
E v o l D i r

April 1, 2008

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

Forward

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.

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Conferences

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Adelaide GeneticsSocAustralAsia Jul7-10

Genetics Society of AustralAsia Annual Conference
GSA2008 Adelaide, 7-10 July 2008

The annual conference of the Genetics Society of AustralAsia will take place in Adelaide, Australia on 7-10 July 2008.

There will be three full days of symposia and concurrent sessions covering the breadth of genetics. Abstracts for oral and poster presentations are welcome on any topic in genetics.

The early registration and abstract submission deadline is 1 May 2008.

Symposia will be held on the following topics:

Teaching Genetics and Evolution Genetics of Development Comparative Genomics Bioinformatics Rates of Evolution Evolutionary Genetics

Confirmed plenary and symposium speakers include:

Ken Wolfe Fred Nijhout Patricia Pukkila Jenny Graves David Penny Allen Rodrigo Eldon Ball Mathew Bellgard Simon Ho Matt Phillips Brett Lidbury Karen Burke da Silva David Adelson Brian Dalrymple Richard Harvey Sally Dunwoodie

For more information please see the conference website:
<http://www.adelaide.edu.au/gsa2008> The GSA2008 Organising Committee

Jack da Silva <jack.dasilva@adelaide.edu.au>

Barcelona EarlyMetazoanEvolution Oct24-25

Dear colleagues,

We are pleased to announce that registration to the “ICREA Conference on the Origin and Early Evolution of Metazoans” is now open through the web page <http://www.originmetazoa.com>. The meeting will be held in the PRBB (Parc de Recerca Biomedica de Barcelona), Barcelona, Spain, 24th-25th October 2008.

Attendance will be free, but registration is required and limited to the first 200 people. Registration will include coffee and tea during breaks. We will not be providing accommodation, so you may want to search for hotels now. We will supply a list of suitable hotels nearby PRBB in the meeting webpage soon.

Registration deadline is July 15th 2008.

Best regards,

Inaki Ruiz-Trillo, Pere Martinez and Andrew J. Roger <http://www.originmetazoa.com> organizers@originmetazoa.com

inaki.ruiz@icrea.es

Barcelona SMBE 2008 Jun5-8 AnimalEvo-DevoSymposium

Dear readers,

We invite submissions of abstracts for the Animal Evo-Devo symposium at the SMBE2008 Conference in Barcelona on June 5-8.

The breadth of genome sequence databases together with the diversity of species under study are enabling a greater understanding of evolutionary change in developmental processes. This symposium aims to balance presentation of invertebrate and vertebrate systems, with a particular focus on phenotype-driven approaches addressing the generation of morphological novelty.

Those of evolutionary or developmental biology backgrounds with an interest in this area are as welcome as those already firmly in the evo-devo field.

Invited Speakers: Gunter Wagner (Yale University, USA) “Molecular Mechanisms of Innovation: different from Adaptation?”

Jukka Jernvall (University of Helsinki, Finland) “How many genes does it take to make mammalian dental diversity?”

Co-organizers: Michel Milinkovitch (Free University of Brussels), Denis Headon (University of Manchester)

Abstract deadline: March 3, 2008

Conference website: <http://www.smb2008.com/>
“Michel C. Milinkovitch” <mcmilink@ulb.ac.be>

Barcelona SMBE 2008 Jun5-8 MolEvolEpidemiology

Dear colleagues,

We would like to invite you to submit your abstracts (talks and posters) for the symposium “Molecular and evolutionary epidemiology at the 2008 annual meeting of the Society for Molecular Biology and Evolution (SMBE) in Barcelona, Spain, from June 5th to 8th, 2008.

Symposium description: The analysis of microbial and viral pathogens represents one of the most prolific areas currently contributing data for the study of genetic variation and molecular evolution. The application of evolutionary theory to these analyses has produced many relevant results with direct application to public health issues, from local to world-wide scales. Identifying the sources of outbreaks, tracing routes of transmission, tracking the natural reservoir(s) of emerging pathogens are among the best known results of molecular epidemiology analyses but the integration of evolutionary thinking into epidemiology extends farther: two recent cases have provided critical evidence for the innocence and culpability, respectively, of medical personnel accused of transmitting HIV to hundreds of Libyan children and HCV to almost 300 patients in Spain. The latter case was taken to court and the evolutionary analysis provided the basis for a 2000-years conviction of an anaesthesiologist. However, by reconstructing the evolutionary history of different pathogens, evolutionary epidemiology allows to gain a much deeper insight on the factors and processes that have led to their current expansion and to make informed predictions about future trends. Also, the modeling of epidemiological scenarios is greatly improved by the incorporation on

information about the genetic variation and evolutionary history of the organisms being considered. The proposed workshop is aimed at presenting the latest results and developments in this area with special emphasis on their application to public health issues, which will hopefully make it very attractive for young investigators looking for new areas in which to develop their recently learned skills, techniques and analytical tools.

Confirmed Main Speakers: Oliver G. Pybus (Oxford University, UK); Fernando Gonzalez-Candelas (Univ. Valencia, Spain).

Symposium organiser: Fernando Gonzalez-Candelas (Univ. Valencia, Spain)

Details of the conference can be found here: <http://www.smbe2008.com/> Abstract submission deadline: March 3, 2008 Early registration deadline: March 10, 2008

– Fernando Gonzalez –

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Barcelona SMBE 2008 Jun5-8 Prok Genomics

Dear colleagues,

We would like to invite you to submit your abstracts (talks and posters) for the symposium on prokaryotic genomics at the 2008 annual meeting of the Society for Molecular Biology and Evolution (SMBE) in Barcelona, Spain, from June 5th to 8th, 2008.

Abstract submission deadline: March 3, 2008!!

THE CROSSROADS BETWEEN PROKARYOTIC GENOMICS, ECOLOGY AND ADAPTATION

The now routine generation of vast nucleotide sequence datasets has transformed our understanding of the dynamics of molecular evolution in prokaryotes and is providing ever more detailed insights into the emergence, spatial structuring, specialisations and interactions between different bacterial lineages in nature. We are

now beginning to understand the trade-offs involved in determining bacterial lifestyle choices: To be a specialist or a generalist? A pathogen or a commensal? To cooperate or to cheat? This symposium captures the continuing erosion of the barriers between comparative genomics, population genetics, biogeography, metagenomics and experimental evolution to explore how bacteria continually adapt in the face of shifting selective landscapes. Four different threads are combined under this banner: i) Comparative genomics overview on how molecular processes (e.g. gene transfer) impact on ecological adaptation, ii) how ecology in turn impacts on sequence evolution iii) Metagenomics: detecting the adaptive basis underlying bacterial diversity using metagenomics, and iv) identifying the molecular basis of adaptation in experimental systems. The synthesis of these threads into a single symposium should prove a timely and invaluable opportunity for world-experts in their respective fields to explore fundamental aspects of bacterial micro-evolution and adaptive radiation. A comparative genomics overview at the start of the session will highlight the role of horizontal transfer in the exploitation of new niches. The role of stochastic forces, in particular relating to the effective population size and selective sweeps, will also be considered in the context of ecological specialisation and host adaptation. The inclusion of experimental evolution will add the basic question of trade-offs between cooperation and competition between populations and cells, how these trade-offs can be studied at the molecular level. The symposium is deliberately broad, and will encapsulate some basic debates concerning the intersection between the ecological and molecular bases of bacterial populations.

Confirmed Main Speaker: Julian Parkhill (Sanger Center, UK);

Symposium organisers: Ed feil (Univ. Bath, UK), Eduardo Rocha (Institut Pasteur, France)

Details of the conference can be found here: <http://www.smbe2008.com/> Abstract submission deadline: March 3, 2008 Early registration deadline: March 10, 2008

CornellU ISBE 2008 Aug15

The ISBE meeting is an important biennial conference mainly attended by evolutionary biologists. This is why we thought that the advert may be attractive for the

audience of EvolDir.

Advances in statistical philosophy and experimental design in behavioural ecology: a new ABC framework ISBE 2008 post-conference symposium, Cornell University, Ithaca, New York, USA, August 15, 2008

We would like to solicit an active discussion among evolutionary biologists who are concerned with recent advancements in the interpretations and analyses of behavioural and ecological data. The Behavioral Ecology Congress in 2008 at Cornell University offers an excellent opportunity for such a discussion, as full-day post-congress symposia are available for this purpose. With the abstract proposed below, we are planning to apply for a possibility to organize a post-congress symposium, for which we seek contributors. We would like to invite participants who would be interested in sharing their experience with a broad audience on the highlighted statistical issues. If you are registered (or planning to register) for the main program of the conference, and are potentially willing to give a short talk in our symposium, please contact either Laszlo or Shinichi for more information:

Laszlo Zsolt Garamszegi laszlo.garamszegi@ua.ac.be

Shinichi Nakagawa itchyshin@yahoo.co.nz

PROPOSED ABSTRACT Advances in statistical philosophy and experimental design in behavioural ecology: a new ABC± framework Laszlo Zsolt Garamszegi & Shinichi Nakagawa Department of Biology, University of Antwerp, Wilrijk, Belgium Department of Animal & Plant Sciences, University of Sheffield, Sheffield, UK

We aim to bring together researchers with different interests in behavioural ecology and evolutionary biology to discuss recent significant developments in the interpretation of behavioural and ecological data. Analytical tools that incorporate statistical philosophies not relying on statistical significance have been highlighted in recent years, but are still in limited use in our field, because of common (mis)beliefs and familiarity with classical approaches. We suggest that conventional hypothesis testing based on statistical significance is often misleading or even incorrect in some circumstances, because it assesses biological hypotheses using an all-or-nothing criterion, instead of along a continuum. It also leads to publication bias, due to unreported non-significant effects, hindering the field from advancing as cumulative science. We propose an ABC framework, in which such problems can be powerfully treated. The ABC framework will open up new horizons for testing evolutionary questions while it sets straightforward guidelines for researchers in the field to follow. In this

framework, A stands for AIC (Akaike Information Criterion), a popular tool of information theoretic IT (information theoretic) approaches that address the trade-off between model complexity and goodness of fit. This allows an objective assessment of the potentially large number of competing models that could describe the data equally well. B refers to Bayesian inference, in which new empirical evidence is combined with past knowledge to update or newly infer the probability of the hypotheses under test. Bayesian approaches also harness us with capabilities of parameter estimation in a way that alternative to the classical framework. C emphasizes the importance of confidence intervals, which give the precision of parameter or effect size estimates. Effect size estimates and their confidence intervals should be at the heart of statistical inference because they relate to biological importance in a way that statistical significance does not. Effect size estimates also facilitate meta-analysis, which has recently established itself as an essential tool for quantitative review in the field. The three components of our ABC framework complement each other. We would like to focus on the basic philosophy behind these approaches by considering pro- and contra arguments, and provide a broad array of examples of biological questions that can be tested in correlative or experimental designs, in intra- or inter-specific contexts, and in different taxonomic groups.

Laszlo Zsolt Garamszegi

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Garamszegi Laszlo <laszlo.garamszegi@ua.ac.be>

Crete Wolbachia Jun9-14

FIFTH INTERNATIONAL WOLBACHIA CONFERENCE ORTHODOX ACADEMY OF CRETE KOLYMBARI, CRETE, GREECE JUNE 9 - 14, 2008

Third Circular – March 18, 2008

This is the final reminder for the registration to the 5th International Wolbachia Conference that will be held from June 9-14 at the Orthodox Academy of Crete (<http://www.oac.gr/>), Kolymbari (<http://www.west-crete.com/holidays-kolymbari.htm>), Crete, Greece.

REGISTRATION AND ACCOMMODATION

Please complete and send the Registration and Accommodation Form to Aggeliki Saridaki (asari-dak@cc.uoi.gr) by March 31, 2008.

The registration fee (150 Euros per participant) should also be sent by check or by wiring funds by March 31.

