 1996, Ins. Mol. Biol. 5: 153) as a control for Wolbachia assays, but its not working as well as I would like, so I wish to give something else a try.

Any suggestions would be much appreciated.

Best,

Zen

Dr Zenobia Lewis

Post-doctoral Research Fellow Laboratory of Evolutionary Ecology Graduate School of Environmental Science Okayama University Japan

zen.lewis@googlemail.com

Lepidopteran housekeeping primers answers

Dear all,

I recently posted a question with regards insect/lepidopteran housekeeping primers as a control for wolbachia assays. My original email was as follows:

> Can anyone recommend a primer set for a general insect or > Lepidopteran-specific housekeeping gene? I have been trying to amplify CO1 > (see Lunt et al 1996, Ins. Mol. Biol. 5: 153) as a control for Wolbachia > assays, but its not working as well as I would like, so I wish to give > something else a try. >

Many many thanks toeveryone that gave me advice - in case anyone else is interested, some of the answers i received are copied below.

Cheers,

Zen

– Dr Zenobia Lewis

Post-doctoral Research Fellow Laboratory of Evolutionary Ecology Graduate School of Environmental Science Okayama University Japan

In our lab, we work on bumblebees and use RPS5 (ribosomal protein S5) as our housekeeping gene, though we do have primers also for actin. RPS5 seems to work very well, and was initially used by Evans (2004) Journal of Invertebrate Pathology 85 (2004) 105'111 for immune studies. Our housekeeping primers were re-designed specifically for bumblebees, but it might be worth a go using Evans's honeybee primers, as RPS5 is very well conserved between bees, butterflies nd wasps (>70% nucleotide homologay).

You might want to check out EF1-alpha. The Lep primers won't amplify the EF1-alpha from Wolbachia. For primers and conditions, see: Monteiro and Pierce. 2001. Mol. Phylogene. Evol. 18: 264-281.

I have had excellent luck with COI primers 1709 and 2353, in a wide variety of Lepidoptera as well as other insects. The reference for those primers is: Simon, C., T. R. Buckley, F. Frati, J. B. Stewart, and A. T. Beckenbach. 2006. Incorporating molecular evolution into phylogenetic analysis, and a new compilation of conserved polymerase chain reaction primers for animal mitochondrial DNA. Annual Review of Ecology, Evolution, and Systematics 37:545-579.

I've been running the Jerry/Pat2 primer pair (Simon et al. 1994 but the Pat is modified in Murray and Pashley Prowell 2004) in my Wolbachia assays.

I'm working on wasps, but some of the primers I use should be general enough to work for Lepidoptera as well. You might want to check Brian Danforth's page, which gives an excellent overview of primers used primarily in bees, but it's also the best one I know for insects in general: http://www.entomology.cornell.edu/-BeePhylogeny/index.html We have successfully sequenced wingless, EF1-alpha, Arginine kinase and LW rhodopsin with the primers given there. Otherwise, you could try beta-actin, which is often used as a housekeeping gene control (if you need it for quantification by qPCR, that's probably the gene of choice). For our wasps, we designed some primers, and Actin-F1 and -R1 worked quite well (over a range of annealing temperatures, from 45-56 C): Actin-F1 5'-GGTAACGAAAGATTCCGTTG-3' Actin-R1 5'-GATCCACATCTGTTGGAAGG-3' They amplify a fragment of about 320 bp of beta-actin. I don't know whether they would work for Lepidoptera, you should check some Lepidopteran actin sequences from GenBank whether the primers match.

In the honeybee Apis mellifera, actin has been used, and also Krh I and Rp49 (Navajas et al 2008, BMC Genomics), or ribosomal protein S5 (Schlüns & Crozier 2007, Ins Mol Biol) etc. Maybe they can also be used for other insects?

Try the primers in : Evolutionary relationships of Drosophila mojavensis geographic host races and their sister species Drosophila arizonae L. K. REED, M. NYBOER, T. A. MARKOW Molecular Ecology Volume 16, Issue 5 , Pages1007 - 1022 I had a lot of luck with these universal CO1 primers.

zen.lewis@googlemail.com

Mac program degenerate sites

Can anyone suggest a program for a Mac that can determine the proportion of fourfold degenerate sites between two species. Thanks, Ron Woodruff

R. C. Woodruff Distinguished Research Professor CoEditor-in-Chief , GENETICA Department of Biological Sciences Corner Merry and N. College Life Sciences Building Bowling Green State University Bowling Green, Ohio 43403 Telephone: 419-372-0376 Fax: 419-372-2024 email: rwoodru@bgnet.bgsu.edu

Ronny C Woodruff <rwoodru@bgsu.edu>

Mark-recapturesoftware answers

Thanks to all of you who have answered! If your favorite software isn't here, please let me know.

//Peter

——— Original Message ———

It depends on what types of questions you are wanting to ask and what forms your data are in. MARK is a great place to start, since you can access most of the other stand-alone software through the MARK interface. I would consider using POPAN (via the MARK interface), provided your data fit the appropriate models. Another package to consider is M-SURGE, which belongs to the U-SURGE/ECARE cluster of programs. It's a bit more troublesome to work with, and results aren't published as much. If you find any others that look promising, please do forward them along - I'd be quite interested to see!

Hi, i think that you have to know what you want to do. Mark is a good software that i used to study population dynamic on subantarctic seabirds. For basic study it is enough but it seems that m-surge is better for multi-state study. if you want to download the programme you should find it at the web site: http://www.cefe.cnrs.fr/BIOM/en/softwares.htm. I will also give you the adress to download a paper of Lebreton: http://www.cefe.cnrs.fr/pdf/Lebreton-EcoMonog-1992.pdf. It can be useful when you start with Mark-recapture. Good luck

---

Your only practical options are either MARK or M-SURGE/E-SURGE. M-Surge used to be much easier to work with than Mark since you could write simple commands that control what you want the program to do instead of more or less manually manipulate matrices as in Mark. In this way even complex analyses is simple to perform. However, Mark can now be run from R.

I mainly use M-Surge. For what it does (including simple and multi-state standard capture-recapture analyses) it is a superb program and as simple to use as it gets. Mark is more general and can do other things.

Information and discussion of capture-recapture software can be found at http://www.phidot.org/forum/-index.php Capture-recapture is not something you learn to do in an afternoon, though. Start with the "Gentle introduction" by Cooch and White: http://-www.phidot.org/software/mark/docs/book/

Dear evoldir, I am about to start a mark-recapture study. Which software would you recommend for analyzing the data? So far I have found the software MARK.

Kind regards, Peter Halvarsson Phd-student, EBC, Uppsala University

peter.halvarsson.1887@student.uu.se peter.halvarsson.1887@student.uu.se

Mark recapture study

Dear evoldir, I am about to start a mark-recapture study. Which software would you recommend for analyzing the data? So far I have found the software MARK.

Kind regards, Peter Halvarsson Phd-student, EBC, Uppsala University

Peter.Halvarsson.1887@student.uu.se Peter.Halvarsson.1887@student.uu.se

Mascarene island paper

Dear all,

I wasn't able to get a pdf file of Cheke, A.S., 1987. An ecological history of the Mascarene Islands, with particular reference to extinctions and introductions of land vertebrates. In: Diamond, A.W. (Ed.), Studies of Mascarene Islands Birds, Cambridge University Press, Cambridge, pp. 5±89.

If someone could send me one pdf file I would appreciate very much. Many thanks.

Salmona Jordi

jordi.salmona@gmail.com

Microarray course help

Dear EvolDir members,

For the first time, I am implementing a course in Special Topics that will include on DNA Microarray topics for Biology students. It is being offered during this summer beginning May 29, 2009 at undergraduate level. If you have and know the basic material including the research papers, please send me and/or suggest the web link. Also, suggest me the books that I may use in the course. I will compile and resend it to Dr. Brian for re-publication.

Your cooperation is highly appreciated

Thank you,

Anand

Anand P. Gupta, Ph.D Johnson C. Smith University Department of Natural Sciences and Mathematics, SHB 307 100 Beatties Ford Road Charlotte, NC 28216

Voice: (704) 378-3580

e-mail to: agupta@jcsu.edu

Web: http://sites.google.com/site/-geneticsandevolution < http://sites.google.com/-site/geneticsandevolution >

"Gupta, Anand P" <agupta@jcsu.edu>

Minimum spaning network

Dear community,

Does someone could advise me how to generate the diagram of a minimum spawning network obtained from Arlequim? Thanks a lot.

– Prof. Dr. Rodrigo A Torres Laboratório de Genômica Evolutiva e Ambiental Departamento de Zoologia Centro de Ciências Biológicas Universidade Federal de Pernambuco Av. Prof. Moraes Rego s/n Cidade Universitária Recife, PE 50670-420 +55(81) 2126-8353 +55(81) 9692-9547

"Rodrigo A. Torres" <rodrigotorres@ufpe.br>

MrBayes consensus answers

Dear colleagues,

Thank you to everyone who sent information on the patch for the 64-bit version. It appears that my problem was much simpler: I used to run MB in a non-parallel version some years ago. Since I have moved to another institution a number of things have changed but I never read the new manual (ooops) or updated my input files accordingly. So here's the fix:

If you use MB that is compiled as a parallel version it is set to run 2 runs by default. In this case, when specifying sumt do NOT include the .t in the file name as MB will add .run1.t / .run2.t and so on. When recalling the tree file MB cannot find the file if you already specified .t as the file ending.

The sump command was ok (I could open the .p files in Tracer) but for continuity reasons I left it out now and is seems to be ok.

Looks like I had a blond moment after all!

Take care, Birgit

On 21/5/09 15:16, "Birgit Meldal" <bhmm2@medschl.cam.ac.uk> wrote:

Dear colleagues,

I am having trouble getting MrBayes saving the consensus file from the sumt command. There is no indication that it shouldn't work automatically, however...

I found a similar posting in the archives where it was pointed out that it was due to compiling it as a 64-bit binary. I don't compile my own program as it is running on the bioinfomatics server. I would be surprised no-one else has this problem as I know MrBayes is very well used on the server. It used to work at my former institution in an older version but not now.

If anyone can enlighten me so I can save time but not doing it manually in PAUP that would be greatly appreciated!

With kind regards,

Birgit

PS: Maybe I am just having a blond moment...

Birgit Meldal, Ph.D. Division of Transfusion Medicine Department of Haematology University of Cambridge NHS Blood & Transplant, Cambridge Centre Long Road Cambridge CB2 0PT U.K.

+44 1223 548049 bhmm2@cam.ac.uk

MrBayes consensus trees

Dear colleagues,

I am having trouble getting MrBayes saving the consensus file from the sumt command. There is no indication that it shouldn't work automatically, however...

I found a similar posting in the archives where it was pointed out that it was due to compiling it as a 64-bit binary. I don't compile my own program as it is running on the bioinfomatics server. I would be surprised no-one else has this problem as I know MrBayes is very well used on the server. It used to work at my former institution in an older version but not now.

If anyone can enlighten me so I can save time but not doing it manually in PAUP that would be greatly appreciated!

With kind regards,

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Birgit Meldal, Ph.D. Division of Transfusion Medicine Department of Haematology University of Cambridge NHS Blood & Transplant, Cambridge Centre Long Road Cambridge CB2 0PT U.K.

+44 1223 548049 bhmm2@cam.ac.uk

Birgit Meldal <bhmm2@medschl.cam.ac.uk>

MrBayes question

Has anyone encountered the following problem with entering text in mrbayes (vers 31.2): After entering (or pasting) about 2.5 lines to define a usertree, I'm prevented from continuing. Not sure what is going on. Program does work with fewer taxa (one line or less). Suggestions? Thanks, Bill Chapco.

Dr. William Chapco Professor Emeritus Department of Biology University of Regina Regina, SK, S4S 0A2 Canada 306-585-4478 306-337-2410 (FAX) chapco@uregina.ca

William.Chapco@uregina.ca

Phil Theory Biology

Dear Colleagues,

Philosophy & Theory in Biology (P&TB) is a new peer-reviewed open- access online journal to be launched in the Fall of 2009, and it aims to bring together philosophers of science and theoretically inclined biologists in order to interact across disciplinary boundaries. The goal of this interaction is to foster a broader conception of what it means to do theory in science and philosophically analyze the sciences, in order to benefit both research communities.

P&TB is for a mixed audience of philosophers of science and biologists, and therefore we seek papers that are methodologically diverse, including but not limited to standard philosophy of biology analyses of concepts or research programs and theoretical papers by biologists. P&TB also publishes select, in-depth reviews and trend articles pertinent to theoretical biology and philosophy of biology in order to stimulate discussion on topics with implications for both biologists and philosophers.

P&TB strives to maintain the highest standards of scholarship while simultaneously making its papers available at no cost to the academic community, independent scholars, and the public at large. P&TB is published only online, a choice that springs from the advantages offered by new technologies and from a desire to reduce publication and environmental costs.

The editorial board consists of a highly distinguished group of philosophers and biologists, including: Alex Badyaev (University of Arizona), John Beatty (University of British Columbia), Carol Cleland (University of Colorado), Deborah Gordon (Stanford University), Paul Griffiths (University of Sydney), Eva Jablonka (Tel Aviv University), David Jablonski (University of Chicago), Elizabeth Lloyd (Indiana University), Jay Odenbaugh (Lewis & Clark College), Samir Okasha (University of Bristol), Anya Plutynski (University of Utah), Sean Rice (Texas Tech University), Elliott Sober (University of Wisconsin), Mike Wade (Indiana University), Gunter Wagner (Yale University) and Mary Jane West-Eberhard (Smithsonian Institution, Panama).

Instruction for authors can be downloaded on the provisional web site of the journal, at www.philosophyandtheoryinbiology.org. Further information can be obtained by writing an email to editors@philosophyandtheoryinbiology.org .

Sincerely, the Editors Massimo Pigliucci (City University of New York) Jonathan Kaplan (Oregon State University) Alan Love (University of Minnesota) Joan Roughgarden (Stanford University)

Massimo Pigliucci www.rationallyspeaking.org "I find television very educational. Every time someone switches it on I go into another room and read a good book." -Groucho Marx

Phylogenetic Handbook

Dear Colleagues,

A second edition of the Phylogenetic Handbook has been published by Cambridge University Press. The book aims at providing a comprehensive introduction to theory and practice of nucleotide and protein phylogenetic analysis. This second edition includes many new chapters and has a stronger focus on hypothesis testing than the previous edition. Many analysis tools are described by their original authors (including MrBAYES, PAUP*, BEAST, HYPHY, RDP3, LAMARC, DAMBE, CLUSTAL, TREE-PUZZLE, IQPNNI, MODELTEST, etc..)

More information, Links to software, data sets, contributors and table of contents can be found at: http://www.thephylogenetichandbook.org We hope that the book will be a useful teaching guide for advanced-level undergraduate and graduate students.

Sincerely, Philippe Lemey Rega Institute, K.U. Leuven Leuven, Belgium

philippe.lemey@gmail.com philippe.lemey@gmail.com

Program for haplotypes answers

Hello,

A few days ago I posted a message asking for help with a program that would estimate or determine individual haplotypes (i.e., gametic phase) from a set of direct sequences of heterozygote individuals.

Thank you so much to those of you who took the time to reply, particularly to those friends who went out of their way to highlight potential problems and alternatives, BTW I will reply personally :^)#. I have compiled excerpts for the suggested programs below for the benefit of the community.

Thanx again and cheers!

Axa

ABOUT PHASE AND fastPHASE

From: John C Garza [mailto:carlosjg@ucsc.edu]

PHASE by Matt Stephens (University of Chicago) is the best program for determining the population frequencies of haplotypes and therefore determining the most likely phase of heterozygous sequences. However, it (and all other phasing algorithms) can run into trouble with MHC, since there is so much gene conversion/recombination.

In what species are you are studying MHC? How we minimize sequencing is by using SSCP with Sybr Gold staining to determine mobility patterns for select sequenced alleles, then do population genetic screening with SSCP.

From: Darren Obbard [mailto:dobbard@staffmail.ed.ac.uk]

phase and fastPhase from Mathew Stephens

http://stephenslab.uchicago.edu/software.html Are both widely used, and trusted.

From: Magdalena Zarowiecki [mailto:m.zarowiecki@nhm.ac.uk]

I've been spending a lot of time with this problem.

The most commonly used software is PHASE, but it doesn't work for my dataset, as it is too big (300 taxa, 80 variable characters.) Instead I've been using fastPHASE, it is available for Mac, PC and Linux, but I only ever got the Linux version to work. I have also used the ELB algorithm in Arlequin, and a new software called BEAGLE, all of which are relatively hassle-free.

You can convert your data to PHASE/fastPHASE input on this website:

http://www.mnhn.fr/jfflot/seqphase/ There is a nice paper that came out last year that compares several different phase-solving algorithms, and also suggests a method for solving a problem just like yours, complete with some useful PERL-scripts.

From: Michael Sorenson [mailto:msoren@bu.edu]

Not sure how well the software will work on MHC, but please see the following paper for a favorable evaluation of PHASE:

Harrigan, R.J., M.E. Mazza & M.D. Sorenson. 2008. Computation versus cloning: evaluation of two methods for haplotype determination. Molecular Ecology Resources 8: 1239-1248.

ABOUT DNAsp/PHASE

From: Mark Chapman [mailto:mchapman@plantbio.uga.edu]

The PHASE algorithm in DnaSP will do this. you make a fasta file of your (aligned) genotypes and open it as "unphase/genotype data file". I have come across some alignments that it cant handle for whatever reason and the program crashes, but this is only maybe 5% of the time and is probably due to very few homozygous genotypes. Each file takes 1 minute to 1 hour to run typically, so it can be frustrating to do this several times. A significant advantage is that once this has been done in DnaSP you can export several filetypes, like nexus, to use in other programs.

See our Plant Cell paper for a little more info (http://markachapman.googlepages.com/ChapmanPlantCell2008.pdf).

From: John Wares [mailto:jpwares@uga.edu]

You can use software like PHASE - it is currently fully implemented in DNAsp, which makes life MUCH easier than only a few months ago when you had to know or use a little PERL to get data in and out for analysis. It is a likelihood-based analysis that considers the frequency of homozygous alleles at each site as well as the combinations of alleles to infer haplotypes directly from sequences.

So, that is the easy answer to your question. The thing I'm worried about with doing this for MHC data is that probably every individual is a heterozygote, so there will be no non-statistical inference of haplotypes, and they are all heterozygotes because MHC harbors so many alleles - maybe hundreds, right? Depends on what you are working on these days but even devil's hole pupfish carries a ton of diversity.

PHASE software works great when you can count the number of segregating sites on your hands, but I think you are going to have a great deal of uncertainty once you cross that threshold. Plus, there is the issue of what is a heterozygous site - we all know that sequencing is usually pretty clean, but probably a few sites - even in haploid mtDNA - that are ambiguous. You would want to sequence in both directions to eliminate most of the sequencing/coding errors, and maybe multiple sequences per individual, because each of those chemistry errors (not actual heterozygous sites) will be used by PHASE

— / —

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

Secondary structure phylogeny

Hello everyone,

I am trying to reconstruct phylogeny using secondary structure of a segment of 28s rDNA in arthropods. Since now I have used 4SALE and CBCanalyser software, but it seems that there is something wrong, cause the cladogram is match different from the cladogram made with the sequences.any ideas of other software packages or anything relative? on the other hand, do you think I could use the structures in other way???is there any software to compare sec.structures?

Thanks! PS: please send your replies at martimianakis@gmail.com , cause I have a few problems with this mailbox.

Stefanos Martimianakis PhD Student Dep. of Biology Sec. of Genetics University of Patras Greece email: martimianakis@gmail.com

stmartim@upatras.gr

Short movies about evolution

Dear members of the Evoldir community,

At http://www.evolution-of-life.com you will find three short (<10 min) movies about evolution / evolutionary research. The movies are the result of a project by Yannick Mahe and myself.

One animation movie is about the evolution of life, one animation movie about life and work of Darwin and one video documentary about coevolution between army ants and myrmecophiles. Four more movies will follow (topics: drug resistance in bacteria, evolution in the lab, lactase persistence and shrinking cod).

The movies are meant for a general audience, but certainly evolutionary biologists will also enjoy them. Great care was taken to make them scientifically correct.

The movies are / will be available in English, German and French. The can be viewed online or downloaded. You are free to show them in lectures, at your local Darwin-year-event or elsewhere. For the exact terms of use, please check the website.

We'd be happy to get feedback. Especially if you are showing the movie to schoolchildren, students or a general audience, we'd love to know about it.

Best wishes, Pleuni Pennings

–

Pleuni S. Pennings PhD

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

* Postdoc in theoretical evolutionary biology

http://www.eeslmu.de/eeswiki/Pleuni_Pennings pennings@zi.lmu.de

pennings@zi.biologie.uni-muenchen.de

Short movies about evolution 2

Dear friends,

I am teaching evolution in a Brazilian University in a place with many creationist students. Thats why sometimes my classes are exausting because I need not just to teach but also try to open some minds! Movies are terrific for this task and then.... congratulations for the Munich team!

After seeing the videos I would like to share some ideas:

1 - The Darwins and the Origin of life videos dont have subtitles. Please include the subtitles! This is very important for teachers in not english countries. This is not a detail but a VERY important tool to improve the concepts understanding. I know there are a rtf file with subtitles but this is not enough because videos like that will be copied and passed to another people by internet and many of them cannot understand english but they can read and have the big picture.

3 - In the ants video the interactions are more discussed

than the ORIGIN of the chemicals and behaviours. If not possible in the video I suggest to include a text in the website asking the people to think about the PROCESS and not ony the PATTERN. Those adaptions came from VARIATION, MUTATION, and after that NATURAL SELECTION. They cannot just happen!

An important final comentary, if this videos are intented to be used for education the approach is very especific; we need to be focused on HOW the information is passed!

Jus as an idea..... maybe I can translate the texts (subtitles) for Brazilian Portuguese and other people could do the same for chinese, japanese, etc. These translations could be available in the website.

Thanks again for the material and I will use them in several classes and courses!

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamiferos (ECOMAM) UNITAU, Depto. Biologia, Taubate, SP. 12030-010. * Grupo de pesquisa ECOMAM: http://jcvoltol.sites.uol.com.br/ * Fotos de projetos e cursos: http://jcvoltol.fotoblog.uol.com.br/ * Exemplo de um curso de ecologia de campo: http://trabiju.blogspot.com/ * Fotos artisticas: http://voltolini.fotos.net.br/texturas —– Original Message —– From: <evoldir@evol.biology.mcmaster.ca>

To: <jcvoltol@uol.com.br>

Sent: Sunday, May 17, 2009 2:51 AM

Subject: Other: short movies about evolution

Dear members of the Evoldir community,

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One animation movie is about the evolution of life, one animation movie about life and work of Darwin and one video documentary about coevolution between army ants and myrmecophiles. Four more movies will follow (topics: drug resistance in bacteria, evolution in the lab, lactase persistence and shrinking cod).

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We'd be happy to get feedback. Especially if you are showing the movie to schoolchildren, students or a general audience, we'd love to know about it.

Best wishes, Pleuni Pennings

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Pleuni S. Pennings PhD

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

* Postdoc in theoretical evolutionary biology

http://www.eeslmu.de/eeswiki/Pleuni_Pennings pennings@zi.lmu.de

pennings@zi.biologie.uni-muenchen.de

jcvoltol@uol.com.br

Skull morphology data sets

Dear friends,

On week ago I sent a message requesting data sets on hominid skulls or dinosaur morphology to use in my stats classes.

Several people wrote requesting also a copy but... sorry guys; nobody sent me any material.

The quest continues....

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamiferos (ECOMAM) UNITAU, Depto. Biologia, Taubate, SP. 12030-010. * Grupo de pesquisa ECOMAM: http://jcvoltol.sites.uol.com.br/ * Fotos de projetos e cursos: http://jcvoltol.fotoblog.uol.com.br/ * Exemplo de um curso de ecologia de campo: http://trabiju.blogspot.com/ * Fotos artisticas: http://voltolini.fotos.net.br/texturas jcvoltol@uol.com.br

Software FastTree1 1

We announce an update to FastTree, a tool for inferring minimum-evolution trees for large alignments.

New in FastTree 1.1:

* FastTree 1.1 uses nearest-neighbor interchanges and subtree-prune-regraft moves to improve accuracy above

distance-matrix methods such as neighbor joining, BIONJ, or FastME. * FastTree 1.1 is even faster: it inferred a tree for 158,000 16S rRNAs in just 11 hours and 2.5 GB. * Pseudocounts improve accuracy for alignments with many truncated sequences. * Fast tools for comparing large trees. * Fast-global bootstrap – analyze 40,000 ABC transporters with 100 bootstraps in just 20 hours, by using the tree for the full alignment as the starting topology for the resampled alignments.

http://www.microbesonline.org/fasttree/ Reference: Price, M.N., Dehal, P.S., and Arkin, A.P. (2009) FastTree: Computing Large Minimum-Evolution Trees \ with Profiles instead of a Distance Matrix. Molecular Biology and Evolution, to appear. http://mbe.oxfordjournals.org/cgi/content/abstract/-msp077?ijkey=DtzbXulQ86zzROU&keytype=ref morgannprice@yahoo.com

Software GenGIS 1 0

Hi everyone,

We have recently released the first full version of GenGIS, a geospatial information system for genetic and genomic data. GenGIS allows the integration of digital maps, sequence information, and trees to build 2D and 3D geophylogenies, and show similarity-based clustering of georeferenced samples.

The software includes a Python console that allows the user to script data analyses and video flythroughs, and hooks into the R statistical language allowing exposed data to be passed directly into R.

GenGIS is extensively documented, with tutorial movies and examples. It is available for Win32 and Mac OSX (tested on Leopard). We are also in the process of using GenGIS to track data from the emerging H1N1 outbreak. Classical examples include the salamander 'ring species' Ensatina eschscholtzii, and Banza katydids from the Hawai'i archipelago.

Main GenGIS page: http://kiwi.cs.dal.ca/GenGIS/-Main_Page Documentation including tutorials: http:/-/kiwi.cs.dal.ca/GenGIS/Documentation H1N1 page: http://kiwi.cs.dal.ca/GenGIS/H1N1 Best wishes, Rob Beiko Faculty of Computer Science, Dalhousie University beiko@cs.dal.ca

TeX LaTeX templates for MBE available

25 May 2009

Dear Folks!

Improved .cls and .bst files for preparing manuscripts for submission to Molecular Biology and Evolution using TeX or LaTeX are now available on the MBE website:

http://www.oxfordjournals.org/our_journals/molbev/-for_authors/msprep_submission.html See you at the SMBE meetings in Iowa City next week!

All the best, Marcy Uyenoyama Editor, Molecular Biology and Evolution

marcy@duke.edu marcy@duke.edu

Tree construction

Dear Evoldirs,

Recently, I am trying to identify the best estimated tree using 10 nuclear DNA intronicsequences. As you might know,each nuclear gene might have different evolutionary rate. I've seen many papers dealing constructing tree by combined nuclear DNA dataset. My question isif it is the best to estimate the tree usingmany nuclear DNAmarkers which has different evolutionary rate. How aboutis the case for mitochondrialgenome? Some use several mtDNA fragments andotheruse complete mtDNA. In mt genome, 13 coding genes, several rRNA, tRNA, andcontrol region are present. If you useonly 2~3 selected mtDNA markers todraw tree, would it tell you the same treewith the onedrawn fromcomplete mtDNA? Are there different evolutionary rate for eachgenes of mtDNA as well? How different are they? Are there good references to read?

Please let me know.

Best Junghwa AN

An Junghwa <junghwa_an@yahoo.fr>

Unifying Biology paper 1992

Dear all,

I wasn't able to get a pdf file of Vassiliki Smocovitis paper Unifying Biology: The Evolutionary Synthesis and Evolutionary Biology, published in the Journal of the History of Biology, 25(1) 1 - 65, 1992. I would like to get this paper to discuss with my students (I have a printed version). If someone could send me one pdf file I would appreciate very much. Many thanks.

Aldo Mellender de Araújo aldomel@portoweb.com.br Departamento de Genética, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brasil

Wanted MultiblockSystem software

Dear Evoldir members

our laboratory has lost the PC CD-rom for the oldish program "Multiblock System version 2.09". This is needed to run Thermo Hybaid PRC machines. The manufacturer claims the program is not available anymore. Does anyone have an idea how to get a copy of this program or another version of it?

Thank you for any tips! e-mail: Kalevi.Trontti((at))helsinki.fi

best wishes,

Kalevi Trontti Coordinator, PhD Laboratory of Molecular Ecology and Systematics Department of Biological and Environmental Sciences P.O. Box 65 (Viikinkaari 1) 00014 University of Helsinki, Finland

Tel: +358(0)9-191 57680 Fax: +358(0)9 191 57694 Mobile: +358(0)40-350 0882

Kalevi Trontti <kalevi.trontti@helsinki.fi>

Web resource EvolverZone

I am pleased to announce the launch of Evolver Zone, a web resource with multimedia and information about databases, journals, societies, software, and web links related to evolution. The collection is meant to be of use to teachers, students, and researchers interested in evolutionary biology. The site is free to access.

http://www.evolverzone.com/ Cheers,

- Ryan Gregory

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

http://www.gregorylab.org/ "T. Ryan Gregory" <rgregory@uoguelph.ca>

PostDocs

CSIRO Australia BeetleEvolution

https://recruitment.csiro.au/asp/-Job_Details.asp?RefNo=2009%2F244 We are seeking an enthusiastic, innovative and highly independent scientist with broad based experience in insect systematics, molecular phylogenetics, and molecular dating methods. Skills and experience in beetle systematics or identification and with insect fossils and/or the insect fossil literature will be highly desirable. Applicants will have completed a PhD in a related discipline and be willing to partake in CSIROs Postdoctoral training program.

The successful applicant will be an early career scientist with (i) a good knowledge of insect systematics and molecular phylogenetics, (ii) excellent communication, personal, and inter-personal skills; and (iii) a documented record of publishing papers in international, peer-reviewed journals. You will be expected to be strongly self-motivated and able to work collaboratively as well as independently on a variety of projects; hence, being able to multi task is high desirable. If successful, you will join the molecular systematics and beetle systematics groups within the ANIC to conduct research into the evolution of Australias beetle fauna. Beetles are the single most diverse animal group both in terms of species numbers but also in terms of life history strategies including highly speciose groups of herbivores, carnivores, fungivores, saprivores, parasitoids. By determining the relationships and divergence times for Australian beetle groups you will develop snap-shots of the evolution of Australias biota across the last 35 million years and how this fauna has responded to floral evolution and climate change.

CSIRO is Australias leading research organisation with over 6,500 staff located across the country. Its aim is to deliver great science and innovative solutions for industry, society and the environment by igniting the creative spirit of its staff. The ANIC is the largest collection of insects in Australia and has the largest research program in insect taxonomy, systematics and evolution.

The OCE Fellowship is a prestigious early career fellowship funded through the Office of the Chief Executive of CSIRO and is available for a maximum of 3 years. These highly competitive fellowships are available to candidates with less than 3 years postdoctoral experience.

Please Note: CSIRO uses some extremely opaque HR-speak to phrase selection criteria which are part of the application process. If you require any explanation as to what they are actually on about please dont hesitate to email or call me.

Details and online application:

https://recruitment.csiro.au/asp/-Job_Details.asp?RefNo=2009%2F244 Stephen Cameron

Senior Research Scientist,

ANIC & CSIRO Entomology,

Black Mountain Laboratories,

Clunies-Ross St, Canberra, ACT, 2601,

AUSTRALIA

ph: +612 6246 4084

fax: +612 6246 4264

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website: http://www.csiro.au/people/-Stephen.Cameron.html seago@nature.berkeley.edu seago@nature.berkeley.edu

EAWAG Switzerland CichlidEvolution

Postdoctoral Position in Comparative Analysis of Cichlid Fish Radiations

A postdoctoral research associate position is available in the labs of Ole Seehausen (http://www.fishecology.ch) at Eawag, Switzerland and Luke Harmon (http://www.webpages.uidaho.edu/˜lukeh/) at University of Idaho to investigate pattern and process of adaptive radiation in cichlid fish.

We are interested in what facilitates or constrains the origin of species diversity. Cichlid fish are an ideal system to address this. They are a wide spread family of freshwater fish and have made many independent adaptive radiations in tropical lakes. Lakes Victoria, Malawi and Tanganyika are well known, but many others are less well known. The Seehausen Lab has collated genetic and phenotypic data on various cichlid fish radiations. The Harmon lab has developed quantitative concepts and analysis tools for investigating adaptive radiations.

The Postdoctoral researcher will engage in phylogenetic and phenotypic analyses, and use comparative analysis tools to address questions about phylogenetic inertia, temporal trends in adaptive radiations, and predictions of neutral and non-neutral models of diversification. The Postdoctoral researcher will be located mainly at the Eawag Centre of Ecology, Evolution & Biogeochemistry in Switzerland, with shorter stays at the University of Idaho.

Candidates have a thorough background in evolutionary biology, and are familiar with sequence-based phylogenetic analysis. Preference will be given to candidates familiar with the R environment and possessing either knowledge of comparative methodology or of African cichlid fish. Funding is available for 10-12 months, depending on the starting date, with a possibility for continuation dependent upon performance. Given the availability of data and analysis tools, we expect the project will quickly begin to generate results. A start date of August 1 2009 or a mutually agreeable date in late Summer 2009 is strongly preferred. Salary will be commensurate with experience and qualifications.