REGISTRATION AND ACCOMMODATION FORM

Name:

Institution:

Postal Address:

Tel:

Fax:

E-mail:

Please give specific dates: arrival: _____ departure: _____

Dates for additional nights: _____

Roommate Request (if any): _____

All rooms are non-smoking

Please advice for special needs

Confirmation will be sent before the meeting Receipts will be given at the meeting

PAYMENT INFORMATION FOR REGISTRATION FEES

PLEASE SEND FEES PAYABLE IN EURO CURRENCY BY MARCH 31, 2008

PREFERABLY WIRE FUNDS to:

Name of Account Holder: Research Committee - University of Ioannina

Bank Name: PIRAEUS BANK (Branch 2405)

Address: Demokratias Square, 45444 Ioannina, Greece

Bank Account Number or IBAN: GR20 0172 4050 0054 0503 4810 310

Bank Code - BIC or SWIFT: PIRBGRAA

ALTERNATIVELY CHECKS payable to:

Research Committee - University of Ioannina SEND checks to:

Attn. Assoc. Prof. Kostas Bourtzis Department of Environmental and Natural Resources Management University of Ioannina

2 Seferi Street

30100 Agrinio, GREECE

Tel. +30-26410-74114 Fax. +30-26410-74171 e-mail: kbourtz@uoi.gr

WIRE FUNDS OR PAYMENT BY CHECK PLEASE NOTE:

Important 1: Please mention the Conference Code Number: 12229

Important 2: If wiring funds, please fax to my attention (+30-26410-74171) the respective certificate with the transfer date and number.

Important 3: Expenses for funds transfer should be paid by the conference participants.

FINANCIAL SUPPORT TO PhD STUDENTS

Financial support covering registration fees, lodging and meals at the meeting (~ \$500 US per person) is available for graduate students attending the Wolbachia meeting. Funds are not available for travel expenses. Support is provided by the US NSF Frontiers in Integrative Biology Research Grant to Jack Werren.

Students wishing to apply for this support should send an application to Cindy Landry at cyly@mail.rochester.edu. Please refer to "Wolbachia Meeting Student Support" in the subject line. Applications should be received by April 15th, although late applications will be considered if residual funds are available. Please include the information below to the email:

Name

Email address

Department & Institution

Advisor's Name

Advisor's email address

Abstract of Your Planned Research Presentation Short Curriculum Vitae in .pdf or .doc format

Please note that students receiving the support award should prepay for their registration and lodging fees and will be reimbursed after the meeting following submission of the receipts. Attendance at the MLST and Education Workshops offered during the meeting is required, as the funds are provided for this purpose.

ABSTRACTS AND PRESENTATIONS

Presentation will be in oral or poster format. Oral sessions will include 20-25 minute talks. The Organizing Committee does encourage poster presentations. The abstracts should be as informative as possible. After a review of the abstracts, the organizing committee will decide on the final scientific program. Deadline for e-mail submission of Abstracts for Presentations and Posters is 15 April, 2008. Please submit them to: kbourtz@uoi.gr, mentioning the following details:

Oral or Poster presentation?

Title: Author(s), affiliation(s) and email of corresponding author Abstract (approximately 250 words)

If you have any questions or suggestions, please do not hesitate to contact me (kbourtz@uoi.gr).

Looking forward to seeing you at Kolymbari, for the Organizing Committee, Kostas Bourtzis

Wolbachia Conference Organizing Committee:

Kostas Bourtzis, University of Ioannina, Greece

Takema Fukatsu, Nat. Inst. of Advanced Industrial Science and Technology, Japan

Greg Hurst, University of Liverpool, United Kingdom

Scott O'Neill, University of Queensland, Australia

Barton Slatko, New England Biolabs Inc., USA

Mark Taylor, Liverpool School of Tropical Medicine, United Kingdom

Jack Werren, University of Rochester, USA

Kostas Bourtzis, PhD Associate Professor in Molecular Biology and Biochemistry,

— / —

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>

DalhousieU EvolutionaryProtistology Jul21-26

The International Society for Evolutionary Protistology (ISEP) is holding its 17th Meeting 21-26 July, 2008, in Halifax, Canada, on the campus of Dalhousie University. This is a joint meeting with the International Society of Protistologists (ISOP).

The meeting website is: <https://protist2008.dal.ca/> In addition to contributed papers, the meeting will host symposia on Protist phylogenomics, Cell compartmentalization in protists, and major events in Protist evolution.

The meeting will be preceded by the Tree of Life Web Project Protist Diversity Workshop (see <https://protist2008.dal.ca/TOL-protist.diversit.php>), an unique event co-sponsored by the Canadian Institute

for Advanced Research (CIFAR) program in Integrated Microbial Biodiversity, and the Tula Foundation. This will be held in Halifax on the 19-20 July.

Registration and abstraction submission for the combined ISEP/ISOP meeting is now open. The deadline for abstract submission and registration at the 'early' rate is May 15th.

In order to make the meeting accessible to all scientists and trainees, on-campus dormitory-style accommodation is available, in addition to nearby hotels. Student accommodation starts at <\$30 Can per day.

Visit <https://protist2008.dal.ca/> for registration, and for more details about the conference.

Sina Adl Alastair Simpson

Alastair.Simpson@Dal.Ca

Einsiedeln Switzerland PhDStudents EMPSEB14 Sep8-13

Dear Prof. Golding,

me and fellow phd-students of the Universities of Basel and Bern, Switerland, are organising the next European meeting of PhD students in Evolutionary Biology in Einsiedeln, Switerland. Could you please put the following text on the evoldir webpage? thanks a lot! Christoph Grüter

We are pleased to announce the next European Meeting of PhD Students in Evolutionary Biology (EMPSEB 14), 8th - 13th September 2008, Einsiedeln, Switzerland. This student conference brings together European students in an informal atmosphere, where they can discuss their work without the pressure of presenting to senior academics. Present your work, discuss your research ideas, meet new collaborators, receive feedback on your talk, and make new friends from all over Europe!

Important date: 1 April 2008: beginning of online registration

Plenary lectures by:

Sebastian Bonhoeffer, ETH Zurich, Switzerland Ashleigh Griffin, University of Edinburgh, UK Angela Hay, University of Oxford, UK David Hosken, University of Exeter, UK Alain Jacot, Max Planck Institute for Ornithology, Germany Hanna Kokko, University of Helsinki, Finland Daniel Rankin, University of Bern,

Switzerland Tom Wenseleers, Catholic University of Leuven, Belgium

For registration and information please consult the EMPSEB 14 website:

<http://www.empseb.unibe.ch/> We are looking forward to see you in Einsiedeln!

The EMPSEB 14 organizing committee

Ralph Dobler, Peter Biedermann, Melanie Dietz, Barbara Fisher, Christoph Grüter, Alexander Kotrschal, Roger Schürch, Francisca Segers

Dr. Christoph Grueter Division of Behavioural Ecology University of Bern Wohlenstrasse 50a CH-3032 Hinterkappelen Switzerland Phone: +41(0)31 631 91 61 Fax: +41(0)31 631 91 41 christoph.grueter@esh.unibe.ch <http://www.zoology.unibe.ch/behav/index.php> and <http://biolo.bg.fcen.uba.ar/inssoc.htm> visit www.empseb.unibe.ch Grüter Christoph <christoph.grueter@esh.unibe.ch>

Estonton Georgia SEPEEG 2008 Oct24-26

Mark your calendars!

The 2008 SouthEastern Population Ecology and Evolutionary Genetics (SEPEEG) meeting will be held on the weekend of October 24 - 26.

The meeting will take place at Rock Eagle conference facility, which is in Eatonton, Georgia. Eatonton is about an hour east of Atlanta, and is easily accessible from Interstate 20.

Keeping with the tradition of SEPEEG, the 2008 meeting will be informal and accommodations will be on the rustic side. Registration will be available June 1st - September 15th, and we expect the cost to be similar to previous SEPEEG meetings (i.e., low!). Talk and poster submissions are encouraged from undergrads, grad students, post-docs, and faculty. This will be a one talk at a time meeting, with no concurrent sessions.

SEPEEG 2008: <http://mendel.genetics.uga.edu/index.php?page=sepeeg-2008> Rock Eagle: <http://www.georgia4h.org/public/facilities/rockeagle/default.htm>

The meeting organizers are Kelly Dyer, David Hall, David Moeller, and the University of Georgia Genet-

ics Department.

Please contact any of us with questions.

Kelly Dyer (kdyer@uga.edu) David Hall (davehall@uga.edu) David Moeller (dmoeller@uga.edu)

kdyer@uga.edu kdye@uga.edu

FloridaStateU SEEC Evolution Mar28-30 2

This is a friendly reminder that early registration for the Southeastern Ecology and Evolution Conference is nearing an end (February 29th). Early registration is only \$15! Once this closes, registration increases to \$35. Registration fees include some meals, a Saturday night social, T-shirt and other conference accouterment. You can find registration information at <http://bio.fsu.edu/~eerdg/seec/index.htm> as well as lodging and directions. Also on the website you can find information on the distinguished speakers we have lined up, including our own Dr. Joseph Travis and Dr. Walter Tschinkel. Additionally, we are still accepting abstracts for poster session and talks- this is a great opportunity to gain experience with an audience of peers. We will be accepting abstracts until March 14th.

We look forward to seeing you this spring in Tallahassee! (See call for abstracts below.)

Florida State University will host the 2008 Southeastern Ecology and Evolution Conference and is announcing a call for abstracts for presentations of research. This is a scientific symposium aimed at graduate, post-doctoral, and undergraduate researchers in the fields of ecology, systematics, and evolutionary biology. The conference will be held on the campus of Florida State University in Tallahassee, Florida on March 28-30, 2008.

Abstract Submission Information

Researchers interested in presenting posters or 15-minute talks are invited to submit abstracts pertaining to: - Animal Behavior - Conservation - Ecology - Evolution - Functional Morphology - History and Philosophy of Science - Systematics

The deadline for the submission of abstracts is Friday March 14, 2008 at 5:00 PM, EST. Please submit your abstract along with registration at the SEEC website, found at <http://bio.fsu.edu/~eerdg/seec/>. Abstracts should be limited to 250 words, and please include any

primary and co-authors as well as session preference. Information about poster and talk requirements is available on the SEEC website.

Please contact David McNutt (dmcnutt@bio.fsu.edu) for questions regarding registration or abstract submission, or general questions about SEEC to Amanda Buchanan (abuchanan@bio.fsu.edu) or Eric Jones (ejones@bio.fsu.edu).

– Nathaniel K. Jue Ph.D. Candidate Florida State University Department of Biological Science Conradi Building Tallahassee, FL 32306

jue@bio.fsu.edu jue@bio.fsu.edu

Fribourg Switzerland Aging May29-30

Symposium Aging: linking evolution with mechanisms Fribourg, Switzerland, 29-30 May 2008.

Information and call for contributed talks

This symposium aims to bring together evolutionary biologists who address the mechanisms of aging, and molecular biologists whose work has implications for understanding evolutionary processes shaping aging.

Invited speakers: Martin Ackermann (ETH Zurich, Switzerland) Adam Antebi (Baylor College of Medicine, Houston, USA) Vera Gorbunova (University of Rochester, USA) Scott D. Pletcher (Baylor College of Medicine, Houston, USA) Marc Tatar (Brown University, Providence, USA) Rudi G.J. Westendorp (University of Leiden, The Netherlands)

We will combine invited talks with 12 contributed talks. We therefore invite submissions of suitable talks. To submit your talk, please send a title and abstract to Tadeusz.Kawecki@unil.ch, with “Aging symposium: talk submission” in the subject field. Deadline: March 31, 2008.

Participation in the meeting is free (no registration fee), and limited funding is available to cover the hotel expenses of contributing speakers. For further information see the meeting website at www.unifr.ch/-/biol/ecology/aging Organizers Tad Kawecki (University of Lausanne) Laurent Keller (University of Lausanne) Fritz Mueller (University of Fribourg)

– Tadeusz J. Kawecki Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lau-

sanne, Switzerland tadeusz.kawecki@unil.ch

Tadeusz.Kawecki@unil.ch Tadeusz.Kawecki@unil.ch

KansasCity ArthropodGenomics Apr11-13 Deadline2

You can still submit a poster abstract and register to attend the 2ND ANNUAL ARTHROPOD GENOMICS SYMPOSIUM: NEW INSIGHTS FROM ARTHROPOD GENOMES April 11-13, 2008, Muehlbach Hotel (operated by Marriott) Downtown Kansas City

The room block at the Muehlbach/Marriott hotel will expire 3/20/08 (or prior to 3/20 if the block sells out); so make your hotel reservations TODAY! A link for making reservations at the discounted room rate can be found at www.ksu.edu/agc/symposium.shtml or telephone 1-800-228-9290.

The deadline to submit POSTER ABSTRACTS for presentation during two poster sessions has been extended!!! We welcome your presentation of a poster at the Symposium. Abstract Guidelines can be found at www.ksu.edu/agc/symposium.shtml.