Send a letter of application, curriculum vitae, and names and addresses of three references to ole.seehausen@eawag.ch

Ole Seehausen (http://www.fishecology.ch) University of Bern, Institute of Ecology & Evolution, & Eawag Centre of Ecology, Evolution and Biogeochemistry (CEEB), Switzerland

Luke Harmon (http://www.webpages.uidaho.edu/˜lukeh/) University of Idaho Department of Biological Sciences

Ole Seehausen Institute of Ecology & Evolution (IEE) University of Bern Baltzerstr. 6, CH-3012 Bern Phone direct +41 31 631 31 31 Phone secr. +41 31 631 30 09 FAX +41 31 631 30 08 & eawag Centre of Ecology, Evolution and Biogeochemistry (CEEB) Seestrasse 79 CH-6047 Kastanienbaum Phone direct +41 41 349 21 21 Phone secr +41 41 349 21 08 FAX +41 41 349 21 68

http://www.fishecology.ch "Seehausen, Ole" <Ole.Seehausen@eawag.ch>

IowaStateU PlantInsectInteractions

Postdoctoral Research Associate Department of Entomology Iowa State University

Available 1 June, 2009

Position Summary: Postdoctoral position studying plant-insect and tritrophic interactions among Bt crops, pest insects, and entomopathogens.

Duties and responsibilities –Work as part of a team to accomplish research goals –Run large-scale field experiments and laboratory bioassays, and assist students participating in these experiments –Prepare manuscripts for publication –Assist with grant writing –Consult with principal investigator, technical personnel and other researchers to improve design of experiments and interpretation of results

Minimum qualifications –Ph.D. in Entomology, Biology, or Ecology and Evolution –Demonstrated ability to publish results in refereed journals –Ability to work independently

Preferred qualifications –Knowledge of population genetics –Knowledge of insect resistance to insecticides or transgenics –Experience designing and conducting field and laboratory experiments –Experience studying entomopathogenic organisms

To apply, send a letter of application, curriculum vitae, reprints of 2 papers, and the names and contract information for three references to Aaron Gassmann (aaronjg@iastate.edu). Although electronic applications are preferred, application materials may also be mailed to, Dept. of Entomology, 110 Insectary Bldg., Iowa State University, Ames, IA 50011

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

Aaron Gassmann Assistant Professor Department of Entomology 18 Insectary Bldg. Iowa State University Ames, IA 50011-3140 Office: 515-294-7623 Lab: 515-294-8675 FAX: 515-294-7406

KansasStateU ComparativeProteomics

Research Associate: Comparative proteomics and speciation at Kansas State University

A postdoc position is available in the laboratory of Dr. Jeremy L. Marshall to work on the NSF-funded project, The genetics of postmating, prezygotic isolation. This project focuses on using cutting-edge proteomic, genomic, and gene-silencing technology to identify the ejaculate proteins in the ground cricket (Allonemobius socius complex) that influence conspecific sperm precedence and other fertilization/reproductive traits.

The three species (A. socius, A. fasciatus, and A sp. nov. Tex) in the Allonemobius socius complex diverged from a common ancestor ˜30,000 years ago and are only isolated from one another by postmating, prezygotic traits (such as conspecific sperm precedence and the ability of males to induce females to lay eggs). These reproductive barriers to gene flow are strong and maintained in zones of secondary contact. Therefore, the main objective of this research is to identify ejaculate proteins that are divergent between species, remain species-specific in zones of secondary contact, and functionally influence the degree of reproductive isolation between species.

The responsibilities of the postdoc will include, but are not limited to, basic statistical analyses, learning and conducting proteomic techniques to identify ejaculate proteins, conducting molecular work such as PCR, cloning, cDNA synthesis, dsRNA synthesis, and overseeing/conducting mating and behavior experiments to test for protein functions. There are also ample opportunities for developing independent projects within this system.

Required qualifications: (1) A Ph.D. in evolutionary biology, molecular biology, biology, or a related field. (2) Experience with basic molecular techniques such as PCR and cloning or a strong background in proteomics. (3) Strong interest in evolutionary genetics and evolutionary biology, as evidenced by dissertation research, publications, and/or previous postdoc experience.

To apply, send the below items as a single PDF to Dr. Jeremy L. Marshall at cricket@ksu.edu

(1) Send a cover letter summarizing your research interests and background as well as a statement on your career goals. (2) A recent CV, including the names and contact information of three persons that I may contact for reference letters and/or more information about you.

Review of applications will begin immediately and continue until the position is filled or closed. Salary and benefits are competitive and have the potential to be renewed for 2 or 3 years. Ph.D. degree must be completed by start date. Kansas State University is an equal opportunity employer.

Dr. Jeremy L. Marshall Department of Entomology Kansas State University Manhattan, KS 66506 cricket@ksu.edu

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KansasStateU PlantEvolutionaryGenet

POST-DOCTORAL POSITION AVAILABLE TO STUDY EVOLUTIONARY GENETICS IN PLANTS

A postdoctoral position is currently available in the laboratory of Mark Ungerer at Kansas State University in the Division of Biology. The successful candidate will contribute to ongoing research investigating the possible causes and evolutionary consequences of massive retrotransposon proliferations that have occurred independently in the genomes of three hybrid sunflower species. Specific responsibilities of the postdoctoral researcher will include oversight of one or more major subprojects that examine the impacts of retrotransposon proliferation on genome function and structure and the environmental and genomic conditions under which such proliferation events take place. The position will require both laboratory and greenhouse work as well as seasonal trips to the southwestern US to collect from natural populations and natural hybrid zones. Candidates must have strong molecular biology skills (including experience working with RNA) and/or interest in the fields of molecular and genome evolution.

To apply, send a cover letter describing your research interests/past research achievements, a C.V., and the names and contact information for three individuals willing to provide letters of recommendation. Materials should be sent to the address below. Review of applications will begin on May 25, 2009 and continue until the position has been filled. Ph.D. degree must be completed by start date. Email applications preferred. KSU is an equal opportunity employer and actively seeks diversity among its employees. Background check required by university policy.

Mark Ungerer Division of Biology Kansas State University Manhattan KS 66506 mcungere@ksu.edu office: 785.532.5845 fax: 785.532.6653

mcungere@ksu.edu mcungere@ksu.edu

KansasStateU SpeciationGenetics

Hi all,

If you are interested in this postdoc position (see ad below) and attending this year's SMBE meeting in Iowa City, I would welcome the opportunity to meet with you. I will be presenting a contributed talk on the below research as part of the Reproductive Protein Function and Evolution Symposium on Friday, June 5, at 4:45. If you would like to discuss this postdoc opportunity with me at this meeting, please feel free to contact me via e-mail to set up a meeting (please e-mail me at the following two addresses: cricket@ksu.edu and the.marshalls@sbcglobal.net) or stop me at any time during the meetings.

Best, Jeremy

P.S. The ad is below.

Jeremy L. Marshall, Ph.D.

Assistant Professor Department of Entomology 123 W. Waters Hall Kansas State University Manhattan, KS 66506-4004

E-mail: cricket@ksu.edu

Office Phone: 785-532-5588 Fax : 785-532-6232

AD: Postdoc: Comparative proteomics and speciation at Kansas State University

A postdoc position is available (to start anytime between now and Fall 2010) in the laboratory of Dr. Jeremy L. Marshall to work on the NSF-funded project, The genetics of postmating, prezygotic isolation. This project focuses on using cutting-edge proteomic, genomic, and gene-silencing technology to identify the ejaculate proteins in the ground cricket (Allonemobius socius complex) that influence conspecific sperm precedence and other fertilization/ reproductive traits. The three species (A. socius, A. fasciatus, and A sp. nov. Tex) in the Allonemobius socius complex diverged from a common ancestor ˜30,000 years ago and are only isolated from one another by postmating, prezygotic traits (such as conspecific sperm precedence and the ability of males to induce females to lay eggs). These reproductive barriers to gene flow are strong and maintained in zones of secondary contact. Therefore, the main objective of this research is to identify ejaculate proteins that are divergent between species, remain species-specific in zones of secondary contact, and functionally influence the degree of reproductive isolation between species.

The responsibilities of the postdoc will include, but are not limited to, basic statistical analyses, learning and conducting proteomic techniques to identify ejaculate proteins, conducting molecular work such as PCR, cloning, cDNA synthesis, dsRNA synthesis, and overseeing/conducting mating and behavior experiments to test for protein functions. There are also ample opportunities for developing independent projects within this system.

Required qualifications: (1) A Ph.D. in evolutionary biology, molecular biology, biology, or a related field. (2) Experience with basic molecular techniques such as PCR and cloning or a strong background in proteomics. (3) Strong interest in evolutionary genetics and evolutionary biology, as evidenced by dissertation research, publications, and/or previous postdoc experience.

To apply, send the below items via e-mail to Dr. Jeremy L. Marshall at cricket@ksu.edu

(1) Send a cover letter summarizing your research interests and background as well as a statement on your career goals. (2) A recent CV, including the names and contact information of three persons that I may contact for reference letters and/or more information about you.

Review of applications will begin immediately and continue until the position is filled or closed. The successful candidate may begin immediately or anytime between now and Fall 2010. Salary and benefits are competitive and have the potential to be renewed for 2 or 3 years. Ph.D. degree must be completed by start date. Kansas State University is an equal opportunity employer.

Dr. Jeremy L. Marshall Department of Entomology Kansas State University Manhattan, KS 66506 cricket@ksu.edu

LaurentianU MinkPopulationGenetics

Post-Doctoral Opportunity in Population Genetics of Domestic and Wild Mink American mink (Neovison vison) have been domesticated for >100 years to supply the fur industry. Although much is known about the effects of escaped domestic mink in Europe and South America where it is an exotic species, little is known about these effects in North America where American mink are native. We have described a decline in American mink across Canada that is associated with the presence of mink farms. In addition, we have documented a large proportion (>50%) of mink in free-ranging populations in Ontario are escaped domestic mink, or hybrids. As part of a NSERC Strategic Grant, we are seeking a Post-Doctoral Fellow to continue our studies in Ontario, and to examine free-ranging populations in Nova Scotia for evidence of escaped domestic mink and wild-domestic hybrids. Nova Scotia has one of the highest mink farm densities in Canada. The candidate will be part of a group of researchers and students at Laurentian University, Trent University and the Ontario Ministry of Natural Resources that are additionally examining the potential spread of a parvovirus (Aleutian disease) from mink farms into wild mink populations, as well as the effects of sexual selection on hybridization between wild and domestic mink. We are especially looking for candidates with expertise in genetic techniques and population genetic analysis. Interested candidates should send a copy of their CV and the names of two referees to Dr. Albrecht Schulte-Hostedde (aschultehostedde@laurentian.ca) and Dr. Jeff Bowman (jeff.bowman@ontario.ca). Applications will be accepted until July 31st, 2009 or until a suitable candidate has been identified.

Albrecht I. Schulte-Hostedde, PhD Associate Professor

Director - Wildlife Research Station (http://www.uoguelph.ca/ ~ wrs/) Department of Biology Laurentian University Sudbury, Ontario, Canada P3E 2C6 aschultehostedde@laurentian.ca (705) 675-1151 x2356 http://laurentian.ca/biology/aschultehostedde Albrecht Schulte-Hostedde <aschultehostedde@laurentian.ca>

MichiganStateU EvolutionInvasions

Post-doctoral Position in Evolutionary Ecology of Biological Invasions

I am searching for a creative, motivated post-doc to work on an NSF-funded project on the evolutionary ecology of biological invasions. The proposed research applies community genetics to the study of biological invasions to investigate how genetic variation in both exotic and native community members influences the outcome of biological invasions and to test the hypothesis that the ?match? between the traits of the invading genotypes and the novel environment determines invasion success. Goals of the project include: 1) Identifying how genetic variation in both native and exotic species impact the invasion process; 2) Assessing genotype-by-genotype interactions in a pair of strongly interacting species, and 3) Investigating how environmental variation influences the outcomes of genotype-by-genotype interactions. For more details on research conducted in the Lau lab see https://www.msu.edu/~jenlau/index.html. The primary responsibility of the post-doc will be to implement experiments, analyze data, and prepare manuscripts. The post-doc will be housed at Michigan State University?s Kellogg Biological Station (http://www.kbs.msu.edu/[1]) in Hickory Corners, Michigan, but the position requires field work in California for several weeks each year.

Applicants must have (or nearly so) a Ph.D. in Ecology, Evolution, Plant Biology or a related field, and should have experience performing large manipulative field and/or greenhouse experiments, analyzing data, and completing manuscripts. Two years of funding are available. Start date is flexible, but Fall 2009 is preferable. Interested parties should email a cover letter explaining why they are interested in the position, a CV, and a brief statement of research interests to jenlau@msu.edu. Evaluation of applications will begin 28 May 2009 and continue until the position has been filled.

Jennifer Lau Assistant Professor Kellogg Biological Station and Dept. of Plant Biology Michigan State University jenlau@msu.edu phone: 269-671-2107 fax: 269-671-2104

[1] http://www.kbs.msu.edu/ jenlau@msu.edu

Munich EvolutionaryBiology

Dear all,

With this e-mail I would like to encourage PhD students and postdocs in the field of evolution, ecology and systematics to consider coming to the University of Munich to do a postdoc. Munich has a very lively community of researchers working on a wide range of topics in evolution, ecology and systematics. We have Master and PhD students from all over the world. See http://www.eeslmu.de/eeswiki Next to the "standard" options (Marie Curie, HFSP, Humboldt) it is possible to apply for postdoc funding at the Volkswagen Foundation. This foundation currently funds projects in the field of evolutionary biology. So if you have an idea for a research project which you would like to do in Munich and which has an evolutionary focus, this funding option may be of interest to you. The next deadline is the 15th of October 2009 (see http://www.volkswagenstiftung.de/funding/thematic-impetus/evolutionary-biology.html?L=1)

For an overview of who works on what in Munich, see the EES website http://www.eeslmu.de/eeswiki/EES_people . If you are considering applying for a Volkswagen Foundation fellowship, please contact the person you would like to work with. Alternatively, you can contact me first (Pleuni Pennings, pennings@lmu.de).

Best wishes, Pleuni Pennings

–

Pleuni S. Pennings

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

* Postdoc in theoretical evolutionary biology

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

Tel: 0049 89 2180 74 234 http://www.eeslmu.de/eeswiki/Pleuni_Pennings pennings@lmu.de

pennings@zi.biologie.uni-muenchen.de

QueenMaryU EvolutionaryBiol

Details of several postdoctoral projects at Queen Mary University of London are advertised at on this site http://www.sbcs.qmul.ac.uk/research/postdoc_projects.shtml The subset with a particularly evolutionary/genetics flavour are â Theoretical and Empirical Studies of Human Cultural Evolution â The statistical analysis of spatial genetic data â Social learning across species boundaries â How fast should colour vision be? An electrophysiological study of the early visual system â Human sexual orientation â Plant cytogenetics and genome evolution â Comparative physiology and evolution of neuropeptide signalling systems â Neurobiology, neuropathology and evolution of endocannabinoid signalling â Computational analysis of the evolution of conserved vertebrate cis- regulatory elements â Functional analysis of vertebrate regulatory elements in the developing embryo â Evolutionary changes in arthropod neurogenesis â Using genomic data to study the evolutionary dynamics of duplicate genes â Developing new approaches to phylogenomics â Research in crossmodal cognition â Two-component regulatory systems in chloroplasts â Genetics of metal metabolism in Drosophila

Richard Nichols <r.a.nichols@qmul.ac.uk>

RutgersU QuantGenetics

Postdoctoral Fellow Quantitative and Molecular Genetics

A postdoctoral associate position in the field of Quantitative/ Molecular genetics and genomics is available. The successful candidate will have the opportunity to work on identifying and characterizing novel clock components using quantitative genetics/genomics and molecular approaches. Candidates with doctoral degrees in genetics, molecular biology, or related fields with strong training in a quantitative field, such as statistics, biostatistics, bioinformatics are encouraged to apply. This project is funded by NSF for three years. Applicants should submit a statement of research interests, curriculum vitae, pdf files of publication, and contact information of three references to kwang1@camden.rutgers.edu.

Kwangwon Lee, Ph.D. Department of Biology Center for Computational & Integrative Biology Rutgers University Science Building, Room 202 315 Penn Street Camden, NJ 08102-1411

Reference: Kim T-S, Logsdon BA, Park S, Mezey JG, Lee K. 2007 Quantitative trait loci for the circadian clock in Neurospora crassa. Genetics 177:2335-2347.

Michael TP, Park S, Kim T-S, Booth J, Byer A, Sun Q, Chory J, Lee K. 2007 Simple sequence repeats provide a substrate for phenotypic variation in the Neurospora crassa circadian clock. PLoS ONE 2: e795

Kim T-S, Booth J, Gauch HGJ, Sun Q, Park J, Lee Y-H, Lee K. 2008 Simple sequence repeats in Neurospora crassa: distribution, polymorphism and evolutionary inference. BMC Genomics 9:31.

Kwangwon Lee <kl272@cornell.edu>

SaoPaulo SugarcaneGenomeOrganization

Post-Doctoral Fellowship in Molecular Biology is available to study sugarcane genome organization and gene expression associated to the presence of Transposable elements under the supervision of Dr. Marie-Anne Van Sluys. Our group has a tradition to study the association of Transposable elements and genomes and their impact in gene/genome structure and gene regulation. Experimental infrastructure to use molecular, cellular, genetic, and transgenic plant techniques are available to investigate the regulation of genome.

The PD position is associated to the Sugarcane genome sequencing initiative within a BioEnergy-FAPESP program. The proposed project involves sequencing of 300 selected BACs using pyrosequencing and Sanger technologies. Assembly and annotation pipelines are available. Three questions will be addressed: How are these elements contributing to allelic variation in sugarcane genome and expression profile of genes of interest (BRIX, drought, RGAs and high CO2 environment? What is the diversity of chromatin target binding sites of selected transposases? How are the identified TE lineages diversifying in Saccharum genome compared to other Saccharineae and Poaceae species?

It is expected to use SSA-P methodology and RBIP derived markers to provide tools for screening allelic variations and dosage in progenies interest. Other high throughput technologies, such as microarray, are available.

For additional information, visit our web site at

GaTE Lab http://www.ib.usp.br/gate/ BIOEN program http://bioenfapesp.org/ Applications should be sent to: mavsluys@usp.br Include a curriculum vitae, bibliography, cover letter with a brief description of research experience and interests, and the names of 3 references along with their postal and e-mail addresses.

Best regards,

Marie-Anne

Marie-Anne Van Sluys, Full Professor GaTE Lab (Genomics and Transposable elements) Departamento de Botânica-IBUSP rua do Matao, 277 05508-900; São Paulo, SP, BRASIL tel:55-11-30917759 fax:55-11-30917724 email:mavsluys@usp.br

mavsluys@usp.br

StonyBrook EvolutionFlightMetabolism

Postdoctoral Position at Stony Brook V Physiological genetics of flight metabolism

A three year NSF-supported postdoctoral position is available in the field of physiological genetics of flight metabolism using Drosophila melanogaster as a model. The project involves the study of the effects of the glycolytic pathway on flight performance [see Eanes, W. F., T. J. Merritt, J. M. Flowers, S. Kumagai, E. Sezgin et al. 2006 Flux control and excess capacity in the enzymes of glycolysis and their relationship to flight metabolism in Drosophila melanogaster. Proc.Natl.Acad.Sci.U.S.A. 103: 19413-19418]. More specifically, the position involves P-element knockout and genetic manipulation of genes involved with pathway steps. Candidates with a Ph.D. in genetics, physiology, molecular biology, or related fields with strong training in a quantitative skills are encouraged to apply. The position is available immediately. Applicants should submit a statement of personal research interests, curriculum vitae, publication PDFs, and addresses for references to walter@life.bio.sunysb.edu. Walt Eanes, Dept. of Ecology and Evolution, Stony Brook University, Stony Brook, New York 11794

Thanks, Walt

Walter F. Eanes Professor Dept. of Ecology and Evolution Stony Brook University Stony Brook, New York 11794

weanes@notes.cc.sunysb.edu

Switzerland RapidEvolution Diversity

Sorry for any cross postings.

Post-doctoral position in physiological and experimental plant ecology

The goal of the interdisciplinary project SPatially Explicit Evolution of Diversity (SPEED) is to understand how evolutionary history and the potential for rapid evolution can influence the response to climate change by species, biotic communities, and regional patterns of biological diversity. The project focuses on species in the Restionaceae, a family of grass-like monocots that are primarily found in the fynbos of South Africa. The project employs the tools of molecular phylogenetics, evolutionary modeling across phylogenies, field experimentation, plant physiology, community phylogenetics and niche modeling. Collaborating institutions include the University of Lausanne, the University of Zurich and the Swiss Federal Research Institute WSL. SPEED is funded by the Sinergia program of the Swiss National Fund for Science (SNF). There are three open positions, each with funding for three years. Here is the post-doc position:

Post-doctoral research in physiological and experimental plant ecology. This position will focus on study of the relationship between the fundamental and realized ecological niches of species in the Restionaceae. Experimental work will be done in greenhouse facilities in Switzerland and potentially include substantial fieldwork in South Africa. The researcher's primary association will be with the Linder lab at the University of Zurich. The position will include some project management (not more than 20%).

Applications MUST be received no later than Sunday, May 31, 2009. Interviews to be held fourth week in June. Start date in September, 2009. For further information about the SPEED project:

http://www.wsl.ch/projects/SPEED Please contact Peter B. Pearman or the relevant person linked to your interest. The SPEED project proposal is available to interested applicants upon request.

To apply, send the following materials, as separate PDF files: 1. PDF of cover letter, addressed to The SPEED Search Committee, indicating –position applied for –your career goals –your research interests in context of the SPEED project –a detail of how the previous experience and skills shown in your CV prepare you specifically for the position for which you are applying 2. PDF of CV, complete, showing contact information, titles of thesis and dissertation, dates, universities, research experience, notable skills, advanced courses, publication list, posters and talks presented, awards, service, etc... 3. PDF of the abstract of your Ph.D. dissertation research 4. PDF of university report of coursework, showing grades and degrees earned (must be in English) 5+. PDF's of published papers and papers in-press.

Send application as e-mail with attachments, with the following subject line:

SPEED Project Postdoc

to:

sibylle.hauser@wsl.ch

Don't forget the deadline!

– Peter B. Pearman, Ph.D. Land Use Dynamics Federal Research Institute WSL Zürcherstrasse 111 8903 Birmensdorf Switzerland

pearman@wsl.ch Tel. ++41 (0)44 739 2524 Fax ++41 (0)44 739 2215

TulaneU HawaiianFishBiogeographyGenetics

Postdoctoral Position in Biogeography and Genetics of Hawaiian Fishes

A postdoctoral research associate position is available in the Blum Lab (www.tulane.edu/~mjblum) in the Department of Ecology & Evolutionary Biology at Tulane University. The incumbent will engage in DoD funded research on the landscape genetics and biogeography of amphidromous fishes native to the Hawaiian Islands. The research focuses on (1) development and use of genetic tools for assessing aquatic environmental condition of oceanic island stream ecosystems (2) assessing metapopulation dynamics and phylogeography of amphidromous fishes across the Hawaiian archipelago and

(3) comparing genetic assays of dispersal with estimates based on otolith microchemistry. The incumbent will be encouraged to develop additional research areas that complement these set objectives.

Preference will be given to candidates possessing in-depth knowledge of molecular techniques and field based studies of stream fishes. An initial appointment will be for one year, with continuation for at least one additional year dependent upon performance. A start date of August 1 2009 or a mutually agreeable date in late Summer 2009 is strongly preferred. Salary will be commensurate with experience and qualifications. Send via email attachment a letter of application, curriculum vitae, statement of research interests, and names and addresses of three references to Dr. Michael Blum at mjblum@tulane.edu .Tulane University is an Affirmative Action/Equal Employment Opportunity Employer. Women and minorities are encouraged to apply.

"Blum, Michael J " <mjblum@tulane.edu>

UAixMarseille SpatialGeneticDiversity

A postdoctoral position (12 moths) is available in IMEP (UMR 6116 CNRS/IRD) at University of Aix-Marseille (France) on the following subject : Spatial ecology in agricultural landscape: from genotypes to plant communities.

This postdoc opportunity is available to start in 2009 and is adressed to doctors who have done and obtained their PhD elsewhere than in France. The salary is about 1945 euros/month.

The objective is to investigate spatial structure of geneitic diversity and plant communities in relationships with hypothesis of effect of landscape structure and history on microevolution process in the Champsaur valley (South Alps). This work will be based on spatially explicite collection of genotypes, floristic relevés, and landscape structure data for two herbaceous species (Primula vulgaris and Moehringia trinervia) occuring within the same habitat.

Qualifications: the candidate should have a strong background in spatial ecology and SIG analysis. Plant population genetic or ecology experiences will be also favourable. The candidate will collaborate to achieve integration of genetic and communities according to landscape or communities genetics approaches. Knowing that field and lab data are already obtained, most of the work will be adressed to data analysis, modelling and publishing. There will be opportunities to develop similar projects on mediterranean landscape within and outside the lab.

DEADLINE : 13/06

For further details or published papers on the subject : Pascal.Campagne@legs.cnrs-gif.fr or alex.baumel@univ-cezanne.fr.

To apply please send a CV to Alex Baumel (alex.baumel@univ-cezanne.fr), Pascal Campagne (Pascal.Campagne@legs.cnrs-gif.fr), and Thierry Tatoni (thierry.tatoni@univ-cezanne.fr).

IMEP web site : http://www.imep-cnrs.com Alex BAUMEL <alex.baumel@univ-cezanne.fr>

UArizona AlgalEvolution

A postdoctoral position is immediately available in the laboratory of Jeremiah Hackett (http://www.eebweb.arizona.edu/Faculty/Hackett/Home.html), Ecology and Evolutionary Biology Department, University of Arizona, Tucson, Arizona. The successful candidate will use genomic approaches to investigate the ecology, physiology and evolution of saxitoxin producing dinoflagellate algae. We are using next-generation sequencing and gene expression methods to understand harmful algal bloom formation and toxin production and comparative genomics to investigate the origin and evolution of genes involved in the production of toxins and other secondary metabolites. This is a NSF-supported position for 1 year, renewable for an additional year with satisfactory performance. With your application, submit a CV and a statement of interest describing your previous research experience and two (2) letters of reference.

Minimum Qualifications: We are looking for a highly motivated individual with a Ph.D. degree and with demonstrated ability to carry out outstanding research in the fields of genetics, genomics, algal ecology, or related fields.

Experience with molecular biology techniques and demonstrated communication skills are essential qualifications.

Preferred Qualifications: Previous research experiences with harmful algae, functional genomics, phylogenetics and molecular evolution, and/or bioinformatics are highly desirable.

Direct questions and inquires regarding this position to Jeremiah Hackett (hackettj@email.arizona.edu)

Please apply to this posting via the University of Arizona's careers website:

www.uacareertrack.com/applicants/-Central?quickFind4658 Jeremiah D. Hackett Assistant Professor University of Arizona Ecology and Evolutionary Biology Department Biosciences West 336 1041 E. Lowell St. Tucson, AZ 85721 Ph: (520) 621-7514 Fax: (520) 621-9190 hackettj@email.arizona.edu

Jeremiah Hackett <hackettj@email.arizona.edu>

UArizona GeneNetworkEvolution

Two postdoc positions are available to work with PI Joanna Masel (http://eebweb.arizona.edu/faculty/-masel) at the University of Arizona in Tucson. The Masel group's main research interests are in evolvability, gene networks, canalization, and evolutionary capacitance, using a mixture of analytical theory, bioinformatic and simulation approaches. Both positions are renewable over multiple years, and are available immediately.

One position will be to study the properties of cryptic genetic variation and evolvability via evolutionary capacitance using theoretical population genetics and/or bioinformatic approaches. Ph.D. with a strong quantitative background and computational and/or modeling experience is required. A background in evolutionary theory is strongly preferred. Some interest in the molecular biology of transcription, translation, protein folding and the errors in each of these processes is an advantage.

The second position involves completing the implementation of a computational model of transcriptional networks that is both realistic enough to be related to yeast data and simple enough for evolution to be rapidly simulated. The model will then be used to study a range of questions, including network topology and the evolution of robustness/canalization to mutation, to the environment, and to the stochasticity associated with small numbers of molecules in cells. This project is a collaboration with Mark Siegal (www.nyu.edu/fas/-dept/biology/faculty/siegal) at NYU. Ph.D. with scientific programming experience is required. Experience in evolutionary biology, genomics, systems biology, mathematical modeling and/or the biology of transcription factors and their binding sites is preferred.

Contact Joanna Masel at masel@u.arizona.edu for more information and to apply for either position.

masel@U.Arizona.EDU masel@U.Arizona.EDU

UBourgogne NeuroEvoParasito

Project title: Neurophysiological basis of parasite manipulation: how do acanthocephalan parasites interfere with the serotonergic pathway of their crustacean host ?

A postdoctoral associate is sought to collaborate on a highly original project at the interface between invertebrate neurophysiology and behavioral ecology. The main goal of the project is to understand the neurophysiological basis of parasite manipulation. Parasite manipulation is defined as the ability, shared by several parasite groups, to modify their hosts behaviour in ways that enhance their own transmission, for instance through increasing the intermediate hosts vulnerability to predation by the final host. We are specifically investigating how parasites interfere with the serotonergic system of their host to alter behavioural perception and/or response to environmental cues (such as phototactism or chemotactism). The project will use the amphipod Gammarus pulex and its acanthocephalan parasites Pomphorhynchus sp. as a model system. It will address how reaction to light and/or odor is controled by serotonin (receptors involved) and whether parasites are altering certain components of the serotonergic pathway (serotonin brain/hemolymph concentrations, post-traductional changes in 5HT-receptors, changes in SERT gene expression...).

The candidates should have a PhD in neurophysiology, or in behavioural ecology with research experience in invertebrate neurobiology. Experience with biochemical techniques (western blot, ELISA, HPLC, immunocytochemistry, analysis of post-traductional modifications) are requested. Skills in proteomics or gene expression analysis will also be considered.

The successful applicant will join the evolutionary ecology lab at University of Dijon, France, and be jointly supervised by Professor Frank Cezilly (www.u-bourgogne.fr/BIOGEOSCIENCE/cv/cezilly) and Dr. Marie-Jeanne Perrot-Minnot (www.u-bourgogne.fr/-

BIOGEOSCIENCE/perrot). The position will be appointed for two years with a net salary of 2500 euros/month Start date is negotiable from september to december 2009. Applicants are requested to email a letter of introduction and motivation, CV, and references to fcezill@u-bourgogne.fr and mjperrot@u-bourgogne.fr. The deadline for application is may the 28th, 2009

*** Marie-Jeanne Perrot-Minnot Associate Professor Ecology Evolution lab UMR CNRS 5561 Biogeosciences Univ. Bourgogne 6 Bd Gabriel 21000 Dijon France

Marie-Jeanne Perrot-Minnot <mjperrot@u-bourgogne.fr>

UBritishColumbia EvolGenomics

A Postdoctoral Fellow position is available in the lab of Dr. Keith Adams at the University of British Columbia in the area of evolutionary genomics. My lab's research combines evolutionary biology with molecular genetics and bioinformatics approaches to study how gene expression, regulation, structures, and sequences evolve. See my web page at http://www.botany.ubc.ca/people/adams.htm for a description of current research. I am looking for a postdoc to study evolutionary genomics of alternative intron splicing patterns in plants. Projects may include examining alternative splicing in hybrids using RNA-seq transcriptome profiling and analyzing selective forces acting on alternatively spliced introns. The postdoc can develop an independent project as well. The postdoc can interact with postdocs in other labs, including the Rieseberg and Cronk labs, who study evolutionary genomics and use next generation sequencing to answer evolutionary questions. My lab is housed in new research building with excellent computational infrastructure.

Candidates should have a strong background in evolutionary genomics, molecular evolution, bioinformatics, or genome analysis in any organism. Experience with computational analysis of sequence or expression data is required as is the ability to do scripting in Perl or Python. Experience with next generation sequence analysis (Solexa, 454, or SOLiD) is desirable but not required. The start date can be any time between late June 2009 and early January 2010. Funding is available for at least two years.

For more information contact Keith Adams at keitha@interchange.ubc.ca Informal inquiries about the research area and projects are welcome. To apply, send a CV, a description of your research interests and your Ph.D. research, and contact information for three references to the above email address.

Keith Adams Assistant Professor Botany Department and Centre for Plant Research University of British Columbia Vancouver, Canada

keitha@interchange.ubc.ca keitha@interchange.ubc.ca

UCaliforniaBerkeley FungalCompartiveGenomics

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Postdoctoral Scholar Position in fungal comparative genomics available July 1, 2009 at the University of California, Berkeley in the laboratory of John W. Taylor

Our research involves comparative genomics and comparative transciptomics among and within species in Ascomycete fungi. With knowledge of species and populations, we are using evolutionary biology to address fungal adaptation in the broad sense. We have compared Sanger genomes of two sibling species and related fungi to find genes whose history of selection makes them candidates for adaptation, including gene family expansions, gene gain and loss, rapid evolution, and an excess of replacement substitutions (in press at Genome Research). Now, we are obtaining data on transcription (Illumina RNA-seq), resequenced population samples (Illumina) and sequences of close relatives (de novo, Illumina) to add population and phylogenetic approaches to detect selection on proteins.

For details, interested applicants with experience in computational biology and evolutionary biology should contact John Taylor at jtaylor@nature.berkeley.edu.