REGISTRATION continues to be open! On-line registration, a schedule, brochure and additional information are available at www.ksu.edu/agc/-symposium.shtml . SYMPOSIUM WEBSITE: www.k-state.edu/agc/symposium.shtml

SYMPOSIUM PROGRAM: The main symposium sessions will take place on Friday-Saturday, April 11-12. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Optional workshops are scheduled for Thursday and Friday evenings. An evening of jazz and KC barbeque is planned for Saturday night. On Sunday morning, participate in a roundtable discussion with the ArthropodBase Consortium. Activities will conclude by noon on Sunday.

FEATURED SPEAKERS: **John Kenneth Colbourne, Indiana University, Preservation, expansion and invention of crustacean genes with reference to insect genomes. **Christine G. Elsik, Georgetown University, Unusual base composition of the honey bee genome. **Sarjeet S. Gill, University of California, Riverside, Mosquito midgut interactions with bacterial toxins. **Catherine A. Hill, Purdue University, Tick genome organization and evolution. **Thomas Kaufman, Indiana University, The latest news from

CNN: What the 12 sequenced *Drosophila* genomes have told us about rapidly evolving genes and positive selection. **J. Robert Manak, University of Iowa, Empirical annotation of arthropod genomes using tiled genomic microarrays. **Subbaratnam Muthukrishnan, Kansas State University, Functional genomics of insect chitin metabolism. **Hugh M. Robertson, University of Illinois at Urbana-Champaign, What we've learned about the insect chemoreceptors from arthropod genome projects. **Bruce R. Schatz, University of Illinois at Urbana-Champaign, BeeSpace: Interactive functional analysis of arthropod genomic data. **Jeff Stuart, Purdue University, Avirulence, sex determination, and a physical map of the Hessian fly genome. **Judy Willis, University of Georgia, Insect cuticular proteins: Annotation, proteomics, expression, evolution. **Evgeny Zdobnov, University of Geneva, Medical School, Switzerland, A comparative perspective on insect genomes.

KANSAS CITY JAZZ AND BARBEQUE: Participants are encouraged to stay Saturday night for an optional evening of jazz and KC barbeque in the historic 18th and Vine district.

WORKSHOPS AND ROUNDTABLE DISCUSSION: On Thursday evening, a workshop on "Community Contributions to Genome Annotation" will feature a presentation on use of the Apollo Genome Annotation Curation Tool by Dr. Chris Elsik (BeeBase). On Friday evening, Dave Clements (NESCent) and Scott Cain (CSHL) will lead a workshop, "Chado Databases and Integration with GMOD Tools." Throughout the meeting, arthropod genome database and bioinformatics tool developers will be available for individual training on Apollo and database use as well as BeeSpace, the automated literature annotation system developed by Bruce Schatz and colleagues. On Sunday morning, participate in a roundtable discussion led by members of the ArthropodBase Consortium regarding the generation of integrated arthropod genome databases and tools for genome analysis, and community curation. Symposium attendees are invited to participate in these additional events.

REGISTRATION: The registration fee of \$325 (\$200 for graduate and undergraduate students), includes a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and light refreshments at the Friday poster session. Additional fees apply for the Apollo Workshop Thursday evening and Saturday night dinner.

We look forward to seeing you in Kansas City! Please share this announcement with colleagues and students!

Susan J. Brown, Professor Director, Center for Ge-

omic Studies on Arthropods Affecting Human, Animal and Plant Health by Doris Merrill, Program Coordinator K-State Arthropod Genomics Center Division of Biology, Kansas State University 116 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, dmerrill@k-state.edu

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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>

Marseilles 11thEvolBiol Videos Sep24-26

Dear All,

We are pleased to inform you that the 12th Evolutionary Biology Meeting at Marseilles will take place on 24th 25th 26th September 2008.

We are also pleased to inform you that the video of the oral presentations are available at http://www.univ-provence.fr/webtv/?liste=biology_meeting_2007

We would like to thank once more all the participants for their outstanding work and we are waiting for you to continue sharing the ideas and works of all next September.

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

Best wishes,

Axelle

Egee@univ-provence.fr

Marseilles 12thEvolBiol Sep24-26 deadline

Dear All,

We are please to inform you that the early dead line of the 12th Evolutionary Biology Meeting at Marseilles (24th 25th 26th September 2008) will be on 31st March.

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

Axelle Pontarotti

Egee@univ-provence.fr

Portland FishAdaptation Jul28-Aug1

We invite abstract submissions for oral presentations in a symposium on the Genomics of Adaptation in Fish Populations to be held at the International Congress on the Biology of Fish in Portland, Oregon from July 28th - August 1st, 2008. A detailed description of this symposium can be found at

<http://fishbiologycongress8.usgs.gov/icbf8/-symposia.htm#Schulte>

While we cannot offer funding to cover travel expenses, the Fish Biology Congress has generous travel awards for postdocs and graduate students. In addition, there is a competition for best student presentation. All information, including details on abstract submission (deadline April 1st), can be found at

<http://fishbiologycongress8.usgs.gov/index.htm> Please also send an email to tymchuk@zoology.ubc.ca if you are interested in participating in this symposium.

Wendy Tymchuk, PhD University of British Columbia Department of Zoology 6270 University Blvd. Vancouver, BC V6T 1Z4 Phone: 604-822-6759 Email: tymchuk@zoology.ubc.ca

tymchuk@zoology.ubc.ca tymchuk@zoology.ubc.ca

PortTownsend Evo-WIBO Apr18-20 2

This a friendly reminder that Monday, March 17 is the registration deadline for the 2008 meeting of "Evo-WIBO: Evolutionary biologists in the Pacific Northwest*."

The meeting will take place April 18-20, 2008 at Ft. Worden State Park in Port Townsend, Washington. For registration and general information visit:

<http://www.zoology.ubc.ca/evo-wibo>

*Evo-WIBO stands for Evolutionary Biologists from Washington, Idaho, British Columbia and Oregon, although we draw much more widely than that, including Alaska, Alberta, California, and Montana.

– Richard Gomulkiewicz gomulki@wsu.edu PHONE: (509) 335-2527 FAX: (509) 335-3184 <http://www.wsu.edu/~gomulki/> Department of Mathematics; P.O. Box 643113 or School of Biological Sciences; P.O. Box 644236 Washington State University Pullman, WA 99164 USA

gomulki@wsu.edu gomulki@wsu.edu

Raleigh NorthCarolina Genomics Jun4-7

The 2008 American Genetic Association Meeting, Genetics and Genomics of Behavior, will be held June 4-7, 2008, at the Raleigh Sheraton Hotel, Raleigh North Carolina. Details and registration at <https://www.agasympoium2008.org> This meeting's goal is to explore and define the emerging field of behavioral genetics and genomics. The 2008 AGA symposium will feature 18 distinguished speakers, providing a kaleidoscope of recent discoveries with different organisms, encompassing laboratory and field studies, and ranging from mechanistic neurogenetic principles through analyses of genetic architecture and evolution of behavior. Behaviors important for human health and disease will also be covered. Talks by invited speakers include three special keynote lectures. There will be poster sessions and invited short talks selected from submitted abstracts.

Travel fellowships for students and postdoctoral fellows will be made available on a competitive basis to defray the costs for airfare and hotel accommodations.

The deadline for abstract submission and advance registration is April 25, 2008.

agajoh@oregonstate.edu agajoh@oregonstate.edu

ROM Toronto BarcodeOfLife Apr28-29

Canadian Barcode of Life Network 2nd Annual Science Symposium April 28-29, 2008, at the Royal Ontario Museum, Toronto, Canada

We are pleased to announce the 2nd Annual Science Symposium of the Canadian Barcode of Life Network. This is a two day conference and registration is open to anyone interested in attending. The conference will address the key issues involved with a DNA barcode-based approach to biodiversity recognition, including recent bioinformatics developments. On day 1, the conference will address what is known of barcodes for Canadian and international biodiversity. On day 2, the conference will focus on the potential impact of this knowledge by considering emerging technological developments and the ensuing implications for public policy.

Keynote Speakers: Daniel H. Janzen, DiMaura Professor, University of Pennsylvania Scott E. Miller, Office of the Under Secretary for Science at the Smithsonian Institution

Network Research Theme Presentations: Spencer Barrett (University of Toronto) - Plants Brian Golding (McMaster University) - Informatics Paul Hebert (University of Guelph) - Animals Donal Hickey (Concordia University) - Fungi Gary Saunders (University of New Brunswick) - Protists

The abstract submission deadline is 28 March 2008. Abstract submission and registration information can be found at: <http://www.bolnet.ca/scientific-conference.2008.php> Organizers: Royal Ontario Museum University of Guelph Biodiversity Institute of Ontario Canadian Centre for DNA Barcoding Department of Integrative Biology Guelph Institute for the Environment

Inquiries can be directed to:

Robert Hanner, Associate Director Canadian Barcode of Life Network Biodiversity Institute of Ontario & Department of Integrative Biology University of Guelph Guelph, ON N1G 2W1 Canada

Phone: 519-824-4120 x53479 Fax: 519-767-1656 Email: rhanner@uoguelph.ca

robert hanner <rhanner@uoguelph.ca>

of Life Network will take place April 28-29, 2008 at the Royal Ontario Museum in Toronto.

The conference will highlight key advances in a DNA barcode-based approach to biodiversity recognition, including recent bioinformatic developments. Taking place over two days, the conference will address what is known of barcodes for both Canadian and global biodiversity. The impacts of this knowledge will be examined in terms of both technology development and the implications for scientific and public policy.

Keynote speakers: Daniel H. Janzen, DiMaura Professor, University of Pennsylvania Scott E. Miller, Office of the Under Secretary for Science at the Smithsonian Institution

With special Network research theme presentations by: Spencer Barrett (University of Toronto) - Plants Brian Golding (McMaster University) - Informatics Paul Hebert (University of Guelph) - Animals Donal Hickey (Concordia University) - Fungi Gary Saunders (University of New Brunswick) - Protists

Registration will include access to all sessions on April 28th and 29th, after-hours admission to Darwin: the Evolution Revolution, reception and dinner April 28th at the ROM, and refreshments at all breaks and lunches on both days.

Abstract submission deadline has been extended until March 28th. Please submit your abstracts to Sue-Ann Connolly at sujohnst@uoguelph.ca For more information, read the Call for Abstracts found at <http://www.bolnet.ca/Announcement%20-%20Call%20for%20abstracts.pdf> Please register for the conference at <http://www.bolnet.ca/scientific-conference.2008.php> Thank you to everyone who has already registered.

If you wish to assist in spreading the word about the conference, please print the poster found at <http://www.bolnet.ca/bolnet-poster.pdf> for distribution.

Please do not hesitate to contact Sue-Ann Connolly (sujohnst@uoguelph.ca) with any questions regarding the symposium.

Sue-Ann Connolly Information Officer Biodiversity Institute of Ontario University of Guelph Guelph, ON N1G 2W1 Phone: (519) 824-4120 x 56393 Fax: 519-824-5703 Email: sujohnst@uoguelph.ca

sujohnst@uoguelph.ca

ROM Toronto BarcodeOfLife
Apr28-29 2

The 2nd annual symposium of the Canadian Barcode

UAlberta EvolutionOfButterflies 2010

Dear Butterfly Evolutionary Biologists,

We are seeking your feedback to allow us to schedule the best dates for the 6th International Conference on the Biology of Butterflies. As some of you know from the successfully concluded 5th conference last year in Rome, we offered to hold the next conference in Alberta, Canada, in 2010. For those of you who don't know about this conference series, it has been held every few years, mainly in Europe but once in Colorado. The long-standing theme of this conference series focuses attention on recent developments in biology that rely on butterflies as research models, particularly in ecology and evolutionary biology. The organization of these meetings has been quite informal, which is why we are also soliciting feedback from people who were not at the previous meeting, but who might want to attend the next one.

Now we would like to get your opinions on the best dates for the conference during summer 2010. We have three weeks available at our University of Alberta conference centre in Edmonton, and we would like you to vote on which one you would prefer. Would you please vote for the single best week at the preliminary conference website, below? We'll leave the survey up for 10 days.

<http://www.biology.ualberta.ca/biobutterfly2010/-survey.php> Comments of any sort are welcome. Although there is a 5-day time period indicated for each week, we intend to keep the actual conference to 3 or 4 days.

Thank you,

Felix Sperling Jens Roland

Department of Biological Sciences University of Alberta

Felix Sperling, Professor Department of Biological Sciences cw405a Biological Sciences Centre University of Alberta Edmonton, Alberta T6G 2E9 Canada Office: 780-492-3991; Fax: 780-492-9234 <http://www.biology.ualberta.ca/faculty/felix.sperling/> Felix Sperling <FELIX.SPERLING@UALBERTA.CA>

UCaliforniaIrvine MEEGID IX Oct30-Nov1 Moved

01/03/08

Dear Colleagues

the MEEGID IX congress (Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases), which was planned to be held in Nairobi (30th October-1st November 2008), has been rerouted to UC Irvine due to the political events in Kenya (attachment). UCI Professor Francisco J. Ayala has provided his full support, and has accepted to be the main coorganizer. The congress will keep high priority for infectious diseases of special interest to developing countries. Thank you for circulating the information around you (http://www.th.ird.fr/site_meegid/doc/MEEGID_IX_new.pdf; http://www.th.ird.fr/site_meegid/menu.htm).

With kind regards,

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) <http://www.elsevier.com/locate/meegid> IRD representative in Thailand IRD Representative Office French Embassy 29, Thanon Sathorn Tai, Bangkok 10120, Thailand Tel : + (66 2) 627 2190 Fax : + (66 2) 627 2194 Cel: + (66 81) 82 64 056 E-mail : Michel.Tibayrenc@ird.fr Website : <http://www.th.ird.fr> Michel.Tibayrenc@ird.fr

UIIdaho CallForSSB Symposia Jun13-17 2009

Call for 2009 SSB Symposia

The Society for Systematic Biologists invites proposals for symposia at the 2009 SSB meeting to be held at the University of Idaho in Moscow, Idaho 13-17 June 2009. The meeting will be held jointly with the American Society of Naturalists and the Society for the Study of Evolution. Proposals should include (1) a descriptive title, (2) one or two paragraphs explaining the purpose of the symposium and its relevance to systematics, (3) a list of presentations including proposed speakers, their institutions or affiliations, and their presentation titles,

(4) an indication of whether the speakers have been invited and whether they have agreed to participate, and (5) the proposed length of each talk. Symposia are restricted to half-day sessions. The society is particularly interested in symposia whose topics do not overlap with those from previous meetings, that introduce new ideas or synthesize important concepts, or those that are particularly good examples of the analysis of empirical data. Proposals that unite systematics with other fields are also desirable. We encourage participation from young investigators and others typically under-represented in symposia. Limited funding is available. The target date for receipt of proposals is June 1, 2008. Proposals will be discussed and two will be selected at the SSB Council meeting during the 2008 annual meeting in Minneapolis, Minnesota. 2009 Symposia will be announced at the SSB business meeting in Minneapolis. Proposals should be sent by email to the Program Chairperson, George D. Weiblen, gweiblen@umn.edu (Department of Plant Biology, University of Minnesota, 1445 Gortner Avenue, Saint Paul, Minnesota 55108 USA).

Reminder: The deadline for receipt of presentation titles for Evolution 2008 is April 1, 2008. Please register at <http://www.evolution2008.org> SSB <SSBMembership@BurkInc.com>

UIIdahoMoscow SSE2009 Jun13-17 Call for Symposia Proposals

Call for Symposia for 2009Annual Meeting

The 2009 annual meeting of the Society for the Study of Evolution will be held from June 13-17, 2009 in Moscow, Idaho and hosted by the University of Idaho. The Council of the Society invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; (3) a rationale for the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society-sponsored symposium; and (4) a budget stating approximate travel (only) costs.

In evaluating symposium proposals, the Council will favor those proposals whose topics concern newly emerging fields, fields ripe for syntheses, and fields different from those that have been included in recent Society

symposia. The Council particularly encourages proposals that include women, younger investigators and others traditionally underrepresented in Society symposia.

The Council will select two proposals for half-day symposia at its meeting in June 2008. All applicants will be notified of the Council's decision in July. The Society provides partial travel support for organizers and participants in sponsored symposia. Details are available on request. To be assured of full consideration, proposals must be received at the following address by midnight Eastern Standard Time on May 19, 2007:

Dr. Charles B. Fenster, Executive Vice President The Society for the Study of Evolution Department of Biology University of Maryland College Park, Maryland, 20742 USA e-mail: CFenster@umd.edu

Proposals can be sent as paper copies by mail or preferably as e-mail attachments in Word or RTF format (under subject heading: SSE Symposia Proposal).

Thank you,

Charlie Fenster (EVP, SSE)

Charles B. Fenster Department of Biology BIOLOGY/Psychology Bldg. Room 3210

University of Maryland College Park, Maryland 20742 USA phone: 301 405 1640 fax: 301 314 9358

<http://www.life.umd.edu/biology/fensterlab/> Charles Fenster <cfenster@umd.edu>

UIowa Evolution of Sex Jun16-19 2

UPDATES:

We are now accepting applications for student/postdoc travel awards and for contributed talks. The deadline for submission is March 16.

<http://cgg.biology.uiowa.edu/sexrec/registration.php>

General registration will be open on or before April 1. Check the meeting website for more information.

EVOLUTION OF SEX & RECOMBINATION: IN THEORY AND IN PRACTICE

June 16-19, 2008, at the University of Iowa, Iowa City, USA.

<http://cgg.biology.uiowa.edu/sexrec> The Roy J. Carver Center for Comparative Genomics and the Department of Biology at the University of Iowa announces an international conference on the evolution

of sex & recombination. This conference will immediately precede the 2008 Evolution meeting taking place in nearby Minneapolis, Minnesota (June 20-24).

Talks will be given by invited speakers at both the junior and senior level. There will also be opportunities for contributed talks and posters to be given by conference attendees at all levels of seniority. A number of travel awards (10-15) 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

Confirmed speakers include: Philip Awadalla University of Montreal Aneil Agrawal University of Toronto Doris Bachtrog University of California, San Diego Graham Bell McGill University Bill Birky University of Arizona Rhona Borts University of Leicester Bernardo Carvalho Universidade Federal do Rio de Janeiro Andy Peters University of Wisconsin-Madison Brian Charlesworth University of Edinburgh Nick Colegrave University of Edinburgh Tim Cooper University of Houston Ursula Goodenough Washington University-St. Louis Joe Heitman Duke University Michael Hood Amherst College Alex Kondrashov University of Michigan Curt Lively Indiana University David Mark Welch MBL, Woods Hole Stephanie Meirmans University of Bergen Andy Peters University of Wisconsin-Madison Steve Proulx Iowa State University Bill Rice University of California, Santa Barbara Isa Schön Royal Belgian Institute of N.S. Marcy Uyenoyama Duke University Jerry Wilkinson University of Maryland Cliff Zeyl Wake Forest University

Check the conference website for details regarding registration, accommodation, etc.: <http://cgg.biology.uiowa.edu/sexrec/registration.php> A symposium issue to be published in Journal of Heredity is being planned.

All enquiries are encouraged (including potential sponsors) and should be directed to the organizers: sexrec@uiowa.edu

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 Biological Sciences 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/>>

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

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

UIowa Evolution of Sex Jun16-19 Registration

More UPDATES:

1. General registration is now open. Space is limited, so please register as soon as possible.

<http://cgg.biology.uiowa.edu/sexrec/regform2.php> 2. We are still accepting applications for student/postdoc travel awards and for contributed talks. The deadline for submission was extended to April 1.

<http://cgg.biology.uiowa.edu/sexrec/registration.php> 3. Information on Venue, Travel and Accommodation are now available:

<http://cgg.biology.uiowa.edu/sexrec/venue.php> 4. The final schedule of talks is being worked out and will be posted shortly. A tentative schedule of events is available at:

<http://cgg.biology.uiowa.edu/sexrec/-SexRecSchedule.pdf> ----- General Announcement:

³EVOLUTION OF SEX & RECOMBINATION: IN THEORY AND IN PRACTICE²

June 16-19, 2008, at the University of Iowa, Iowa City, USA.

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Confirmed speakers include: Philip Awadalla University of Montreal Aneil Agrawal University of Toronto Doris Bachtrog University of California, San Diego Graham Bell McGill University Bill Birky University of Arizona Rhona Borts University of Leicester Christina Burch University of North Carolina-Chapel Hill Bernardo Carvalho Universidade Federal do Rio de Janeiro Brian Charlesworth University of Edinburgh Nick Colegrave University of Edinburgh Tim Cooper University of Houston Ursula Goodenough Washington University-St. Louis Joe Heitman Duke University Michael Hood Amherst College Alex Kondrashov University of Michigan Curt Lively Indiana University David Mark Welch MBL, Woods Hole Stephanie Meirmans University of Bergen Andy Peters University of Wisconsin-Madison Steve Proulx Iowa State University Bill Rice University of California, Santa Barbara Isa Schön Royal Belgian Institute of N.S. Marcy Uyenoyama Duke University Jerry Wilkinson University of Maryland Cliff Zeyl Wake Forest University

A symposium issue to be published in Journal of Heredity is being planned.

All enquiries are encouraged (including potential sponsors) and should be directed to the organizers: sexrec@uiowa.edu

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 Biological Sciences 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://euplotes.biology.uiowa.edu> >

ULondon SAGE2009 Sep14-17

SAGE2009 - Southeast Asian Gateway Evolution Conference

14-17 September 2009: Royal Holloway University of London

In September 2009 we are holding an international

meeting at Royal Holloway that will focus on the Indonesian Gateway, the current connection between the Pacific and Indian Oceans. The meeting is aimed to bring together Life and Earth Scientists to discuss the history, development and current state of the region.

We shall run SAGE2009 meeting as two parallel scientific meetings, with several plenary sessions and keynote speakers who will be encouraged to explain their subject and give overviews that can be useful to all scientists who attend.

We welcome contributions on all aspects of the geology, oceanography, climate, biology and development of this region, particularly those that cross discipline boundaries, and can explain the relevance of their work to other scientists including non-specialists in the field.

Please download the 1st Circular at <http://sage2009.rhul.ac.uk> To register your interest in attending this meeting, please click on the following link

http://sage2009.rhul.ac.uk/interest/-express_interest_form.html or mail your name and contact details to

SAGE2009 SE Asia Research Group Royal Holloway University of London Egham, Surrey TW200EX, UK

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

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

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

UMinnesota Evolution 2008 Jun20-24 CallForMentors

For the sixth consecutive year, the Undergraduate Diversity at SSE/SSB program, funded originally by the Undergraduate Mentoring in Environmental Biology (UMEB) program at NSF, will take place again at the 2008 meeting of the Society of the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB) in Minneapolis, MN. This year we have teamed up with staff at the National Evolutionary Synthesis Center (NESCent) to send up to 25 undergraduates to the meetings to present posters and receive mentoring from

graduate students, postdocs and faculty in evolutionary biology.

In addition to applications from undergraduates, we hope to hear from graduate students, postdocs and faculty who wish to serve as undergraduate mentors for the meetings. 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. No costs for travel, housing or registration are covered.

If you are interested in serving as a mentor, please send an email to either Rich Kliman (rmkliman@cedarcrest.edu) or Scott Edwards (sedwards@fas.harvard.edu). Please also indicate your broad field of interest, so that we can pair you with appropriate students. And please help spread the word about this very rewarding activity.

Richard Kliman <Rmkliman@cedarcrest.edu>

UMinnesota Evolution 2008 Jun20-24 deadline

Evolution 2008 June 20-24, 2008 University of Minnesota - Twin Cities campus

The deadline for presentation titles is April 1, 2008. Please visit www.evolution2008.org < <http://www.evolution2008.org/> > for more information.

This is the annual meeting of the Society for the Study of Evolution, the Society of Systematic Biologists, and the American Society of Naturalists.

The deadline for receipt of presentation titles including posters and talks is April 1, 2008. Participant registration should be completed by May 2, 2008 to qualify for discounted rates. Evolution 2008 is the premier annual opportunity for sharing scientific research related to evolution.

We look forward to welcoming you to Evolution 2008 and are eager to answer your questions to make your participation a productive and memorable experience. Questions may be directed to Heather Dorr (cceconf3@umn.edu <<mailto:cceconf3@umn.edu>>).

On behalf of the societies, the organizing committees, and the University of Minnesota, thank you for your participation.

George Weiblen Evolution 2008 Program Chair Associate Professor, Department of Plant Biology Herbarium Curator, Bell Museum of Natural History

Carey Madsen <careymadsen@biology.utah.edu>

UMinnesota Evolution 2008 Jun20-24 deadline2

Call for Symposia for 2009 Annual Meeting

The 2009 annual meeting of the Society for the Study of Evolution will be held from June 13-17, 2009 in Moscow, Idaho and hosted by the University of Idaho. The Council of the Society invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; (3) a rationale for the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society-sponsored symposium; and (4) a budget stating approximate travel (only) costs.