John Taylor Department of Plant and Microbial Biology 111 Koshland Hall Berkeley, CA 94720 jtaylor@nature.berkeley.edu http://pmb.berkeley.edu/~taylor/ –

John Taylor, Department of Plant and Microbial Biology, 111 Koshland Hall, University of California, Berkeley, CA 94720-3102 Tel(510) 642-5366, Fax(510) 642-4995, jtaylor@nature.berkeley.edu lab web site: http://pmb.berkeley.edu/ ~ taylor/ jtaylor@nature.berkeley.edu jtaylor@nature.berkeley.edu

UCaliforniaIrvine PlantComparativeGenomics

POSTDOCTORAL RESEARCHER/SCHOLAR POSITION

A postdoctoral position in plant evolutionary genetics is available immediately in the Department of Ecology & Evolutionary Biology at the University of California, Irvine. The aim of the project is comparative evolutionary analysis of plant genomic sequence data, particularly comparisons of Arabidopsis thaliana to the new genome sequences of Arabidopsis lyrata and Capsella rubella.

The successful applicant must have a PhD and demonstrated expertise in molecular evolution and bioinformatics methods. To apply for this position, please send a statement of interest, a CV, and contact information for 3 references to:

Dr. Brandon S. Gaut bgaut@uci.edu

You can learn more about the interests and projects in the lab by visiting titus.bio.uci.edu

The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program.

bgaut@uci.edu

UCalifornia SantaBarbara EvolutionaryTheory

A postdoctoral position in evolutionary theory is currently available in the Proulx lab at UCSB. The postdoc would participate in an NSF funded project to develop theory describing the evolution of genetic interactions in an ecological context. The postdoc is expected to design their own research project within the broader scope of the funded research. Interested applicants should have a strong background in evolutionary theory, mathematical modeling, and interests in either organismal adaptation or molecular evolution.

UCSB has an active group working in several areas of theoretical biology. Areas of expertise include population dynamics, ecological epidemiology, systems biology, complex systems, and population genetics.

To apply, please send an email with a letter of interest and cv to postdoc@proulxresearch.org and include “theory postdoc” in the subject.

For more information on the lab and our research see http://www.lifesci.ucsb.edu/eemb/faculty/proulx/index.html http://dx.doi.org/10.1086/426873 http://dx.doi.org/10.1111/j.0014-3820.2006.tb01168.x – Stephen Proulx Assistant Professor Ecology, Evolution, and Marine Biology UC Santa Barbara proulx@lifesci.ucsb.edu

stephen.proulx@gmail.com

UCDavis StatPopGenomics

A postdoctoral position in statistical population genomics is currently available in the Rannala research group at the Genome Center < http://genomics.ucdavis.edu > and Department of Evolution and Ecology at UC Davis. The postdoc would participate in an NIH funded project aimed at developing statistical methods and algorithms for analyzing genome-wide SNP data to infer recombination rates, demographic parameters, and human genetic disease associations. Candidates should have a recent Ph.D. in theoretical population genetics, statistics, or a related area, and strong programming skills. Prior experience analyzing human population genomic data is desirable but not essential. Funding is available for a period of up to 3 years.

To apply, please send an email with a letter of interest, CV, and the names (and email addresses) of two references to brannala@ucdavis.edu.

– Bruce Rannala, Professor Genome Center and Department of Evolution and Ecology University of California Davis Ph: 530-754-4060

Bruce Rannala <brannala@gmail.com>

UEastAnglia WarblerFitness

The following postdoc position has become available again due to the previously chosen candidate being unable to take up the position

Telomeres as biomarkers of costs and quality in the Seychelles warbler

UEA SCHOOL OF BIOLOGICAL SCIENCES

SENIOR RESEARCH ASSOCIATE Ref: RA519

29,704 to 35,469 per annum

This NERC funded postdoctoral position is available from June 2009 for a period of two years and nine months to undertake a comprehensive longitudinal study of telomere shortening in a wild avian population. The researcher will help to develop and then utilise molecular protocols to screen for telomere length in the Seychelles warbler. You must have, or shortly obtain, a PhD (or equivalent) in a relevant discipline, have a keen interest in understanding life history trade-offs and senescence and have practical experience in modern molecular techniques.

Closing date: 12 noon on Thursday 2 April 2009. This is a readvertisement but previous applicants are welcome to apply.

Further particulars and an application form are available on our website: www.uea.ac.uk/hr/jobs/ <file:///C:\Documents%20and%20Settings\k483\Local%20Settings\Temporary%20Internet%20Files\OLK1A\www.uea.ac.uk/hr/jobs/> or Tel. 01603 593493.

David S Richardson Centre for Ecology, Evolution and Conservation School of Biological Sciences University of East Anglia e-mail: david.richardson@uea.ac.uk Norwich NR4 7TJ ph: (44) 01603 591496 ENGLAND fax: (44) 01603 592250

http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=325

"Richardson David Dr (BIO)" <David.Richardson@uea.ac.uk>

UIdaho EvolutionaryGenomics

Postdoctoral Researcher in Evolutionary Genomics: University of Idaho

Position Description: A postdoctoral position is available in the laboratory of Dr. Erica Rosenblum to study evolutionary genomics of the deadly chytrid fungus, the pathogen implicated in global amphibian declines. The postdoctoral scientist will be involved in research using comparative and functional genomics tools to better understand the genetic basis of chytrid pathogenicity and the dynamics of host- pathogen interactions. The postdoctoral scholar will specialize on the empirical and/or computational aspects of the project depending on interest and prior experience. The ideal candidate will have a strong bioinformatics background and will be involved in the analysis and synthesis of genome-scale datasets, with a particular emphasis on computational analysis of next generation 454 and Solexa data. However, applicants with a background in molecular biology or genetics will also be considered for empirical aspects of the project. The successful candidate will contribute to existing collaborative projects across multiple institutions and will also be expected to develop new independent research directions. The start-date for this position will be summer or fall 2009, and salary will be commensurate with current NIH guidelines.

Qualifications: Minimum qualifications include a Ph.D. in Biological Sciences, Computer Science, Statistics, Molecular Biology or a related field. For computational applicants, demonstrated experience in bioinformatics and proficiency in programming is necessary. For empirical applicants, demonstrated experience in molecular biology and genetics is required. For all applicants, experience with next generation sequencing is desirable but not required. Ability to communicate clearly, work independently, and interact collaboratively is essential.

To Apply: Details about the job responsibilities and the necessary qualifications can be found at https://www.sites.uidaho.edu/AppTrack/Agency/Applicant/ViewAnnouncement.asp?announcement_no=12508082883 . Applications consisting of 1) a CV, 2) a statement of research interests and experience including how previous experience relates to the position description (2 page max) and 3) contact information for three references must be submitted online at www.hr.uidaho.edu. Review of applications will begin June 11th, 2009 and continue until the position is filled. Informal inquiries are welcome. Please contact Erica Rosenblum at rosenblum@uidaho.edu. General information about the lab can be found at ttp://people.ibest.uidaho.edu/~bree/.

About University of Idaho: The successful applicant will be affiliated with the Department of Biological Sciences (http://www.uiweb.uidaho.edu/biology), the Bioinformatics and Computational Biology Program (http://www.bcb.uidaho.edu), and the Initiative for Bioinformatics and Evolutionary Studies (http://www.ibest.uidaho.edu). These groups support a world-class genomics facility and have a strong culture of collaboration among evolutionary, statistical, mathematical and computational biologists. The postdoctoral researcher will join a community of highly interactive research labs working on disease genomics. The University of Idaho is in the Palouse region of northern Idaho and is ten miles from the main campus of Washington State University. The successful candidate will also work closely with collaborators at the University of California (Berkeley and Riverside campuses), the University of Michigan, and Florida State University. The University of Idaho is hosting the 2009 Evolution meetings this summer.

Erica Bree Rosenblum, Ph.D. Assistant Professor Department of Biological Sciences Life Sciences South 346 University of Idaho Moscow, ID 83844-3051

office phone: (208) 885-1007 email: rosenblum@uidaho.edu

Erica Bree Rosenblum <rosenblum@uidaho.edu>

UKoblenzLandau EvolutionaryGenetics

POSTDOCTORAL POSITION IN EVOLUTIONARY GENETICS AT THE UNIVERSITY OF KOBLENZ-LANDAU

Academic appointment is within the University's Department of Environmental Sciences, section MOLECULAR ECOLOGY, and the position is based at Landau (Rhineland-Palatinate). The position's distribution is 60% research and 40% administration and education. The successful candidate is expected to establish an extramurally funded research program, attract and mentor successful graduate students, and mentor undergraduate researchers. Area of research is ecological genetics using model organisms such as Daphnia. Research activities should complement existing strengths at the environmental sciences department. Possibilities include (but are not limited to) invasive species ecology, restoration ecology and experimental evolutionary biology.

The successful candidate should have the equivalent of a master's degree, diploma or Ph.D. in biology, a firm background in evolutionary biology, experience with molecular techniques and a strong commitment to basic research. The applicant should have a strong publication record, very good written and oral English language skills, fluency in German and interest in joining a multidisciplinary research team are required. The position is open starting June 2009 and available at maximum for six years; pay and conditions are according to the German 1,0 EGr. 13 TV-L scale for civil servants.

The University Koblenz-Landau advocates gender equality. Women are therefore strongly encouraged to apply.

Equally qualified severely handicapped applicants will be given preference. Closing date for applications is 26st May 2009. Please send your application (using the reference number 31/2009) including a detailed CV, 3 references, a list of publications and three selected reprints, to the Präsident der Universität Koblenz-Landau, Präsidialamt, Isaac-Fulda-Allee 3, 55124 Mainz, Germany. For enquiries about the scientific framework and practical work please write to Prof. Dr. Klaus Schwenk. E-mail: schwenk@uni-landau.de

schwenk@uni-landau.de

ULausanne SocialEvolution

POSTDOCTORAL POSITION, SOCIAL EVOLUTION AND ANTI-PARASITE DEFENCES, LAUSANNE

Applications are invited for a Postdoctoral position in the research group of Michel Chapuisat (Department of Ecology and Evolution, University of Lausanne). We study social evolution, social conflicts and collective defences against parasites in ants. Please look at http://www.unil.ch/dee/page7000.html for information and references.

The project will focus on (1) the impact of entomopathogenic fungi on ant societies of various degrees of complexity and (2) the collective defences of ants against fungi. The main model system will be the socially polymorphic ant Formica selysi and several of its naturally occurring fungal pathogens. The project can take various directions and there will be scope to accommodate personal ideas or individual research projects. Along with solid background in evolutionary biology, experience in one or more of the following areas would be an asset: behavioural ecology, host-parasite relationship, microbiology, fungal biology, chemical ecology, molecular techniques, population genetics.

The position is funded by the Swiss National Science Foundation and is available for three years, with a possibility of extension. The gross salary starts at 58'994 CHF per annum. Starting date is negotiable, from September 2009 onwards. The Department of Ecology and Evolution is large and thriving, and provides excellent facilities for research and training (see http://www.unil.ch/dee/).

Informal enquiries and applications should be sent to Michel.Chapuisat@unil.ch. Applications should include a cover letter, complete CV with publication list, and contact details of three referees, preferentially embedded in a single pdf file.

I will review the applications on 22 June 2009, but will continue to consider incoming applications until the position is filled.

Michel Chapuisat <Michel.Chapuisat@unil.ch>

Michel Chapuisat

Department of Ecology and Evolution Biophore, Quartier Sorge University of Lausanne CH-1015 Lausanne (Switzerland)

Ph: +4121 6924178 http://www.unil.ch/dee/page7642.html Michel Chapuisat <Michel.Chapuisat@unil.ch>

ULyon SexChromosomeEvolution

Postdoctoral position on the origin and evolution of young plant sex chromosomes

An ANR-funded postdoc position (2 years) is available in Gabriel Marais' lab at the University of Lyon (France).

The project will focus on Silene latifolia a dioecious plant species with X and Y chromosomes. This species is emerging as a model species for the understanding of the evolution of sex chromosomes. The aim of the project will be to use the genomic resources that have recently become available in S. latifolia (BAC sequences, ESTs and microarrays) to investigate several points in relation to the origin and evolution of XY in this species: XY recombination suppression, Y degeneration, and sex determination. We collaborate on this project with Prof. Alex Widmer's lab (ETH Zurich).

We seek a highly motivated candidate with skills in data analysis and a strong interest in genome evolution and evolutionary biology in general. A PhD in one or several of the following fields is expected: bioinformatics, genomics, molecular evolution, population genetics, biostatistics. The applicant does not need to be a French speaker.

We are part of the Bioinformatics and Evolutionary Genomics group, which includes about 25 people (including Laurent Duret and Manolo Gouy). The BGE group has a long-standing experience in bioinformatics and offers a very stimulating scientific environment (highest rate by CNRS at last evaluation in 2006). We have a vast range of locally available bioinformatics tools and excellent computing facilities (UNIX servers, PC clusters). Our weekly lab meeting and journal club are held in English. Find more details at http://lbbe.univ-lyon1.fr/ . Lyon is the 2nd largest French city. Its city center has been classified "world heritage" by UNESCO and Lyon is considered French capital of gastronomy. Excellent public transports exist within the city (metro, bus, tramway, public bikes), and to the nearby Alps, Paris (two hours by train) and the rest of Europe.

To apply, please send to Gabriel Marais (email: marais@biomserv.univ-lyon1.fr): a letter describing your research motivation and experience, a CV including publication list, full contact details of two scientific referees.

The position should start on fall 2009. Annual gross salary will be about 28,000 euros. Review of materials will begin late April and will continue until the position is filled. For further information, please contact:

Dr. Gabriel Marais Bioinformatics and Evolutionary Genomics group Institute for Biometrics and Evolutionary Biology University of Lyon Campus de la Doua, Villeurbanne Email: marais@biomserv.univ-lyon1.fr Website: http://lbbe.univ-lyon1.fr/-Marais-Gabriel-.html?lang=en Gabriel Marais <marais@biomserv.univ-lyon1.fr>

UManchester VertebrateComparativeGenomics

Post Doctoral Research Associate - Comparative Genomics of Gene Regulation in Vertebrates

University Of Manchester Faculty Of Life Sciences Reference: LS/90559 Closing date: 28/05/2009

Based in the laboratory of Dr. Casey Bergman, we seek a capable and enthusiastic computational biologist to study the comparative genomics of gene expression in vertebrates as part of an FP7-funded consortium of experimental and computational groups in France, Germany, Italy and the UK. This project will involve the analysis of genome-wide sequence and expression data in vertebrates to gain insight into the cis- regulatory logic and evolution of transcriptional control in neural stem cells.

You should have (or expect to hold shortly) a relevant PhD or equivalent appropriate postdoctoral level experience in Bioinformatics/ Computational Biology, Evolutionary Genetics, Comparative Genomics, Gene Expression, Computer Science or related disciplines. This position is tenable for up to 2 years and salary will be £28,839 - £31,514 per annum.

Informal enquiries can be addressed to: Dr. Casey Bergman Tel: +44 (0)161 275 1713 Email: casey.bergman[at]manchester.ac.uk < http://www.bioinf.manchester.ac.uk/bergman/ >

Application forms and further particulars can be obtained at: < http://www.ls.manchester.ac.uk/about/jobs/job/index.asp?ref=3D154458 > <http://www.manchester.ac.uk/_contentlibrary/_vacancies/furtherparticularsmax10mbpdf,154458,en.pdf >

Information on computational biology research at the University of Manchester can be found at: <http://www.manchester.ac.uk/ bioinformatics>.

casey.bergman@manchester.ac.uk
casey.bergman@manchester.ac.uk

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, including changes of gene expression noise. 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 for three references to jianzhi@umich.edu. The position is available immediately.

For further information about the Zhang lab, see http://www.umich.edu/~zhanglab/ Jianzhi George Zhang Department 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 http://www.umich.edu/~zhanglab/ jianzhi@umich.edu jianzhi@umich.edu

UOxford SocialEvolutionTheory

University of Oxford Department of Zoology Postdoctoral Research Assistant: Social Evolution Theory

Grade 07S Salary: Â£28,839 â 35,469 per annum

Applications are invited for a Postdoctoral Research Assistant to work under the supervision of Prof Stuart West to study social evolution theory. The post is funded by the European Research Council, and is available for three years, extendable up to five.

The main part of the proposal will be to develop models which can explain the evolution and maintenance of cooperative social behaviours in bacteria. The other part of the proposal is to develop models which can explain the evolution and maintenance of cooperative social behaviours in humans and cooperative breeding vertebrates. Some related papers on this can be found at http://www.zoo.ox.ac.uk/group/west/social.html. Depending upon the applicant, the work could be taken in a number of directions, ranging from issues such as cultural evolution to sex allocation, to the development of general methodology.

Further particulars and application forms can be downloaded from http://www.zoo.ox.ac.uk/jobs/adverts/at09020.pdf or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS, tel: 01865 271190. E-mail: recruit@zoo.ox.ac.uk Applications, together with CV and contact details of three referees, should be sent to the above address, quoting reference number AT09020 The closing date for applications is noon on 19 June 2009.