In evaluating symposium proposals, the Council will favor those proposals whose topics concern newly emerging fields, fields ripe for syntheses, and fields different from those that have been included in recent Society symposia. The Council particularly encourages proposals that include women, younger investigators and others traditionally underrepresented in Society symposia.

The Council will select two proposals for half-day symposia at its meeting in June 2008. All applicants will be notified of the Council's decision in July. The Society provides partial travel support for organizers and participants in sponsored symposia. Details are available on request. To be assured of full consideration, proposals must be received at the following address by midnight Eastern Standard Time on May 27, 2007:

Dr. Charles B. Fenster, Executive Vice President The Society for the Study of Evolution Department of Biology University of Maryland College Park, Maryland, 20742 USA e-mail: CFenster@umd.edu

Proposals can be sent as paper copies by mail or preferably as e-mail attachments in Word or RTF format (under subject heading: SSE Symposia Proposal).

Charles Fenster <cfenster@umd.edu>

UMinnesota Evolution 2008
Jun20-24 LifeHistoryEvol

SSE SYMPOSIUM, EVOLUTION MEETINGS, Minneapolis 2008 (June 20-24, 2008)

MOLECULAR MECHANISMS UNDERLYING LIFE HISTORY EVOLUTION

Dear Colleague,

We would like to invite you to attend the half-day symposium "MOLECULAR MECHANISMS UNDERLYING LIFE HISTORY EVOLUTION" at the 2008 EVOLUTION MEETINGS, the annual meeting of the Society for the Study of Evolution (SSE) hosted by the University of Minnesota in Minneapolis (June 20-24, 2008).

SYMPOSIUM DESCRIPTION: Evolution by natural selection is due to variation in Darwinian fitness, and variation in fitness is caused by variation in life history traits. Life history theory seeks to understand the causes and consequences of variation in life history traits within and among species. While the field has witnessed rapid progress in explaining the diversity of life history strategies among species, our understanding of many fundamental problems in life history evolution remains limited because we lack information on proximate mechanisms. This interdisciplinary symposium brings together evolutionary biologists from various fields (life history theory, molecular biology, aging, phenotypic plasticity, social behavior, and endocrinology) who use studies of molecular mechanisms to solve fundamental problems in life history evolution in a variety of organisms (plants, insects, echinoderms, birds, and amphibians). Integrating molecular mechanisms into life history evolution is one of the most exciting tasks for integrative evolutionary biologists in the near future; together with the affiliated poster session, this symposium will foster stimulating discussions among biologists interested in this novel, emerging field.

DETAILS on the symposium can be found at:

<http://www.cce.umn.edu/conferences/evolution/-symposia.html> or at

http://www.metamorphnet.org/pb/wp_f6dd1963.html

INVITED SPEAKERS: Derek Roff (University of California), Paul Schmidt (University of Pennsylvania), Gro V. Amdam (Arizona State University), Kathleen

Donohue (Harvard University), Peter McCourt (University of Toronto), Michaela Hau (Princeton University), Daniel R. Buchholz (University of Cincinnati), Andreas Heyland (University of Florida), and Anthony J. Zera (University of Nebraska).

POSTERS: Please note that there is no specific affiliated poster session to this symposium. However, we encourage poster submissions (at <http://www.cce.umn.edu/conferences/evolution/>) which directly and explicitly deal with molecular (genetic, physiological, developmental, and cellular) mechanisms of life history evolution, with a particular emphasis on candidate life history genes and endocrine signaling. If you think that your poster is relevant to our symposium, please feel free to contact us with the title and abstract of the poster and we will add this information to our symposium page.

FURTHER INFORMATION: The SSE meetings, jointly held with the American Society of Naturalists (ASN) and the Society of Systematic Biologists (SSB), will take place between 20-24 June, 2008, at the University of Minnesota in Minneapolis. Details on registration, accommodation, program, and online abstract submission are available at: <http://www.cce.umn.edu/conferences/evolution/> **IMPORTANT DATES AND DEADLINES:** The deadline for presentation titles is April 1, 2008. The deadline for early bird registration at discounted rates is May 2, 2008.

SPONSORS: Society for the Study of Evolution, Dean's Office of the Brown University Division of Biology and Medicine, and Fisher Scientific.

SUGGESTED READING:

Flatt, T., M. P. Tu, and M. Tatar. 2005. Hormonal pleiotropy and the juvenile hormone regulation of *Drosophila* development and life history. *Bioessays* 27:999-1010.

Heyland, A., J. Hodin, and A. M. Reitzel. 2004. Hormone signaling in evolution and development: a non-model system approach. *Bioessays* 27:64-75.

Houle, D. 2001. The character problem in life history evolution. Pp. 109-140 in, *The Character Concept in Evolutionary Biology*. G. P. Wagner, ed. Academic Press.

Roff, D. A. 2007. Contributions of genomics to life-history theory. *Nature Reviews Genetics* 8:116-125.

Zera, A. J., and L. G. Harshman. 2001. The physiology of life history trade-offs in animals. *Annual Review of Ecology and Systematics* 32:95-126.

SYMPOSIUM ORGANIZERS: Thomas Flatt (Brown University, Department of Ecology and Evolutionary

Biology, Providence, USA) and Andreas Heyland (University of Guelph, Department of Integrative Biology, Guelph, Canada). Contact: thomas_flatt@brown.edu or aheyland@uoguelph.ca

We apologize for multiple posting.

Thomas Flatt, Ph.D. Brown University Division of Biology and Medicine

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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>

UMinnesota Evolution 2008 Jun20-24 UndergraduateDiversity

For the sixth consecutive year, the Undergraduate Diversity at SSE/SSB program, funded originally by the Undergraduate Mentoring in Environmental Biology (UMEB) program at NSF, will take place again at the 2008 meeting of the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB) in Minneapolis, MN. This year we have teamed up with staff at the National Evolutionary Synthesis Center (NESCent) to send up to 25 undergraduates to the meetings to present posters and receive mentoring from graduate students, postdocs and faculty in evolutionary biology.

The deadline for applications this year is May 1, 2008. However, proposals will be reviewed and accepted on a rolling basis, SO IT IS ADVANTAGEOUS TO APPLY BEFORE APRIL 15. Applications will consist of a title, author line and abstract of the poster to be presented by the undergraduate; and a one-page statement of academic interests and career goals. The statement should address how attending the Evolution meetings will help meet these goals, and should indicate whether or not the student plans to attend graduate school, if this is known. A letter of recommendation, ideally from the undergraduate's research advisor, should indicate how inclusion of the student will increase diversity of the group participants. It is essential that the student's contact information (both e-mail and mailing address) be included in the materials. All materials should be submitted as pdf files and emailed to Alison Pirie at apirie@oeb.harvard.edu. Details on selection criteria are available at <http://www.oeb.harvard.edu/faculty/>

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

Contact one of the program organizers for more information: Scott V. Edwards (sedwards@fas.harvard.edu) Richard Kliman (rmkliman@cedarcrest.edu) at NESCent: Brian Wiegmann (brian.wiegmann@ncsu.edu) Jory Weintraub (jory@nescent.org)

Richard Kliman <Rmkliman@cedarcrest.edu>

UMinnesota SSE Jun20-24 LifeHistoryEvolution

SSE SYMPOSIUM, EVOLUTION MEETINGS, Minneapolis 2008 (June 20-24, 2008)

MOLECULAR MECHANISMS UNDERLYING LIFE HISTORY EVOLUTION

Dear Colleague,

We would like to invite you to attend the half-day symposium "MOLECULAR MECHANISMS UNDERLYING LIFE HISTORY EVOLUTION" at the 2008 EVOLUTION MEETINGS, the annual meeting of the Society for the Study of Evolution (SSE) hosted by the University of Minnesota in Minneapolis (June 20-24, 2008).

SYMPOSIUM DESCRIPTION: Evolution by natural selection is due to variation in Darwinian fitness, and variation in fitness is caused by variation in life history traits. Life history theory seeks to understand the causes and consequences of variation in life history traits within and among species. While the field has witnessed rapid progress in explaining the diversity of life history strategies among species, our understanding of many fundamental problems in life history evolution remains limited because we lack information on proximate mechanisms. This interdisciplinary symposium brings together evolutionary biologists from various fields (life history theory, molecular biology, aging,

phenotypic plasticity, social behavior, and endocrinology) who use studies of molecular mechanisms to solve fundamental problems in life history evolution in a variety of organisms (plants, insects, echinoderms, birds, and amphibians). Integrating molecular mechanisms into life history evolution is one of the most exciting tasks for integrative evolutionary biologists in the near future; together with the affiliated poster session, this symposium will foster stimulating discussions among biologists interested in this novel, emerging field.

DETAILS on the symposium can be found at:

<http://www.cce.umn.edu/conferences/evolution/-symposia.html> or at

<http://www.metamorphnet.org/pb/wp-f6dd1963.html>

INVITED SPEAKERS: Derek Roff (University of California), Paul Schmidt (University of Pennsylvania), Gro V. Amdam (Arizona State University), Kathleen Donohue (Harvard University), Peter McCourt (University of Toronto), Michaela Hau (Princeton University), Daniel R. Buchholz (University of Cincinnati), Andreas Heyland (University of Florida), and Anthony J. Zera (University of Nebraska).

POSTERS: Please note that there is no specific affiliated poster session to this symposium. However, we encourage poster submissions (at <http://www.cce.umn.edu/conferences/evolution/>) which directly and explicitly deal with molecular (genetic, physiological, developmental, and cellular) mechanisms of life history evolution, with a particular emphasis on candidate life history genes and endocrine signaling. If you think that your poster is relevant to our symposium, please feel free to contact us with the title and abstract of the poster and we will add this information to our symposium page.

FURTHER INFORMATION: The SSE meetings, jointly held with the American Society of Naturalists (ASN) and the Society of Systematic Biologists (SSB), will take place between 20-24 June, 2008, at the University of Minnesota in Minneapolis. Details on registration, accomodation, program, and online abstract submission are available at: <http://www.cce.umn.edu/conferences/evolution/> IMPORTANT DATES AND DEADLINES: The deadline for presentation titles is April 1, 2008. The deadline for early bird registration at discounted rates is May 2, 2008.

SPONSORS: Society for the Study of Evolution, Dean's Office of the Brown University Division of Biology and Medicine, and Fisher Scientific.

SUGGESTED READING:

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SYMPOSIUM ORGANIZERS: Thomas Flatt (Brown University, Department of Ecology and Evolutionary Biology, Providence, USA) and Andreas Heyland (University of Guelph, Department of Integrative Biology, Guelph, Canada). Contact: thomas_flatt@brown.edu or aheyland@uoguelph.ca

Thomas Flatt, Ph.D. Brown University Division of Biology and Medicine Department of Ecology and Evolutionary Biology

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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>

UOregon EvoDevo Symposium Apr4-6 deadline extended

UOregon.EvoDevo.Symposium.Apr4-6

We have extended the early registration deadline by two weeks to allow everyone to register!

WEBSITE: <http://evodevo.uoregon.edu/-symposium.html> WHERE: Eugene, Oregon at the Valley River Inn

WHEN: April 4 - 6, 2008.

KEYNOTE SPEAKERS: Jerry Coyne - University of Chicago Greg Wray - Duke University

SCHEDULED SPEAKERS: Detlev Arendt - European Molecular Biology Laboratory Bill Cresko - University

of Oregon Bernie Degnan - University of Queensland
Hopi Hoekstra - Harvard University Mark Martindale
- University of Hawaii Daniel Meulemans - California
Institute of Technology Leonie Moyle - Indiana Univer-
sity Fred Nijhout - Duke University Kevin Peterson -
Dartmouth College Stephan Schneider - University of
Oregon Mike Wade - Indiana University Deneen Wellik
- University of Michigan

The symposium has been organized by the NSF
IGERT-associated graduate students at the University
of Oregon. We are very proud of the invited speakers
and we look forward to an intellectually stimulating and
enjoyable symposium. We hope that you can attend!

Please feel free to contact me with any questions.

Cheers, Conor O'Brien

Cresko Lab / Bradshaw-Holzappel Lab Center for Ecol-
ogy & Evolutionary Biology University of Oregon co-
brien1@uoregon.edu cobrien1@uoregon.edu

Warsaw Bioinformatics Apr24-27

Dear Colleague,

We would like to remind you that the early bird reg-
istration deadline for the Bioinformatics-2008 is March
24, 2008. Also the abstract submission deadline passed
at the same day.

The conference is organized by SocBiN - Society
for Bioinformatics in the Northern Europe (<http://www.socbin.org/>). It is already the 10th edition. All
previous conferences in this series have been a great suc-
cess with many excellent talks from high-profile speak-
ers and 300-400 participants from Europe and the rest
of the world. The conference will be held in Warsaw,
Poland (24-27 April 2008). The website for the confer-
ence is <http://bioinformatics2008.icm.edu.pl/> and we
invite you to take a look at the programme and regis-
ter.

There is a number of bioinformatics activities in
Poland, and we believe that this meeting will attract
many participants from Northern Europe, as well as
Poland and other countries of Central Europe, and
elsewhere. Our ambition is that the meeting should
provide a bridge between biologically-motivated and
mathematically-motivated aspects of bioinformatics.
Life scientists from outside the field of bioinformatics
are also encouraged to participate.

We have put together a programme with three dis-
tinguished keynote speakers (Janet Thornton, Andrzej
Kolinski, and Gunnar von Heijne), and 20 excellent in-
vited speakers. There will be two additional sessions
with 10-12 talks selected from presented posters. All
participants will have a chance to be selected for a talk
during the meeting, therefore we encourage you to ar-
ticipate and present your work.

We would also appreciate if you could disseminate in-
formation about this conference among your cowork-
ers and collaborators and anybody who might be in-
terested. A pdf flyer is accessible at the conference
page and at the following address: <http://tinyurl.com/-299scb> - please print it and post it at a message board
at your institution and send it by email to anybody who
might be interested.

We would like to promote the participation of young sci-
entists, therefore the registration fee for students (incl.
PhD students) has been reduced to a minimum (120
Euro). Additionally, if budget allows, the organizers
will provide travel or accommodation grants for stu-
dents

On Tuesday-Wednesday 22-23 April (just before the
conference) there will be an optional guided tour to
KrakÅ³w and Wieliczka.

We look forward to see you in Warsaw!

Best regards,

On behalf of the Programme and Local Committees

Janusz Bujnicki (PC Chair) Witold Rudnicki (LC
Chair)

Programme Committee

Janusz M. Bujnicki, Warsaw, Poland Arne Elofsson,
Stockholm, Sweden Mikhail Gelfand, Moscow, Russia
Jan Komorowski, Uppsala, Sweden Ceslovas Venclovas,
Vilnius, Lithuania Witold Rudnicki, Warsaw, Poland

Local Committe

Witold Rudnicki, Warsaw University Janusz Bu-
jnicki, IIMCB Krzysztof Ginalski, University of War-
saw Marek Niezgadka, University of Warsaw Jerzy
Tiuryn, University of Warsaw Piotr Zielenkiewicz, Pol-
ish Academy of Sciences

W.Rudnicki@icm.edu.pl W.Rudnicki@icm.edu.pl

Warsaw Bioinformatics Apr24-27 deadline extended

Dear Colleague,

Due to the numerous requests we extend the deadline for the abstract submission for the Bioinformatics-2008 until April 5, 2008.

The conference will be held in Warsaw, Poland (24-27 April 2008). The website for the conference is <http://bioinformatics2008.icm.edu.pl/> and we invite you to take a look at the programme and register.

We have put together a programme with three distinguished keynote speakers (Janet Thornton, Andrzej Kolinski, and Gunnar von Heijne), and 20 excellent invited speakers. There will be two additional sessions with 10-12 talks selected from presented posters. All participants will have a chance to be selected for a talk during the meeting, therefore we encourage you to participate and present your work.

We would also appreciate if you could disseminate information about this conference among your coworkers and collaborators and anybody who might be interested. A pdf flyer is accessible at the conference

page and at the following address: <http://tinyurl.com/-299scb> - please print it and post it at a message board at your institution and send it by email to anybody who might be interested.

We would like to promote the participation of young scientists, therefore the registration fee for students (incl. PhD students) has been reduced to a minimum (150 Euro).

We look forward to see you in Warsaw!

Best regards,

On behalf of the Programme and Local Committees

Janusz Bujnicki (PC Chair) Witold Rudnicki (LC Chair)

Programme Committee

Janusz M. Bujnicki, Warsaw, Poland Arne Elofsson, Stockholm, Sweden Mikhail Gelfand, Moscow, Russia Jan Komorowski, Uppsala, Sweden Ceslovas Venclovas, Vilnius, Lithuania Witold Rudnicki, Warsaw, Poland

Local Committe

Witold Rudnicki, Warsaw University Janusz Bujnicki, IIMCB Krzysztof Ginalski, University of Warsaw Marek Niezgódka, University of Warsaw Jerzy Tiuryn, University of Warsaw Piotr Zielenkiewicz, Polish Academy of Sciences

Witold Rudnicki <W.Rudnicki@icm.edu.pl>

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Austria HoneyBeeEvolution

Dear Evoldir members,

Please bring this advert to the attention of potential applicants.

Best wishes, Gerald Kastberger

Position available from Sept. 2008 for three years: FWF (Austrian Science foundation)-funded PhD studentship.

Research topic: Ethological basis of social waves in Giant honeybees. Giant honeybee research group (group leader: Gerald Kastberger)

Short summary. This project investigates the phenomenon of social waving in Giant honeybees which is a main component of colony defence and which has been termed 'shimmering behaviour' in literature. While focussed on its uniqueness in Giant honeybees, the research topic does have relevance for a series of hot spots of the biology of social systems in general. It refers, in particular, to 'task partitioning', to 'collective decision-making', to 'social communication', and to 'social defence'. Shimmering also relies on unexplored principles of 'information transfer' and introduces itself as a compelling example of 'self organisation'. It addresses 'proximate' questions (HOW does shimmering function?) and ultimate questions (WHY has been shimmering evolved?) and therefore, it gives rise to discovery of interdependencies between giant honeybees as prey and its predators as part of a 'co-evolutionary arms race'.

Reference:

Kastberger G, Raspotnig G, Biswas S, Winder O [1998] Evidence of Nasonov scenting in colony defence of the Giant honeybee *Apis dorsata*. *Ethology* 104, 27-37; Oldroyd BP, Wongsiri S [2006] Asian honeybees. *Biology, Conservation and Human interactions*. Harvard University Press, Cambridge; Paar J, Oldroyd BP, Kastberger G [2000] Giant honey bees return to their nest sites. *Nature* 406, 475.

Additional background information available at <http://www.kfunigraz.ac.at/zoowww/personal/kastberger/-kastberg.html> Enquiries and applications (including covering letter, CV & contact details of 2 referees) to: Dr. Gerald Kastberger: email: gerald.kastberger@uni-graz.at. Applicants ought to have a good degree in a relevant subject. Interest, enthusiasm, and technical and methodological background for evolutionary

biology, ethology, sensory ecology would be beneficial. Applicants need to meet residency criteria of Austrian Research Councils. Closing date May 31th 2008.

Univ.Prof.Dr. Gerald Kastberger Institut für Zoologie Universität Graz

Adresse Universitätsplatz 2, A 8010 Graz TEL (0043) (0)316 380 5612 FAX (0043) (0)316 380 9875 email gerald.kastberger@uni-graz.at

gerald.kastberger@uni-graz.at

DalhousieU FishComparativePhylogeography

PhD position in Comparative Phylogeography/Conservation Genetics of Patagonian or northern fishes

Support for a PhD position is expected to become available at Dalhousie University (Halifax, Nova Scotia, Canada) for research in comparative phylogeography and conservation genetics of fish in Patagonia or in the north. The student will develop a research project that uses molecular genetic and phenotypic approaches to examine issues in phylogeography, adaptive radiation and/or conservation genetics. The successful candidate should have experience with molecular techniques and should have a strong interest in population genetics and statistics. Fieldwork in Patagonia will take place in collaboration with scientists from Argentina and Chile. The position is expected to start in the 2008/2009 academic year, pending funding approval and is contingent upon acceptance to the Department of Biology graduate program. Potential applicants may consult: Ruzzante et al 2006 *ME* 15:2949-2968; Palstra et al 2007 *ME* 16:4504-4522; and Ruzzante et al 2008 *ME* available online.

If interested please send an e-mail application including CV, names and addresses of two to three referees and a statement describing the reason(s) for your interest in this research to: Daniel E Ruzzante, Associate Professor and Canada Research Chair in Marine Conservation Genetics, Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1. (email: daniel.ruzzante@dal.ca, <http://myweb.dal.ca/~ruzzante>)

Daniel Ruzzante, Associate Professor Canada Research Chair in Marine Conservation Genetics Department of Biology, Dalhousie University, Halifax, Nova Scotia,

Canada, B3H 4J1 phone: (902) 494-1688 fax: (902) 494-3736 e-mail: daniel.ruzzante@dal.ca

<http://myweb.dal.ca/ruzzante>
[/patagonia.byu.edu](http://patagonia.byu.edu) Canada
 Chairs <http://www.chairs.gc.ca>
 <Daniel.Ruzzante@Dal.Ca>

<http://>-
 Research
 ruzzante

DurhamU PigPopGenet

PhD studentship (funded by the Leverhulme Trust) available starting Oct. 2008

Closing date: April 21, 2008

A PhD studentship - based jointly in the departments of Archaeology and Biological & Biomedical Sciences at Durham University (UK) - will investigate wild and domestic pig population genetics from Europe over the last 10,000 years using ancient and modern DNA in the context of *Sus* population dynamics, patterns of environmental change and human dispersal.

This project will form an integral part of a much broader collaborative and multi-disciplinary research effort at Durham University (funded by the Wellcome Trust, AHRC and most recently NERC), which is using a wide variety of archaeological, anthropological, and genetic methodologies (including molecular evolution, population genetics, introgression, and the molecular basis of phenotypic diversity) to understand the origins and spread of early farmers around the world.

The studentship will cover the full cost of tuition fees for UK/EU students, and will pay a tax-free stipend of £38,755 over a period of three years. Non-UK/EU students are encouraged to apply, but will be responsible for additional University fees charged to international students. There are also additional funds for related laboratory consumables and travel.

The studentship will be supervised jointly by Dr. Greger Larson, Prof. Rus Hoelzel and Dr Keith Dobney.

Applications should be sent electronically to Prof. Rus Hoelzel and cc to Dr. Greger Larson at the email addresses given below and should include:

- 1) Your Curriculum Vitae
- 2) Course results for undergraduate and any post-graduate work
- 3) A cover letter explaining why you are well qualified

for this project

Please also have two letters of recommendation in support of you application sent on your behalf.

In addition, please complete the online University postgraduate application form found at:

https://banners.dur.ac.uk/blive_ssb/-bwskalog.P_DisLoginNon A. Rus Hoelzel School of Biological and Biomedical Sciences a.r.hoelzel@dur.ac.uk

Greger Larson Department of Archaeology greger.larson@imbim.uu.se

Durham University, Durham, UK

Related web links: <http://www.dur.ac.uk/archaeology/research/projects/?mode=project&id=260> <http://www.dur.ac.uk/archaeology/research/projects/?mode=project&id=261> <http://www.dur.ac.uk/archaeology/research/projects/?mode=project&id=258> <http://www.dur.ac.uk/archaeology/research/projects/?mode=project&id=259> <http://www.dur.ac.uk/archaeology/staff/?id=1221> <http://www.dur.ac.uk/archaeology/staff/?id=5502> <http://www.dur.ac.uk/biological.sciences/staff/profile/?username=dbl0arh> a.r.hoelzel@durham.ac.uk

ETH Zurich MicrobialGeneticDiversity

PhD position in Microbial Genetic Diversity

A 3-year PhD position is available at the Forest Pathology & Dendrology Group, Institute of Integrative Biology, ETH Zürich, to study the influence of genetic diversity and temperature on the fungal root endophyte *Phialocephala fortinii* s.l. Our study organism is a dominant root colonizer in conifer forests and operates across a wide range of the symbiotic continuum, ranging from parasitism to mutualism. The project seeks to understand the role of the genetic diversity of *P. fortinii* s.l. in shaping host communities in a changing world. The work includes inoculation experiments in microcosms, virulence assessments and molecular studies.

The applicant is expected to hold an University degree in Natural Sciences (environmental sciences, environmental microbiology, experimental mycology, phytopathology or a related discipline, ideally with good background in molecular biology and statistics) which allows entering a PhD program, and very good organizational, analytical and writing skills. Applicants

should submit a letter that summarizes motivation, interests and relevant experience, a cv including undergraduate and masters/diploma transcripts, and contact information for 2-3 references (all as pdfs) to: ottmar.holdenrieder@env.ethz.ch

Yearly salary 38000-44000.-SFr.

Starting date: Ideally by the 1st of April 2008 or according to mutual agreement. Review of applications will continue until the position has been filled.