Mirella Lingwood <mirella.lingwood@zoo.ox.ac.uk>

UPierreMarieCurie PigeonGenetics

A one-year post-doctoral position funded by the Centre National de la Recherche Scientifique is available in our research unit "Ecology & Evolution" CNRS/ University Pierre & Marie CURIE (Paris 6).

In the context of growing urbanisation, understanding the functioning of natural populations inhabiting cities is required. The research project aims at identifying the particular selective pressures exerted by the urban environment, focusing on genetic and phenotypic differentiation of feral pigeons in relation to environmental factors. It is in line with an interdisciplinary project (more details in French at http://pigeons.u-psud.fr/).

The candidate will have strong interest and experience in evolutionary ecology, population genetics, ornithology, and/or GIS, and being able of strong autonomy, creativity, organisational and relational skills.

Contact Adrien Frantz at adrien.frantz@snv.jussieu.fr for more information and to apply (before 15 June 2009).

– Adrien FRANTZ

Assistant Professor/Lecturer UMR 7625 "Ecologie et Evolution" Université Pierre et Marie Curie - Paris 6 7, quai Saint-Bernard Bât. A 7ème étage - Case 237 F-75252 Paris cedex 05 Tél: +33 (0)1 44 27 38 23 Fax: +33 (0)1 44 27 35 16

adrien.frantz@snv.jussieu.fr

UTartu OptimalityModeling

Position in evolutionary ecology available: optimality modeling

We wish to recruit a post-doctoral researcher to undertake OPTIMALITY MODELING in the field of LIFE HISTORY research. The position will be opened at the recently established Centre of Scientific Excellence 'Frontiers in Biodiversity Research' (FIBIR, http://fibir.ut.ee) at the University of Tartu, Estonia (http://www.ut.ee). The successful candidate will work in Prof. Toomas Tammaru's (http://www.ut.ee/~tammarut) research group, whose primary focus is the life history evolution of insects (the evolution of body size in particular). Having mainly relied on experimental methods to date, the group is looking to strengthen the modeling component of its research activity. We have various ideas waiting to be formalized, and empirical data are available to serve as the foundation of empirically based models. However, the work profile is largely flexible, and the researcher will be able to develop his or her own ideas. The successful candidate will be encouraged to collaborate with other research groups, both at FIBIR and elsewhere. Funding is presently available for 24 months, though there is a strong possibility that this can be extended, subject to the candidate's performance. FIBIR offers an excellent research environment within a modern infrastructure. The salary level corresponds to that of European Union framework projects and is open to negotiation. The position is available from 1st June, 2009, though the start date is flexible. The successful candidate is expected to have a strong publication record that demonstrates his or her ability to apply either analytical or numerical methods to model biological systems. Competence in the field of mathematical statistics would be an advantage. Previous experience with insect life history research is not essential. In the case of very strong candidates, it would be possible to transform the post-doctoral position into that of a senior researcher. If interested, provide your CV, a list of publications and the contact details of at least two academic referees by 11th May, 2009. For this purpose, and for informal enquiries, please contact Toomas Tammaru at toomas.tammaru@ut.ee (cc to maarika.maesalu@ut.ee).

tammarut@ut.ee tammarut@ut.ee

UTartu PhylogeneticComparativeMethods

Position in evolutionary ecology available: phylogenetic comparative methods

We wish to recruit a post-doctoral researcher in evolutionary ecology to undertake research using PHYLOGENETIC COMPARATIVE METHODS. The position will be opened at the recently established Centre of Scientific Excellence 'Frontiers in Biodiversity Research' (FIBIR, http://fibir.ut.ee) at the University of Tartu, Estonia (http://www.ut.ee). The successful candidate will work in Prof. Toomas Tammaru's (http://www.ut.ee/˜tammarut) research group, whose primary focus is the life history evolution of insects. Having mainly relied on experimental methods to date, the group is now looking to develop its expertise in the field of phylogenetically explicit comparative approaches. The strengths of the group include a rare combination of in-depth knowledge about the taxonomy and life-history of insects (mainly Lepidoptera), and a productive interest in various questions in the field of evolutionary biology. While we have well-defined research questions in mind for the post-doctoral researcher (evolution of body size, egg size, host specialization etc.), and respective data sets available, the work profile is largely flexible. The successful candidate will be encouraged to collaborate with other research groups, both at FIBIR and elsewhere. Funding is presently available for 24 months, though there is a strong possibility that this can be extended, subject to the candidate's performance. FIBIR offers an excellent research environment within a modern infrastructure. The salary level corresponds to that of European Union framework projects and is open to negotiation. The position is available from 1st June, 2009, though the start date is flexible. The successful candidate is expected to have a strong publication record that features research using a phylogenetic comparative approach. However, we may also consider candidates with experience of other phylogeny-based analyses or statistical analysis of autocorrelated data). Previous experience with insect life history research is not essential. In the case of very strong candidates (excellent publication record and very good skills in comparative analyses), it would be possible to transform the post-doctoral position into that of a senior researcher. If interested, provide your CV, a list of publications and the contact details of at least two academic referees by 11th May, 2009. For this purpose, and for informal enquiries, please contact Toomas Tammaru at toomas.tammaru@ut.ee (cc to maarika.maesalu@ut.ee).

tammarut@ut.ee tammarut@ut.ee

UVienna DrosophilaAgingGenetics

1 POSTDOCTORAL POSITION IN DROSOPHILA AGING

A postdoctoral position in the genetics of Drosophila aging is available in the research group of Dr. Thomas Flatt at the University of Veterinary Medicine in Vienna, Austria (Institute of Population Genetics) (http://i122server.vu-wien.ac.at/pop/-Flatt_website/flatt_home.html). The postdoc position is funded by a grant from the Austrian Science Foundation (FWF) and will be for three years.

This research project will focus on the identification of the molecular basis of the trade-off between reproduction and lifespan in the fruit fly, Drosophila melanogaster, a powerful genetic model system. In many organisms, from fruit flies to humans, reproduction shortens lifespan, but the underlying mechanisms remain unknown (e.g., Flatt & Kawecki 2007, Evolution; Flatt & Promislow 2007, Science). Experiments in C. elegans suggest that hormonal signals from the gonad affect longevity (Hsin & Kenyon 1999, Nature), and we have recently found that germline ablation extends lifespan and affects insulin signaling in Drosophila (Flatt et al. 2008, PNAS). However, the details of this systemic regulation of lifespan by the reproductive system remain unclear. In our project we are interested in dissecting the hormonal mechanisms that modulate the reproduction-longevity trade- off. By employing mutant and transgene analysis, genetic manipulation of the gonad, epistasis experiments, and hormonal manipulations we will examine the endocrine mechanisms whereby signals from the reproductive system modulate longevity.

We are seeking a highly talented, dynamic, independent, and self- motivated young biologist with good social skills. The successful candidate will have a Ph.D. and a strong background in genetics and molecular biology using the Drosophila system. Some background in the biology of aging, evolutionary biology, and/or endocrinology would be ideal, but is not required. The postdoc will work closely with a PhD student and the PI on this project. The working language in the laboratory is English, so the candidate should be proficient in spoken and written English. German skills, although helpful, are not essential. The initial appointment will be made for one year, with a possible extension to up to three years. The annual salary is 54,180 Euro. The position is available as of now, but the starting date is negotiable.

In a 2009 world-wide survey by the William M. Mercer Institute, Vienna ranked first world-wide in terms of standards of living. Vienna is a beautiful, historical yet modern city, located in the heart of Europe, close to the Alps and to major cities like Munich, Zurich, Prague, and Budapest. Being famous for its concert sites, opera houses, theathers, museums, and coffee shops, Vienna also provides great outdoor activities, such as sailing on the Neusiedler See, ice skating, biking and hiking in the Viennese woods and the nearby Alps. Moreover, the city has a wide range of great restaurants, bars, wineries, cinemas, clubs, libraries, galleries, and art collections. The Vienna area is also an exceptional and highly international research environment. Four major life science universities and three world-class research institutes (GMI, IMBA, IMP) provide a dynamic and interactive setting. Vienna hosts an active Drosophila community, and the onsite availability of the Drosophila RNAi center (VDRC) provides a great opportunity for functional Drosophila work. In population genetics and evolutionary biology, the Vienna research area also provides excellent prospects, due to a growing number of evolutionary research groups.

To apply for this position, please send a single pdf file including: (1) a cover letter explaining why you would like to join our group, (2) your Curriculum Vitae (including a description of your skills), (3) your publication list, (4) a statement of research interests, and (5) contact details for 2-3 academic references who are willing to write a reference letter on your behalf to the following email address: thomas.flatt@vu-wien.ac.at

Informal inquiries are welcome and should be sent to the same e-mail address. For further information see (http://i122server.vu-wien.ac.at/pop/-Flatt_website/flatt_home.html).

The deadline for submission is 1 July 2009.

Dr. Thomas Flatt University of Veterinary Medicine Department of Biomedical Research Institute of Population Genetics Veterin?rplatz 1 / Josef Baumann Gasse 1 A-1210 WIEN Austria

VOX +43(0)1-25077-4334 FAX +43(0)1-25077-4390

E-mail: Thomas.Flatt@vu-wien.ac.at

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1 RESEARCH ASSISTANT/TECHNICIAN POSITION IN DROSOPHILA AGING

A research assistant/technician position in the biology of Drosophila

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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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UWisconsinMadison Disease Evolution

UWisconsinMadison.Disease.Evolution

The Goldberg lab at University of Wisconsin-Madison invites applications for a post-doctoral position focused on the ecology and evolution of infectious disease. This is a unique opportunity for a post-doctoral scholar with broad interests in infectious disease ecology, evolution, and molecular approaches to engage in creative research as part of a dynamic team. Projects include (but are not limited to):

1) Ecology and evolution of West Nile virus in urban areas. Ecology of West Nile virus transmission in suburban Chicago, with an emphasis on molecular epidemiology and viral evolution, funded by the NIH/NSF Ecology of Infectious Diseases Program.

2) Diversity, evolution, and immunology of porcine reproductive and respiratory syndrome virus (PRRSV). Molecular epidemiology of PRRSV, with an emphasis on the development of broadly effective polyvalent vaccines, funded by USDA.

For more information, please see the Goldberg lab website:

http://svmweb.vetmed.wisc.edu/goldberglab/

Applicants should have a primary interest in infectious disease ecology and evolution (experience with viral systems is a plus), strong quantitative skills in molecular phylogenetics/phylodynamics, and a demonstrated ability for creative research. Projects involve a flexible combination of fieldwork, lab work, and computational analyses. The successful applicant will be expected to explore new research directions of her/his choosing, assisted by a strong team of collaborators.

University of Wisconsin-Madison is a top-notch institution for research and training in the biomedical sciences, with strong programs in ecology, evolution, and microbial sciences (www.wisc.edu). Madison, WI, is a vibrant city with outstanding culture and exceptional opportunities for outdoor recreation (www.wisc.edu/-about/location.php).

Applicants should send a CV, a brief statement of research interests, and a list of three people (names, addresses, e-mails) who can serve as references.

Materials and inquiries should be sent to tgoldberg@vetmed.wisc.edu. Application materials should be received by June 15 2009 for full consideration; the position is available starting September 1, 2009 and is for a minimum of 2 years, with an option to extend.

Thanks very much!

Tony

Tony L. Goldberg, PhD, DVM, MS Professor of Epidemiology Department of Pathobiological Sciences School of Veterinary Medicine University of Wisconsin-Madison 1656 Linden Drive Madison, Wisconsin 53706 Phone: 608-890-2618 FAX: 608-262-7420 e-mail: tgoldberg@vetmed.wisc.edu Website: http://svmweb.vetmed.wisc.edu/goldberglab/ Tony L Goldberg <tgoldberg@vetmed.wisc.edu>

YaleU BacterialEvolution

A one-year postdoctoral position is available immediately under the co-supervision of Paul Turner and David Post in the Department of Ecology and Evolutionary Biology at Yale University. The project concerns empirical tests of theory at the interface of ecology and evolution, via high-throughput experiments with microbes using a liquid-handling robot. Experience in a bacterial system such as E. coli is preferred, but all strong candidates will be considered. Please direct inquiries to paul.turner@yale.edu

Paul Turner <paul.turner@yale.edu>

WorkshopsCourses

Budapest Levels of Selection Sep13-16

CALL FOR EXTENDED ABSTRACTS

Levels of Selection and Individuality in Evolution: Conceptual Issues and the Role of Artificial Life Models

*** One day Workshop at ECAL 2009 conference (13th-16th September, Budapest, Hungary)

Submission deadline: Monday 22 June 2009

Understanding how new levels of biological organisation, selection and individuality can arise are exciting and open challenges in both evolutionary biology and artificial life. In attempting to understand these issues we are forced to ask questions that challenge our existing preconceptions of evolutionary theory, such as what kinds of entities can natural selection act on, what are the properties that define an individual, and how can new levels of heredity arise? In this workshop we aim to provide a forum to discuss and debate these issues, drawing on the philosophical and modelling expertise of artificial life researchers in areas such as autonomy, emergence and self organisation.

Confirmed Invited Speaker: Prof. Eors Szathmary (Collegium Budapest)

The main focus of this workshop will be on discussion of important conceptual issues and the application of techniques and philosophy from artificial life in addressing these. Submissions are invited that discuss any aspect of levels of selection, organisation, and individuality in evolution, including:

* Multi-level selection * Evolution of cooperative behaviour * Prebiotic evolution and the origins of life * Philosophical issues in levels of selection and the major transitions * Comparisons of the utility of different types of model * Cultural evolution and other non-genetic sources of heredity * Inclusive fitness / kin selection * Species-level selection; ecosystem selection * How to recognise genuine higher-level selection * Niche construction * Self-organisation as a support for higher-level selection

Submission Process

Extended abstracts of up to 1000 words (optional: up to 2 figures) should be submitted in the ECAL 2009 format (10pt minimum, single space, wide margins). Please email submissions to Simon Powers (stp05r@ecs.soton.ac.uk).

All suitable submissions will undergo peer review by 3 members of the program committee for relevance, quality, and ability to generate discussion. Accepted submissions will be allocated either a brief oral presentation or a poster. Submissions to this workshop may be based on papers submitted to ECAL 2009 or elsewhere, but must focus on raising issues for discussion.

Important dates

Submission : Monday 22 June 2009 Notification of acceptance : Monday 13 July 2009 Workshop: During ECAL 2009 (13th-16th September 2009)

Organising Committee

Simon Powers Rob Mills Richard A. Watson Alexandra Penn Hywel Williams

Program committee TBA.

Workshop website: http://www.sense.ecs.soton.ac.uk/-levels-of-selection-workshop-2009/ ECAL 2009 website: http://www.ecal2009.org/ – Simon T. Powers Natural Systems Group University of Southampton http://www.ecs.soton.ac.uk/people/stp05r stp05r@ecs.soton.ac.uk

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Bydgoszcz Poland ForestGeneFlow Jun15-19

Workshop on Estimating Gene Flow in Forest Trees

Bydgoszcz, Poland, June 15-19, 2009

Organized by Institute of Experimental Biology, Department of Genetics, Kazimierz Wielki University of Bydgoszcz and Evoltree Network of Excellence

The intention of the workshop is to cover the state-of-the art of current methods for estimating gene flow - with special emphasis to forest trees. The lectures will be given by a number of highly qualified scientists with strong scientific background in this field.

Topics will include (among others): introduction to gene flow issues; genetic markers for gene flow studies - benefits and problems; parentage exclusion and parentage assignments; TwoGener method and its derivatives; gene flow based on population structure; mating models for pollen mediated gene flow; modeling seed and pollen dispersal based on established seedlings - seedling model; inverse modeling of seed dispersal, direct vs. indirect methods, covariates of mating success affecting estimation of gene flow. Course will consist of lectures by teachers (morning session) and practicals (with hands-on-computer) where specific software for estimating gene flow will be presented and training provided. There will also be a field trip to one or two local experimental sites where gene flow studies have been done recently.

Registrations will be treated on a first-come first-served basis. The number of attendants is limited to 20 persons. No registration fees are planned at the moment. EVOLTREE members have support through their group project budgets.

Confirmed teachers include: Sylvie Oddou (INRA-Avignon), Olivier Hardy (University of Brussels), Frederick Austerlitz (CRNS), Etienne Klein (INRA-Avignon), Juan Jose Robledo-Arnuncio (CIFOR-INIA

Madrid), (Local organizers/teachers: Jaroslaw Burczyk, Igor Chybicki, Elzbieta Koralewska, Magdalena Trojankiewicz)

For more information:

http://members.upcpoczta.pl/j.burczyk1/index.htm jjrobledo@gmail.com

Colombia Bioinformatics Aug23-30 DeadlineMay1 2

Tomorrow (Friday 1st May) is the last day for applications for the EMBO course "Advanced bioinformatic methods in the study of gene and genome evolution" which will be held in Medellin, Colombia, 23 - 30 August, 2009.

In response to a number of questions: The course is open to anybody, anywhere in the world at any level of their career. Acceptance on the course will be based on whether you are most deserving of a place.

You can find out more here:

http://cwp.embo.org/wpc09-04/ James

– Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@nuim.ie – Work — http://bioinf.nuim.ie/

James McInerney <james.o.mcinerney@nuim.ie>

Iceland ArabidopsisEvolution Aug14-17

Iceland â Arabidopsis Molecular Ecology Group (AMEGO) 14-17 August 2009

The Arabidopsis Molecular Ecology Group (AMEGO) is a network financially supported by NordForsk, including research groups from Denmark, Finland, Norway and Sweden. AMEGO will be hosting international workshops and Ph.D. courses on Arabidopsis molecular ecology and evolution in the period 2007-2009. The last Arabidopsis molecular evolution workshop and Ph.D. course will be held 14-17 August 2009 in Reykjavik, Iceland.

Preliminary program: 14 August Arrival and registration 15 August Workshop with talks and posters 16 August Excursion to Arabidopsis lyrata sites. Participants will also get the opportunity to experience some of the natural wonders of Iceland. 17 August Ph.D. course: âNatural selection in the wild: exploring the magnitude and mechanisms of selection in the fieldâ. Participants should bring their own laptop. Responsible: Professor Jon Ãgren, Uppsala University.

Deadline for registration is 7 June 2009

- invited speaker will be Rodney Mauricio, University of Georgia

For more information about AMEGO 2009 workshop and Ph.D. course, please see our home page at http://www.molecol.net. The registration page can be found at http://www.bio.ntnu.no/amego/pomelding/-skjema.php . Best regards, Sverre Lundemo

Sverre Lundemo Department of Biology Norwegian University of Science and Technology N-7491 Trondheim Norway

lundemo@bio.ntnu.no

Sverre Lundemo <lundemo@bio.ntnu.no>

Lisbon ComputationalPhyloinformatics Jul9-19

Computational Phyloinformatics: A GTPB-NESCent Course 9 July - 19 July 2009

http://gtpb.igc.gulbenkian.pt/bicourses/-PHYLOINF09/ http://www.nescent.org/courses/-2009/comphy/ Course Contacts: Pedro Fernandes (pfern@igc.gulbenkian.pt) and William Piel (piel@treebase.org) Organizing Committee: Pedro Fernandes, Hilmar Lapp, William Piel, Todd Vision

Computational Phyloinformatics is a 10-day summer course co-sponsored by the Gulbenkian Training Programme in Bioinformatics and the U.S. National Evolutionary Synthesis Center (NESCent), and will take place at the Oeiras campus of the Instituto Gulbenkian de Ciência near Lisbon, Portugal. This course aims to give students practical knowledge and hands-on skills in phyloinformatics.

SYNOPSIS Biologists are faced with ever-larger datasets, more complex evolutionary models, and increasingly elaborate analytical methods. Seldom is it sufficient to run a dataset with an off-the-shelf program on a desktop PC; increasingly, biologists need to write scripts to interface with internet services and databases, build analytical pipelines, customize analyses, and distribute computation over multiple processors. This course is designed for graduate students, postdocs, and researchers in phylogenetics interested in receiving practical, hands-on training in the use of Perl and SQL for phyloinformatics applications.

The course is divided into three parts:

- Part I: A tutorial review of of Perl, including object oriented programming and building packages - Part II: Introduction and practical use of BioPerl and Bio::Phylo, (e.g. scripting for large tree inference engines, automating model testing, supertree assembly, rate smoothing and branch calibration, tree traversal, etc). - Part III: Introduction to database design; computing and querying nested sets and transitive closure; BioSQL; BioPerl-BioSQL bindings.

Students will learn how to write basic phylogenetic or comparative analysis scripts, parse NEXUS files, traverse and compute over trees, and make practical use of phylogenetic software libraries. These skills will be learned in a biological context, touching on a diverse array of topics such as analysis of large datasets, automation of supertree assembly, querying for topological patterns in large collections of trees, etc.

INSTRUCTORS Hilmar Lapp, Darin London, William Piel, Rutger Vos

PREREQUISITES Biology: A solid understanding of phylogenetics - for example, having already taken the Workshop on Molecular Evolution (http://www.molecularevolution.org/), the GTPB Molecular Evolution, Phylogenetics and Adaptation course (Molecular Evolution, Phylogenetics and Adaptation), or equivalent coursework or experience.

Computing: Prior experience with Perl or careful study of the suggested reading materials (see web site). Students should have experience with basic Unix shell commands. All students are expected to bring either their own Mac OSX computer or a LINUX computer; otherwise computers will be rented for them and the fee will be included in their tuition.

FEES Full tuition is 650 (˜ $878), and includes housing, lunches, coffee, and computer rental. Participants who bring their own computers receive a discount of 150 (˜ $203) off of their tuition. Participants who find their own housing receive a discount of 200 (˜ $270) off of their tuition.

HOW TO APPLY Apply through the course website (http://gtpb.igc.gulbenkian.pt/bicourses/PHYLOINF09/application.html). You will be asked to provide a resume and a motivation statement (including a self-assessment of your skills, experience, and knowledge of both phylogenetics and computing). Applications are due by June 8 2009.

piel@treebase.org

Montana PopulationGenetics DataAnalysisCourse Aug31-Sep4

4th ConGen- Population Genetics Data Analysis Course Recent Approaches for Estimation of Population Size, Structure, Gene flow, Selection Detection focusing on conservation and beyond

31-Aug/4-Sep 2009, Flathead Lake Biological Station, Montana, USA

APPLICATIONS FOR 2009 ARE OPEN!

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 20 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program).

Deadline for application is 30 June, 2009

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

For detailed information see http://popgen.eu/congen2009/ Instructors: Fred Allendorf, University of Montana, USA Sam Cushman, US Forest Service, Missoula, USA Jonathan Pritchard, The University of Chicago, USA Robert Lacy, Chicago Zoological Society, USA Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, CIBIO, Portugal & University of Montana Albano Beja-Pereira, CIBIO, Portugal Tiago Antao, Liverpool School of Tropical Medicine, UK Mike Schwartz, US Forest Service, Missoula, USA David Tallmon, University of Alaska, Juneau, USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, USA

congen@popgen.eu

conservation genetics course <congen@mail.icav.up.pt>

Albano Beja-Pereira <albanobp@fc.up.pt>

Munich HostParasiteCoevolution Sep20-25

Subject: conference, summer school

Last Call for applications for summer school on Host-Parasite Coevolution

The Munich Graduate Program for Evolution, Ecology and Systematics (EES) invites applications for the international EES summer school on Host-Parasite Coevolution held at Frauenchiemsee (80 km east of Munich) from September 20th to September 25th, 2009.

The 5-day summer school will consist of lectures, discussions and exercises organized by the local and invited instructors, as well as oral and/or poster contributions by the students. We will cover theoretical aspects of host-parasite evolution and discuss empirical approaches for studying coevolution. Specific topics will include the evolution of virulence and resistance, local adaptation and spatial structuring in host-parasite systems, and the molecular signature of coevolution.

Instructors (confirmed): Mike Boots, University of Sheffield, UK (theoretical analysis of disease dynamics in humans and wildlife) Jukka Jokela, ETH Zurich, Switzerland (maintenance of sex driven by host-pathogen coevolution) David Nash, University of Copenhagen, Denmark (coevolution on geographical scales) Peter Tiffin, University of Minnesota, USA (molecular coevolution between plants and parasites)

Local Instructors/Organizers at Ludwig-Maximilians-University Munich: Susanne Foitzik, Pleuni Pennings, Laura Rose, Aurelien Tellier, Volker Witte, and Justyna Wolinska.

The summer school is open to all graduate students (PhD, Masters, Diplom biologists). The summer school will be taught in English. Participants should plan to arrive Sunday, Sept. 20th. The summer school will wrap up on Friday, Sept. 25th in the early afternoon.

Costs: Thanks to support from the Volkswagen Foundation, the University of Munich's EES program will cover housing and meals during the Summer School. Participants are required to cover their own travel expenses and pay a 50 Euro registration fee. A small amount of funding is available to subsidize travel costs for students from the most distant locations.

The Application Procedure: Applicants should submit a single pdf file containing the following: a) a one page CV b) a one page motivation letter for attending the summer school c) a short abstract of your research project (maximum 200 words) Email applications to Dr. Elisabeth Brunner (brunner@biologie.uni-muenchen.de). Application Deadline: June 1st, 2009.

Further information is available at: http://www.eeslmu.de/eeswiki/Summer_school_2009 – Justyna Wolinska Ludwig-Maximilians-Universität, München Department Biologie II Evolutionsökologie Grosshaderner Str. 2 82152 Planegg-Martinsried, Germany

Phone: +49 (0)89 2180 74201 Fax: +49 (0)89 2180 74204 email: wolinska@bio.lmu.de http://www.biologie.uni-muenchen.de/ou/ecology/evol_e/people_wolinska_e.html Justyna Wolinska <wolinska@bio.lmu.de>

Portugal PopulationGenetics Jun15-19

Applications are now open for

MMPG09 Molecular Markers and Population Genetics June 15th - June 19th 2009

Course description: Genetic data are increasingly used by ecologists and evolutionary biologists in general. It has thus become important for many biologists with different levels of experience to produce and analyse genetic data. In this course we shall take a practical approach to the analysis of genetic data, but we will also provide some of the theoretical background required to understand the outputs of the software used. Mornings will usually be devoted to introduce notions that will be applied in the afternoon using freely available software. In particular the following software will be used: ARLEQUIN and GENETIX to analyse classical population genetic data, STRUCTURE and GENECLASS2 to look for hidden structure and assign multilocus genotypes, Bottleneck and msvar to detect and quantify population size changes, IM to estimate gene flow and divergence times, Fdist and/or BayesFst to detect selection. The R statistical package will also be introduced and used to analyse genetic data and outputs of the software, and to simulate simple processes. The software ms that allows to simulate genetic data will also be introduced together with a user-friendly version called Gms.

All the necessary info, important dates, instructions for applicants at the GTPB website, as usual

http://gtpb.igc.gulbenkian.pt Best wishes

Pedro Fernandes GTPB Coordinator Instituto Gulbenkian de Ciência Apartado 14 2781 OEIRAS PORTUGAL

Pedro Fernandes <pfern@igc.gulbenkian.pt>

Regensburg EvoDevo Sep24-25

Dear colleagues,

together with Matthias Gerberding and Gregor Bucher, we are organizing a workshop with the question: "What we can learn about evolutionary changes by studying development at different levels of organismic diversity?" we think that some members of your lab might be interested in the topic and we would like to invite your students to join the workshop. Keynote talks given by Martin Klingler (Erlangen, comparison of Drosophila and Tribolium segmentation) and Alistair McGregor (Vienna, comparing Drosophila sister species). Besides, the students will practice the presentation of their data in a short talk. Finally, we hope that the workshop will also help to give the students an overview on current work and to network with other students in the field.

The workshop takes place immediately before the annual meeting of the DZG (German Zoological Society) at Regensburg (www.dzg2009.de) which this year is devoted to evolution.

The official website of the workshop is http://m.gerberding.googlepages.com/dzgevo-devomtg . Please forward this information to students (focus on PhD students) and young postdocs in your lab. We hope to see them in Regensburg!

Louis Boell

Regensburg 24./25. Sept. 2009

Evo-Devo tries to infer mechanisms of evolutionary innovation by identifying similarities and dissimilarities of developmental processes and mapping them onto the phylogenetic tree of life. Starting from the classical model systems, comparisons have been extended towards other species being closely related ("satellite organisms") or more distantly related to the well-established developmental models. The choice depends on which evolutionary transitions are to be elucidated. Comparisons are now applied at widely different levels of organismic divergence, ranging for instance from sister species in Drosophila to phylum level comparisons between insects and annelids or deuterostomes.

The aim of this workshop is to discuss the respective potential and drawbacks of the different levels of comparison and consequences for evolutionary inferences. For example, is there a fundamental difference between "microevolutionary" modification of existing structures and the generation of "evolutionary novelties", or is this distinction an artefact resulting from the use of different comparative approaches? If we study how distantly related organisms develop the same structures - will we learn how these different modes of development evolved? This topic lies at the heart of any attempts at generalization in evolutionary developmental biology.

In this context, Dr. Alistair McGregor will present results on the molecular dissection of small morphological differences between closely related species of Drosophila, and Prof. Martin Klingler will talk about differences in the segmentation cascade between Drosophila and the flour beetle Tribolium and their relevance for evolution.

The workshop takes place immediately before the annual meeting of the DZG at Regensburg which this year focuses on evolution. PhD students but also Master/Diploma students or young postdocs are welcome to join the discussion.

Louis Boell MPI für Evolutionsbiologie, Plön August-Thienemannstr.2 D-24306 Plön Tel.: 0049 4522 763 280

lboell@evolbio.mpg.de

Roscoff France MarineEvolutionaryGenomics

Summer Course - Marine Genomics Europe Marine Evolutionary & Ecological Genomics May 25th â June 5th, 2009 Station Biologique de Roscoff, France

Aims to give an introduction on genetic and genomic approaches to analyze biological diversity, evolution and adaptation at the species and population level in the ocean

Confirmed teachers

Sandie Baldauf, Univ of York, UK

Erik Bonivard, Univ. Paris 6, FR

Galice Hoarau, Univ of Groningen, NL

Wiebe Kooistra, SZN, IT

FrÃ©dÃ©ric Partensky, SB-Roscoff, FR?

Klaus Valentin, AWI-Bremerhaven, DE

FrÃ©dÃ©rique Viard, SB-Roscoff, FR

ClÃ©mentine Vitte, Univ. Paris 6, FR

Filip Volckaert, KULeuven, BE

Organizing committee

HÃ©lÃne Huelvan, SB-Roscoff, FR

Jeanine Olsen, Univ of Groningen, NL

Anne Saisi, SB-Roscoff, FR

Arnaud Tanguy, SB-Roscoff, FR

FrÃ©dÃ©rique Viard, SB-Roscoff, FR

Filip Volckaert, KULeuven, BE

Target group

PhD students (at least in their second year) and post docs with a solid knowledge in phylo- and/or population genetics. This course is open to MGE members as well as non-members.

Topics

The course will consist of lectures, tutorials and computer based exercises in the following subjects.

* Phylogeny - sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies * Population genetics â allele and genotype analyses, population genetic structure and gene flow, assignment tests, effective size and population dynamics, case studies * Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies * Environmental, functional and comparative genomics - 1. Genome structure and architecture. 2. Markers in the genomics realm. 3. Methods for detecting structure. 4. Introduction to functional genomics. 5. Methods for detecting adaptive variation (including selective sweeps) within and among populations; linking hydrographical/environmental and demographic data to population structure and local adaptation. 6 Quantitative genetics: evolution of traits. 7. EST libraries: why and how. 8. Introduction to comparative genomics (whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, transposable elements in marine species) 9. Case studies * Phylogenomics - 1. What is comparative genomics? 2. Genomics and genetics of speciation/ what makes a species from a genome point of view? 3. Comparative marine genomics. 4. Case studies

Costs; course, accommodation and meals

* The course fee is paid by the MGE Network for all academics (pre and post doc). Welcome reception, excursion (incl lunch) and farewell dinner are included. * All participants pay their own travel, accommodation and board (self catering is possible) * Participants are offered to be accommodated at the SBR guesthouse which is situated directly at the institute. The cost for this is 13 per night in double room incl. breakfast. The guesthouse can also offer lunch and supper for a cost of 5.50 per person and meal.

Application and contact

To apply please fill in the application form and send to Anne Saisi (saisi@sb-roscoff.fr) together with a 2-paged CV before April 10, 2009. This information + application form can also be found on the MGE website: www.marine-genomics-europe.org under Training & Education.

16 participants will be selected by the following criteria:

1. Relevance of the course for their PhD or post-doc project

2. Background and experience of applicant

3. We will aim at mixing people from different research areas and therefore probably no more then one person per institute will be considered. We will also aim at an equal distribution of women and men.

The selected persons will receive a notification at the end of April that has to be confirmed within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Contact

Anne Saisi

European Project Manager

Station Biologique de Roscoff

BP 74, 29680 ROSCOFF CEDEX

France

Email: saisi@sb-roscoff.fr

Phone: (33)2 98 29 23 45

Fax: (33)2 98 29 23 80

Disclaimer: http://www.kuleuven.be/-cwis/email_disclaimer.htm Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Roscoff France MarineEvolutionaryGenomics May25-Jun5

MGE Summer Course

Marine Evolutionary & Ecological Genomics May 25th â June 5th, 2009 Station Biologique de Roscoff, France

Confirmed teachers Sandie Baldauf, Univ of York, UK Erik Bonivard, Univ. Paris 6, FR Galice Hoarau, Univ of Groningen, NL Wiebe Kooistra, SZN, IT FrÃ©dÃ©ric Partensky, SB-Roscoff, FR Klaus Valentin, AWI-Bremerhaven, DE FrÃ©dÃ©rique Viard, SB-Roscoff, FR ClÃ©mentine Vitte, Univ. Paris 6, FR Filip Volckaert, KULeuven, BE Simon Creer, UBangon, UK Mathias Wegner, UZurich, CH

Organizing committee HÃ©lÃne Huelvan, SB-Roscoff, FR Jeanine Olsen, Univ of Groningen, NL Anne Saisi, SB-Roscoff, FR Arnaud Tanguy, SB-Roscoff, FR FrÃ©dÃ©rique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

Aims to give an introduction on genetic and genomic approaches to analyze biological diversity, evolution and adaptation at the species and population level in the ocean

Target group

PhD students (at least in their second year) and post docs with a solid knowledge in phylo- and/or population genetics. This course is open to MGE members as well as non-members.