Ottmar Holdenrieder

Ottmar Holdenrieder <ottmar.holdenrieder@env.ethz.ch>

Kiel Germany DiseaseEvolution

GENETICS OF GRANULOMATOUS DISEASES
PhD position in Molecular Biology and Genetics at the Institute of Molecular Biology, Kiel, Germany.

A PhD student position is available at the Institute for Molecular Biology (IKMB), Christian-Albrechts-University Kiel, Germany. The position relates to a scientific research project in the area of Human genetics, Quantitative genomics and Bioinformatics. The project deals with systematic genetic studies identifying susceptibility mechanisms for sarcoidosis and other human granulomatous diseases (e.g. tuberculosis, Berylliosis) using genome-wide SNP data. The research involves analysis of high density SNP association studies of large population samples, sequencing, gene expression and related bioinformatics.

GENERAL INFORMATION We are using state-of-art DNA technologies, including genome-wide scans and dedicated follow-up studies to identify and characterize novel susceptibility loci for granulomatous diseases. The candidate will work with an internationally recognized team of scientists in this area of research within IKMB, with the access to high throughput, state-of-the-art experimental (e.g. SNPlex, next-generation sequencing, immunological and cell biological analytic) and computational facilities and large genomic databases. The successful candidate will be enrolled at the University of Kiel. He/She will be supervised by Dr. Sylvia Hofmann at the IKMB. Relevant project information can be found at the IKMB website <http://www.ikmb.de>. **ELIGIBILITY AND PAYMENT** A high quality honours or Masters degree or similar in the field of molecular genetics or population genetics or animal/plant genomics/breeding or bioinformatics or evolutionary biology or similar field is required. Exceptional B.Sc. students are also encouraged to apply. Experience in molecular biology methods, a computer programming knowledge and use of statistical analysis software is desirable. The position is open to international applicants but German citizenship or residencies are preferred. Financing is available for at least three years. The salary is according to the standard guidelines of German universities.

APPLICATION Applications including a short CV (max 3 pages), list of publications, and the names and contact information including e-mail addresses of two researchers willing to write a letter of reference should be sent via e-mail to: s.hofmann@ikmb.uni-kiel.de (write "HumGen - Granuloma - PhD position" on the subject line)

Applications close by April 30, 2008. The position will remain open until filled.

Dr. S.Hofmann Institute of Clinical Molecular Biology Christian-Albrechts-University Schittenhelmstrasse 12 24105 Kiel, Germany e-mail: s.hofmann[at]ikmb.uni-kiel.de <http://www.ikmb.uni-kiel.de/> sylvia.hofmann@zoologie.uni-halle.de

Lisbon ComputationalBiology

Applications are now open for the 2008 academic year PhD programmes at the Instituto Gulbenkian de Ciencia, in Lisbon, Portugal.

The IGC is once again hosting 3 international PhD programmes:

Gulbenkian/Champalimaud PhD Programme in Neuroscience

PhD Programme in Computational Biology

IGC International PhD Programme in Multidisciplinary Life Sciences

Information on the programmes and application procedures are available at www.igc.gulbenkian.pt <<http://www.igc.gulbenkian.pt/>>.

The deadline for applications is 4 April 2008.

Henrique Teotonio <teotonio@igc.gulbenkian.pt>

NorthCarolinaStateU TermitePopGenetics

Graduate Assistantship in Molecular Population Genetics of Termites or Bed Bugs

Department of Entomology North Carolina State University

A Graduate Assistantship is available for an MS or Ph.D. student in the laboratory of Ed Vargo. Research in our lab focuses on colony and population genetic studies of subterranean termites using microsatellite and mtDNA markers, and we are initiating studies of bed bugs. A variety of thesis projects involving termites are possible, including phylogeography, comparative studies of breeding systems of subterranean species, population dynamics and intercolonial interactions, effect of inbreeding on disease resistance, and biology of invasive species. Potential bed bug projects include identifying source populations of infestations, mating system, and modes and patterns of dispersal at varying spatial scales. NCSU has a large and dynamic Department of Entomology, with a particularly vigorous program in Urban Entomology, and is closely associated with the Keck Center for Behavioral Biology, an interdepartmental program focused on the fundamental processes governing animal behavior (<http://www.cals.ncsu.edu/beh.bio/>). Graduate Fellowships and Scholarships are available to students working on structural pests.

For more information, contact:

Ed Vargo Department of Entomology Box 7613 North Carolina State University Raleigh, NC 27695-7613

Tel. (919) 513-2743 Fax (919) 515-7746 Email: ed_vargo@ncsu.edu < <http://www.cals.ncsu.edu/entomology/vargo/> > <http://www.cals.ncsu.edu/entomology/vargo/> ed_vargo@ncsu.edu

PompeuFabraU Barcelona EvolutionaryGenomics

Funded PhD scholarship in evolutionary genomics

and Systems Biology in Pompeu Fabra University (Barcelona).

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

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

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

– Hafid Laayouni CIBER Epidemiología y Salud Pública (CIBERESP). Universitat Pompeu Fabra Parc de Recerca Biomèdica de Barcelona (PRBB) Departament de Ciències Experimentals i de la Salut Dr. Aiguader, 88. 08003 Barcelona Tel. (34) 93-316-0845 Fax: (34) 93-316-0901 Spain

[hafid.laayouni](mailto:hafid.laayouni@upf.edu) <hafid.laayouni@upf.edu>

UArkansas EnvironmentalGenomics

Ph.D. Graduate Assistantship, Environmental Genomics

University of Arkansas

An NSF-funded graduate research assistantship is available to support a Ph.D. candidate interested in functional genomics of adaptation and evolution. The project involves laboratory and field experiments designed to discover patterns of gene expression in populations of cactophilic *Drosophila mojavensis* exposed to different host plants in stressful and non-stressful thermal regimes. Our general goals are to uncover whole-genome patterns of gene expression in populations exposed to natural abiotic and biotic stress. Ultimately, we wish to pinpoint clusters of functionally interacting

genes expressed throughout the life cycle in different environments, and predict limits of phenotypic plasticity and adaptation, particularly in response to stressful environments and long-term global climate change.

Laboratory experiments involve DNA microarrays to study gene expression changes due to different host cacti and temperature stresses, as well as differences in epicuticular hydrocarbons. Field-related work will include multiple field trips to Mexico to monitor wild flies, assess demography of wild populations, and analyze cuticular hydrocarbon and RNA profiles. Other related research projects are also possible. This position is part of a collaborative project involving the Univ. of Arkansas, Fayetteville, and the Univ. of Nevada, Las Vegas.

Applicants must gain admission to the Ph.D. program in the Department of Biological Sciences at the University of Arkansas. Application information is available at <http://biology.uark.edu/1251.htm>. Full stipend, tuition, and benefits are included. Supplemental funding is available on a competitive basis for applicants qualifying for Doctoral Fellowships at the Univ. of Arkansas (<http://biology.uark.edu/1255.htm>).

William J. Etges Program in Ecology and Evolutionary Biology Department of Biological Sciences University of Arkansas Fayetteville, AR 72701 USA 479-575-6358 wetges@uark.edu <http://comp.uark.edu/~wetges/wetges.html> wetges@uark.edu

UCalgary CommunityPhylogenetics

I am looking for a highly motivated student for September 2008 at the PhD or MSc level who is interested in studying phylogeography and/or phylogenetic community structure of predeaceous diving beetles. Field work will take place in western Canada, with most of the anticipated sampling occurring from coastal BC to the western edge of the prairies, including montane sites. I am currently building up facilities for isolating and amplifying DNA in my laboratory, and anticipate using third party providers for the sequencing component. Therefore, the ideal candidate will be equally comfortable in the field waist deep in water, in the lab with a pipette in hand, or in front of a computer aligning sequences and running comparative analyses. The successful candidate will join a group of graduate students investigating the ecology of temporary ponds, the role of predation in community struc-

ture of diving beetles, and the influence of larval competition on female fitness in seed beetles. For more, see: < <http://homepages.ucalgary.ca/~smvamosi/> >. The Department has a strong EEB group < <http://www.bio.ucalgary.ca/research/EEB.html> >.

Guaranteed funding of at least \$20,000 CAD/year for 4 years (PhD) or 2 years (MSc) is available through a combination of teaching and research assistantships. Candidates with strong GPAs will find themselves eligible to apply for several provincial funding sources, in addition to federal sources available to Canadian citizens.

Requirements: Potential applicants must have a *minimum* GPA of 3.20 (on a four-point system), and preferably higher. For students entering an MSc, this is based on the last two years of the undergraduate degree consisting of a minimum of 10 full-course equivalents. For those entering a PhD with an MSc, the overall GPA from the MSc will be considered.

Canadian citizens will be given first priority, but I am open to applications from qualified international candidates. Please note that proficiency in the English language is essential for the pursuit and successful completion of graduate programs at the University of Calgary.

To inquire, submit (via email) a cover letter with a brief review of your research experience, interests and goals (~ one page), resume, transcripts, and names of three academic references to:

Dr. Steven M. Vamosi Department of Biological Sciences University of Calgary 2500 University Dr NW Calgary AB T2N 1N4

smvamosi@ucalgary.ca

UdeLaCoruna PlantGeneticDiversity

We seek a college graduate interested in using molecular markers to investigate population structure and genetic diversity in various endangered plants endemic to NW Iberian Peninsula and catalogued as priority species by the Habitats Directive (92/43/CEE). Research will be conducted in the Área de Ecología of the Universidad de La Coruña, funded by the Environment and Sustainable Development Programme of the Consellería de Innovación e Industria, Xunta de Galicia. The project will entail both molecular evolution laboratory activity and fieldwork. Given the length of this position, it is

expected that this research should lead to obtain a PhD degree.

Eligibility

- College graduate in biology or other similar disciplines.
- Commitment to get a PhD degree is important.
- Knowledge of molecular evolution techniques and previous research experience advantageous but nonessential.

Details of the position

- 1 research contract for 31 months, full-time from Monday to Friday.
- Monthly stipend of about 1498.15??? gross salary (1284.13??? net salary).
- Working place: Facultad de Ciencias, Campus A Zapateira s/n, Universidad de La Coruña

Application procedure

- Closing date for applications: 11th April 2008.
- Send a CV no longer than 5 pages and a 1-page covering letter with a description of your background and goals to Rodolfo Barreiro either by electronic (rodbar@udc.es) or postal mail (Facultad de Ciencias, A Zapateira s/n, 15071-La Coruña).

Please, use reference CT-MDS in any correspondence.

Rodolfo Barreiro Lozano Área de Ecología Facultad de Ciencias Universidade da Coruña Campus A Zapateira s/n 15071-A Coruña España/Spain

Tf.- +34-981167000 x 2053 Fax.- +34-981167065
Correo-e.- rodbar@udc.es

Rodolfo Barreiro <rodbar@udc.es>

UdeLaCoruna SeaWeedGeneticDiversity

We seek a college graduate interested in using molecular markers to investigate population structure and genetic diversity in various seaweed species of conservation concern in NW Iberian Peninsula. Research will be conducted in the Área de Ecología of the Universidad de La Coruña, funded by the Environment and Natural Resources Programme of the Ministerio de Educación y Ciencia (Spain). The project will entail both molecular evolution laboratory activity and fieldwork.

Eligibility

- College graduate in biology or other similar disciplines. - Interest in getting a PhD degree will be advantageous. - Knowledge of molecular evolution techniques and previous research experience advantageous but nonessential.

Details of the position

- 1 research contract for 15 months, full-time from Monday to Friday. - Monthly stipend of about 1390.40 ??? gross salary (1191.77??? net salary). - Working place: Facultad de Ciencias, Campus A Zapateira s/n, Universidad de La Coruña

Application procedure

- Closing date for applications: 11th April 2008. - Send a CV no longer than 5 pages and a 1-page covering letter with a description of your background and goals to Rodolfo Barreiro either by electronic (rodbar@udc.es) or postal mail (Facultad de Ciencias, A Zapateira s/n, 15071-La Coruña).

Please, use reference CT-MAR in any correspondence.

Rodolfo Barreiro Lozano Área de Ecología Facultad de Ciencias Universidade da Coruña Campus A Zapateira s/n 15071-A Coruña España/Spain

Tf.- +34-981167000 x 2053 Fax.- +34-981167065
Correo-e.- rodbar@udc.es

Rodolfo Barreiro <rodbar@udc.es>

UExeter AquaticFungiDiversity

A NERC funded PhD studentship is available at the University of Exeter to study the molecular diversity and ecology of aquatic chytrid fungi.