Topics

The course will consist of lectures, tutorials and computer based exercises in the following subjects.

* Phylogeny - sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies * Population genetics â allele and genotype analyses, population genetic structure and gene flow, assignment tests, effective size and population dynamics, case studies * Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies * Environmental, functional and comparative genomics - 1. Genome structure and architecture. 2. Markers in the genomics realm. 3. Methods for detecting structure. 4. Introduction to functional genomics. 5. Methods for detecting adaptive variation (including selective sweeps) within and among populations; linking hydrographical/environmental and demographic data to population structure and local adaptation. 6 Quantitative genetics: evolution of traits. 7. EST libraries: why and how. 8. Introduction to comparative genomics (whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, transposable elements in marine species) 9. Case studies * Phylogenomics - 1. What is comparative genomics? 2. Genomics and genetics of speciation/ what makes a species from a genome point of view? 3. Comparative marine genomics. 4. Case studies

Costs; course, accommodation and meals

* The course fee is paid by the MGE Network for all academics (pre and post doc). Welcome reception, excursion (incl lunch) and farewell dinner are included. * All participants pay their own travel, accommodation and board (self catering is possible) * Participants are offered to be accommodated at the SBR guesthouse which is situated directly at the institute. The cost for this is 13 per night in double room incl. breakfast. The guesthouse can also offer lunch and supper for a cost of 5.50 per person and meal.

Application and contact

To apply please fill in the application form and send to Anne Saisi (saisi@sb-roscoff.fr) together with a 2-paged CV before April 10, 2009. This information

+ application form can also be found on the MGE website: < http://www.marine-genomics-europe.org/- > www.marine-genomics-europe.org under Training & Education.

16 participants will be selected by the following criteria:

1. Relevance of the course for their PhD or post-doc project 2. Background and experience of applicant 3. We will aim at mixing people from different research areas and therefore probably no more then one person per institute will be considered. We will also aim at an equal distribution of women and men.

The selected persons will receive a notification at the end of April that has to be confirmed within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Contact

Anne Saisi European Project Manager Station Biologique de Roscoff BP 74, 29680 ROSCOFF CEDEX France Email: saisi@sb-roscoff.fr Phone: (33)2 98 29 23 45 Fax: (33)2 98 29 23 80

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Trento Italy PopulationGenomics Jul22-24

Dear Colleagues, * INTERNATIONAL WORKSHOP*: “Population and Ecological Genomics in Changing Forest Environments” *LOCATION*: Centro di Ecologia Alpina (CEA; http: www.cealp.it), Fondazione Edmund Mach, on Monte Bondone, near Trento, Italy *DATES:* July 22-24, 2009. * HOW TO APPLY*: Potential participants are kindly requested to submit an e-mail (events@iasma.it) along with a one-page cv and 1-page statement describing why they would like to attend the workshop.

*Deadline for registration is May 21, 2009. *

*FEE: *200 includes lunches and dinners (from July 22-24) and the course manual. * CONTACTS:* Floriana Marin, Research and Innovation Centre, Fondazione Edmund Mach, (events@iasma.it), phone: +39 0461 615543 - Fax + 39 0461 615183

DESCRIPTION: This workshop will be hosted by CEA, in collaboration with the University of California, Davis, USA (Department of Plant Sciences).

The aim of the workshop is to provide up-to-date knowledge of theoretical and computational approaches to studying adaptation in changing forest environments. The workshop will emphasize the use bioinformatics tools and software packages. Participants must have their own laptop computer and have software applications installed before arriving at the CEA. Information regarding obtaining software and computer hardware requirements will be provided by the organizers in advance of the workshop.

The workshop is primarily intended for young researchers at the doctoral and post-doctoral stages, but is also open to people working outside academic institutions seeking to acquire basic knowledge useful for implementing practical management and conservation plans.

ORGANIZERS: David Neale (Dept. of Plant Sciences, UC Davis) Cristiano Vernesi (Centro di Ecologia Alpina, Research and Innovation Centre, Fondazione Edmund Mach) Claudio Varotto (IASMA Research and Innovation Centre, Fondazione Edmund Mach)

INSTRUCTORS: David Neale (UC Davis, USA) , Jill Wegrzyn (UC Davis, USA), Andrew Eckert (UC Davis, USA) and Elena Mosca (UC Davis, USA). Invited speakers: Sally Aitken (University of British Columbia, Canada) and Brad St. Clair (USDA Forest Service, Corvallis, Oregon, USA)

LOCAL COMMITTEE: Cristiano Vernesi and Floriana Marin (secretary), Fondazione Edmund Mach.

Cristiano Vernesi Centro di Ecologia Alpina Centro Ricerca e Innovazione - Fondazione Edmund Mach postal address: Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skypename: cvernesi

jillylee@gmail.com

UAzores PhylogeneticComputing Jul20-25

INTRODUCTION TO PHYLOGENETIC COMPUTING AND ANALYSIS

20-25 July 2009 University of the Azores, Ponta Delgada, São Miguel I., Azores

Instructors: Endre Willassen and Manuel Malaquias (Bergen Museum of Natural History, University of Bergen, Norway)

Overview: Phylogenetic methods have become an essential tool across several fields of biology with particularly emphasis on systematics, biogeography and evolution. This practical course addresses the fundamentals but also the latest advances in phylogenetic computing methods with a focus on the analysis of molecular sequence data. It is designed to fulfil the needs of those looking to have a first grasp into the science and of those looking to develop further competences in phylogenetic analysis. Therefore, undergraduate, graduate, and academics/researchers are welcome to attend. The course will cover topics such as: phylogenetic principles and concepts; use of DNA web-based databases; edit, assembling, and alignment of DNA sequences; distance, parsimony and Bayesian methods of tree reconstruction; models of molecular evolution; tree optimization; interpretation of phylogenetic trees; single and combined gene-trees; molecular-clocks, relaxed phylogenetics, and age estimate of tree-nodes; tree drawing.

Language: English (with supportive Portuguese when required)

Structure of the course: 6 days; 8.30h /day (Lectures: 2.30h + Practicals: 6h). Total number of hours: 51h (15h lectures + 36h computational practical).

Pre-requisites: Attendees should have some background knowledge in evolutionary biology and phylogenetic thinking, but previous experience with programs for phylogeny reconstruction is not expected.

Further queries should be addressed to: Sérgio Ávila (avila@notes.uac.pt).

Manuel Malaquias <Manuel.Malaquias@bm.uib.no>

UBern PlantMicrevolution Jul7-10

Dear all,

on 7-10 July 2009 several colleagues at the University of Bern (Markus Fischer, Mark van Kleunen and Daniel Prati) and I are organising a

WORKSHOP ON GLOBAL CHANGE AND PLANT MICROEVOLUTION (Website: http://www.staff.unibe.ch/bossdorf/workshop.html)

Global environmental change does not only affect the ecology but also the evolution of plants. Climate change, land use and biological invasions affect the direction and strength of natural selection, as well as the amount and distribution of plant genetic diversity. The resulting microevolution could buffer or accelerate environmental change. Understanding this anthropogenic evolution might be important for our ability to predict global change impacts. However, evolutionary processes are still a very understudied aspect of global change biology. While there has been quite some recent research on evolutionary consequences of biological invasions, much less is known about evolution in response to climate change, and even less about evolutionary consequences of land use. The purpose of our workshop is to bring these questions together under a common conceptual framework, discuss the current research in this field, and develop an agenda for future research. The scale of the workshop will be rather small, with a total of about 40 participants. The workshop will thus have a pleasant retreat character. It will be divided into two parts: a symposium part where the invited speakers and some of the participants will give lectures, and a workshop part where participants, assisted by the invited experts, will form small discussion groups and jointly develop ideas for future research.

The workshop venue will be on 7-10 July in Mürren, a beautiful and car-free mountain village in the Swiss Alps, about 75 km south of Bern. Mürren can be reached only by foot or cable-car. Hotel Regina is a 100 year old mountain hotel with a special charme and a breathtaking view of the famous Eiger, Mönch and Jungfrau mountain panorama.

Invited speakers: Rob Colautti, University of Toronto, Canada Julie Etterson, University of Minnesota, USA Markus Fischer, University of Bern, Switzerland Steven Franks, Fordham University, USA Alistair Jump, University of Stirling, UK Jennifer Lau, Michigan State University, USA

If you are interested in participating in the workshop, please visit the workshop website (http://www.staff.unibe.ch/bossdorf/workshop.html) and follow the instructions. Please register as early as possible, as the total number of participants is limited.

See you in Mürren, Oliver

– Dr. Oliver Bossdorf University of Bern Institute of Plant Sciences Altenbergrain 21 CH-3013 Bern, Switzerland

bossdorf@ips.unibe.ch Phone: +41 31 631-4923 (Fax -4942) http://www.staff.unibe.ch/bossdorf/ Oliver Bossdorf <bossdorf@ips.unibe.ch>

Uganda BiodiversityConservation Jun21-25

Dear all,

The Network for Conservation Educators and Practitioners of the Albertine Rift Region (NCEPARR), in conjunction with the Institute of Environment and Natural Resources, Makerere University (MUIENR) and the National University of Rwanda (NUR) are organizing a workshop on the theme: BIODIVERSITY CONSERVATION IN THE ALBERTINE RIFT REGION.

The workshop will take place between the 21st - 25th June 2009 in Uganda.

The workshop is aimed at promoting collaborations in teaching and research among Conservation Educators and Practitioners in the Albertine Rift Countries, government and non-government organizations, policymakers, and decision makers; and also to create opportunities and approaches for conservation scientists at universities and research institutes in the Albertine Rift to interact.

The workshop sub-themes are:

1. Climate change and biodiversity conservation 2. Research and Monitoring as a conservation tool in the Albertine Rift 3. Ethnobotany and value addition 4. The status of biodiversity resources within the Albertine Rift and implications for their conservation 5. Role of conservation educators and practitioners in attaining MDG 7 in the Albertine Rift : opportunities and challenges

If you are interested to participate in this workshop, please submit an abstract. I wish to inform all that only a limited number of participants will be hosted and that the selection of participants to be hosted will be based on submission of a good abstract.

THE DEADLINE FOR ABSTRACTS SUBMISSION IS 5TH JUNE 2009.

Yours sincerely,

John R.S. Tabuti

Chairperson, Organizing committee

John R.S. Tabuti (Ph.D.), Associate Professor/Ethnobotanist Institute of Environment and Natural Resources, Makerere University. P.O. Box 7062 Kampala, Uganda. Alternative e-mail: jrstabuti@yahoo.com Tel: +256 (0) 414 530 135; Mobile: +256 (0) 772 960 880 Fax: +256 (0) 414 530 134 Africa Regional representative for the International Society of Ethnobiology

"John R.S. Tabuti" <jtabuti@muienr.mak.ac.ug>

ULisbon BioinformaticsCompBiol

Dear all

I am pleased to announce the new edition of the Bioinformatics and Computational Biology Master Course at the University of Lisbon, Portugal. For this edition (2009-2010) the courses are Lectured in Portuguese only, in due time some courses will be lectured in English again. For further information check our webpage http://bbc.fc.ul.pt Octávio S. Paulo Ph.D. Assistant Professor Centro de Biologia Ambiental Departamento de Biologia Animal Faculdade de Ciências da Universidade de Lisboa P-1749-016 Lisboa Portugal

ofpaulo@fc.ul.pt

UMichigan EvolutionaryEpidemiology Jul27-31

The University of Michigan School of Public Health is offering a one-week, one credit course from July 27-31 on *Evolutionary Epidemiology (< http://www.sph.umich.edu/epid/GSS/courses/1week.html > **EPID 788) < http://www.sph.umich.edu/epid/GSS/courses/1week.html >** *taught by Betsy Foxman and Randolph Nesse. For details and an application, click above.

Description: New applications of evolutionary theory to medicine are growing and helping to explain apparent paradoxes, such as rapidly increasing rates of breast cancer, increased asthma vulnerability in certain populations and the metabolic syndrome (For details see The Evolution and Medicine Review at http://evmedreview.com. Epidemiologists have begun to apply these principles and ask new questions, such as do genes that vary by latitude explain hypertension, and how might public health interventions for infectious disease be "evolution-proofed" (see discussion of the American College of Epidemiology 2008 meeting: Dawn of Evolutionary Epidemiology (http://acepidemiology.org/meetings/-2008Tuscon/08AMSpeakerHandouts.asp). This course will explore how epidemiologists and other public health workers can make use of these advances in their own work. Applying evolutionary theory can sharpen research questions, raise new possible explanations for observed phenomena and identify new types of exposure and outcome measures. Pre-requisite: No prior training in evolutionary biology is assumed. Full info at http://www.sph.umich.edu/epid/GSS/-courses/1week.html rmnesse@gmail.com

UWashington SummerInstStatGenetics EarlyRegistration

The early-bird registration fee for the Summer Institute in Statistical Genetics will not be available after May 18. Some modules have now closed and other modules are close to being full. Details about the Institute are at http://www.biostat.washington.edu Bruce S Weir Professor and Chair Department of Biostatistics University of Washington Seattle, WA 98195-7232

Phone: (206) 221-7947 Email: bsweir@u.washington.edu

Bruce Weir <bsweir@u.washington.edu>

Valencia MolEvol Jun15-19

Fourth Course on Molecular Evolution, Phylogenetics, Phylogenomics and Adaptation

15 - 19 June 2009, Valencia. Spain

Hernán Dopazo, Co-ordination

The course aims to provide the necessary background to understand the basic concepts from comparative and evolutionary biology that are frequently used in molecular biology and bioinformatics analyses. The course consists in five full-day sessions with an adequate balance between theory and computer practice, oriented to solve frequent problems and hypothesis testing. The course includes a session of phylogenomic analysis and functional annotation including the most recent developments in this area. Among other tools, attendees will become familiar with Phylip, Phyml, PAML, TreePuzzle, MrBayes, Modeltest, ProTest, JModelTest programs and tools developed in our department such as Phylemon, FatiGO and FatiScan. The course is mainly intended for professionals in the field of biology and chemistry who work on areas related to biological sequence analysis.

Course fee is 300 euros

Application Deadline: 18th May 2009

More information at: http://bioinfo.cipf.es/courses/-mol_evol_phylo_4ed/ Language: the official language of the course will be english unless all attendees speak spanish.

Phylemon web server: http://phylemon.bioinfo.cipf.es Comparative Genomics Unit Bioinformatics and Genomics Department Centro de Investigación Príncipe Felipe (CIPF) Valencia, Spain.

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Hernán J. Dopazo, PhD 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 http://hdopazo.bioinfo.cipf.es/ hernan dopazo <dopazoh@gmail.com>

Venice EvoDevo Sep14-17

Summer School on Evolutionary Developmental Biology Venice, September 14th-17th 2009

Organizers Alessandro Minelli, Michael Akam, Gerd B. Müller and Giuseppe Fusco

A summer school on Evolutionary Developmental Biology will be held at the Istituto Veneto di Scienze, Lettere ed Arti (Venice, Italy) from September 14th to September 17th 2009.

The school will be articulated into eight theoretical/practical units introducing the students to a diversity of resources and working tools in evo-devo, and to likely pitfalls in their use.

The School is sponsored by the Istituto Veneto di Scienze, Lettere ed Arti, the Konrad Lorenz Institute for Evolution and Cognition Research, Vienna, and the University Museum of Zoology, Cambridge.

The teaching panel includes M. Akam (Cambridge), M. Babu (Cambridge), G. Fusco (Padova), J. Jaeger (Barcelona), R. Jenner (London), J. Jernvall (Helsinki), A. Minelli, (Padova), G.B. Müller (Vienna), S.A. Newman (New York), I. Salazar-Ciudad (Barcelona), E. Schierenberg (Köln).

The school is hosted in Palazzo Franchetti, a splendid, recently restored building, located in the very centre of Venice and facing the Grand Canal.

Participants will be asked to pay a fee of 300 Euros, to contribute to their living expenses in Venice.

Deadline for applications: May 30th 2009.

For details, visit < http://www.istitutoveneto.it/-EDB/ >http://www.istitutoveneto.it/EDB/

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Giuseppe Fusco <giuseppe.fusco@unipd.it>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.