Fungi represent a biochemically and ecologically diverse kingdom of eukaryotes with members including important symbionts, parasites and saprotrophs in all environments. However many fungal groups, such as the chytrids (flagellated fungi), remain poorly characterised. This is despite the fact that they are recyclers of complex compounds such as cellulose, chitin and keratin, making them key agents for carbon and nitrogen recovery in aquatic ecosystems.

By understanding the habitat range and diversity of chytrids we can start to better understand their ecological roles in global cycles. This project will develop molecular tools to assess the distribution, diver-

sity and abundance of specific chytrid lineages in diverse aquatic environments. Methods will include environmental gene surveys, RNA sampling and fluorescent in situ hybridization, and the student will receive full training in these techniques.

The project will be hosted in the Centre for Eukaryotic Evolutionary Microbiology (CEEM) <http://www.projects.ex.ac.uk/ceem/>, which includes a total of 10 researchers who work on related themes. In 2009 we will enter a new research centre equipped with microscopy suites, tissue culture rooms and facilities for large-scale environmental sample analyses.

Funding is open to UK residents or EU nationals who have spent the last three years in the UK for education or employment. Applications should be made before the 5th of April 2008 CV by and covering letter saying why you would like to apply and giving the names of two referees. These should be sent to Mrs S. Mudge, Postgraduate Secretary, School of Biosciences, University of Exeter, Geoffrey Pope Building, Stocker Road, Exeter EX4 4QD or by email to BS-PGadmissions@ex.ac.uk. For informal enquiries please contact Bryony Williams, (B.A.P.Williams@exeter.ac.uk), Tom Richards (T.A.Richards@exeter.ac.uk) or Mark van der Giezen (M.vanderGiezen@exeter.ac.uk)

B.A.P.Williams@exeter.ac.uk

B.A.P.Williams@exeter.ac.uk

UHull Morphological Evolution

PhD studentship on “Patterns and processes of morphological evolution in vertebrates”.

A NERC-funded PhD studentship supervised by Dr. Leandro Monteiro, Evolutionary Biology group, Department of Biological Sciences, The University of Hull, is available to develop a project dealing with a quantitative approach to patterns and processes of morphological evolution. The quantitative study of shape variation of biological structures is essential for the understanding of the evolutionary and developmental processes of organisms. Shape variation may be associated with patterns of phenotypic evolution in large scales of time and space, to genetic and environmental factors causing variation within and between populations. Our current research projects deal with macroevolutionary patterns of morphological divergence and evolutionary integration in the skulls and mandibles of echimyid rodents

and phyllostomid bats; microevolutionary processes responsible for body shape differentiation in recently isolated populations of a livebearer fish, and evolutionary processes and patterns of shape variation in otoliths of sciaenid fishes, which can also be used for otolith-based stock identification in fisheries management.

Further information about published papers and ongoing research projects at Monteiro’s lab and the Evolutionary Biology group at The University of Hull is available at <http://www.hull.ac.uk/evolution/people/-Monteiro/> Applicants should have a keen interest in morphological evolution, statistical analysis and morphometrics, and hold at least an upper second class honours degree in the life sciences. Eligibility for the NERC studentship depends on the student being a UK citizen or a UK resident for at least 3 (three) years for EU citizens (more detailed information on eligibility can be found in the studentship handbook at <http://www.nerc.ac.uk/funding/application/studentships/>).

Informal enquiries should be directed to Dr. Leandro Monteiro (l.monteiro@hull.ac.uk).

Closing date for applications is 22nd March 2008. Interviews will be held in Hull during the second week of April. The start date is 1st October 2008.

Postgraduate application forms can be downloaded from our website at: http://www.hull.ac.uk/-biosci/studying_in_hull/postgrad_courses/-Application_information/ To apply for the studentship, please fill in the Postgraduate application form (note that at this stage you don’t need to get a referee to fill in the red sections of the form) and submit a cover letter to support your application, which gives details of your research interests, relevant experience and skills and why you want the PhD, then send your application to:

Dr. Leandro R. Monteiro Department of Biological Sciences The University of Hull Cottingham Road, Hull HU6 7RX Tel: 44 1482-466425 E-mail: L.Monteiro@hull.ac.uk <http://www.hull.ac.uk/-evolution/people/Monteiro/> lrabellom@gmail.com

Uillinois BeeEvolGenomics

Graduate Student Research Assistantships

At least one graduate student assistantship is available for students interested in one or more areas of evolutionary research on bees, including sys-

tematics/phylogenomics of corbiculate bees, genetic regulation and ecological determinants of Müllerian mimicry patterns in bees, and population genetics/phylogeography.

A student interested in phylogenomics and bioinformatics will have access to EST libraries under development for corbiculate bees (bumble bees, stingless bees, orchid bees and honey bees), which can be used both for assessing phylogeny of these taxa (noted for their differences in social evolution) and for discovering genomic patterns that could help elucidate behavioral differences among these distinct lineages.

Müllerian mimicry research would involve laboratory experiments and/or studies of bumble bees in the wild to understand some of the underlying regulatory mechanisms of color pattern and selective forces that lead to convergent patterns among multiple species.

Given the threatened status of multiple species of bumble bee pollinators in both Europe and North America, it is essential to understand the population structure and gene flow patterns of different taxonomic groups of these bees. Research in this area would include both field and lab work to sample populations across the ranges of focal species, develop molecular markers (e.g., mtDNA and nuDNA fragments, microsatellites, SNPs) and apply or develop statistical approaches to delimiting populations and species, their relationships and ancestral origins. This research is complimentary to a larger effort in the lab to determine the current status and causes of decline in North American bumble bees.

Interested applicants have the opportunity to apply through the Department of Entomology or the Program in Ecology, Evolution and Conservation Biology (PEEC) at the University of Illinois. Admissions information can be found on the relevant links at <http://www.life.uiuc.edu/entomology/admissions.html> and <http://www.life.uiuc.edu/peeb/index.htm>. Prospective candidates should have strong academic records and some research experience is preferred, either at the M. S. level or via undergraduate projects. The assistantship is suited to motivated, energetic students interested in scientific careers, who can work both independently and collaboratively, enjoy problem solving and are well organized. Review of applications will begin immediately and continue until a candidate is selected.

Please send 1) a statement of interest and 2) a CV including GPA and GRE scores, research experience and general research interests, and the names and contact information for at least three referees familiar with your work.

Application deadline is 1 June 2008 or until suitable candidates are selected.

– Sydney A. Cameron Assoc. Prof. Department of Entomology University of Illinois 320 Morrill Hall 505 S. Goodwin Ave. Urbana, IL 61801

ofc ph. 217-333-2340 lab ph 217-333-2170

www.life.uiuc.edu/scameron Sydney Cameron
<scameron@life.uiuc.edu>

ULondon TheoreticalBiology

The following 2 PhD studentships are currently advertised in my group:

Project 1: The evolution of pseudogamy and the emergence of diversity and altruism.

Project 2: Lymphocyte homeostasis in man; Measurement and modelling of thymic versus peripheral generation of naïve lymphocytes in the maintenance of normal T-cell pools

Description project 1:

The evolution of pseudogamy and the emergence of diversity and altruism.

Main supervisor: Prof. Vincent Jansen, co-supervisor: Dr Ian Barnes

This PhD Studentship aims to investigate how diversity of and altruism emerge using mathematical modelling and simulation studies. The research will be inspired by the evolution of pseudogamy. Pseudogamy is a form of reproduction where the males do not contribute genetic material to the next generation, despite the fact that the females can only reproduce if they have mated. This studentship is suitable for candidates with a degree (UK 2.1 degree or higher or equivalent thereof) in biology and proven skills in mathematical modelling/computer programming or for applicants with a degree in a quantitative subject (e.g. physics, mathematical or computer science) and an affinity for biology. The studentship will cover fees at UK-EU level and a maintenance stipend of approximately £14,000 per annum for 3 years. We will not consider candidates from outside the EU unless the candidate has additional funding available. The selected candidate will start in or close to October 2008 will work in the research groups of Jansen (Mathematical Biology) and Barnes (Molecular phylogenetics and ecology).

If you require further information on this studentship, see or http://www.rhul.ac.uk/Biological-Sciences/Vacancies/2008_Jansen.doc contact Vincent.jansen@rhul.ac.uk. The deadline for applications is 19 March 2008. The interviews are planned for the week of 21 April 2008. To apply, use the form on http://www.rhul.ac.uk/Biological-Sciences/Vacancies/2008_PhDapplicationForm.pdf or generate your own form using <http://www.rhul.ac.uk/Registry/Admissions/applyonline.html>. Please send the completed form, together with a recent CV, to Prof. Vincent Jansen, School of Biological Sciences, Royal Holloway, University of London, Egham, Surrey TW20 0EX by post or e-mail. If you use the online application, please make sure you send a copy of the application form by email to Vincent.jansen@rhul.ac.uk.

Description project 2: Joint PhDStudentship with Royal Holloway- St Georges University of London Lymphocyte homeostasis in man; Measurement and modelling of thymic versus peripheral generation of naïve lymphocytes in the maintenance of normal T-cell pools

Lead Supervisor: Derek Macallan, Professor in Infectious Diseases and Medicine, Centre for Infection, St George's, University of London. Co-supervisor: Vincent Jansen, Professor of Mathematical Biology, School of Biological Sciences, Royal Holloway, University of London.

Project Description

Lymphocyte populations persist because dying cells are continually replaced, unless replacement fails, as in HIV infection, with devastating consequences. Within this context, some clonal populations must be retained long-term in order to confer "immunological memory". How this is achieved is poorly understood. This project seeks to extend our understanding of human lymphocyte physiology by combining in vivo measurements of lymphocyte kinetics in human studies in Dr Macallan's laboratory at St George's with theoretical modelling and in silico experiments in Dr Jansen's group at RHUL. We will specifically study the role of naïve cells (defined by surface markers such as CD31) in regenerating peripheral naïve populations and investigate the effect of ageing on this process. We will compare in vivo naïve T-cell labelling data with data on rates of recent thymic emigration from the abundance of T-cell receptor rearrangement DNA excision circles (TREC). This combined approach will provide important new insights by relating new in vivo data with novel mathematical and statistical tools for interpretation in order to develop new conceptual frameworks. The proposed project will consist of both laboratory and theoretical

elements. Supervision would be jointly undertaken by the two supervisors; the student would need to spend time on both campuses across all three years.

How to apply

— / —

This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at <http://life.biology-untel.net/~brian/evoldir.html>

UNewOrleans PlantPhylogenetics

DOCTORAL FELLOWSHIPS IN PLANT PHYLOGENETICS, EVOLUTION, & CONSERVATION BIOLOGY UNIVERSITY OF NEW ORLEANS

The Department of Biological Sciences at the University of New Orleans announces one Doctoral Fellowships in Plant Phylogenetics, Evolution, & Conservation Biology beginning Fall 2008. The fellowships provide support for four years at an annual stipend of \$23-25,000 and include a full tuition waiver. The Department of Biological Sciences offers exciting opportunities for graduate student research in ecology, evolution, systematics, genetics, reproductive biology, physiology, and biochemistry. For more information on the Department, faculty research interests, and other resources, please see the departmental website: <http://biology.uno.edu/>. Or lab website: <http://www.phylodiversity.net/cbell> Applicants must be US citizens.

Interested applicants should contact:

Dr. Charles Bell Department of Biological Sciences
Email: cdbell1@uno.edu

Charles Bell <valerianaceae1969@gmail.com>

UOslo MicrobialMolEvol

DOCTORAL RESEARCH FELLOWSHIP

Four year PhD position in molecular evolution with 25% compulsory work available from 1. June 2008 at the Microbial Evolution Research Group (MERG), De-

partment of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo

In this project the community structure of mycorrhizal fungi and other fungal root symbionts associated with an alpine plant species will be analyzed. One of the main aims is to analyze which factors that determine the diversity and composition of fungal root symbionts, implementing both experimental and empirical inferences.

The candidate will work together with a group of researchers in the Microbial Evolution Research Group (MERG) and outside. The research program MERG has status as a Strategic Research Initiative at the University of Oslo. The vision of MERG is to develop an internationally leading and dynamic multidisciplinary research environment focusing on ecological, evolutionary and systems biology research on prokaryotic and eukaryotic microbes, their communities and interactions.

The candidate will be expected to participate in both field work, generating data, perform data analyzes, to work cooperatively with other lab members and outside collaborators and to actively publish and present results. 25% of the working time is allocated to duties besides research and project work, and typically includes lecturing and co-supervision of master students. The ideal candidate will be enthusiastic, highly motivated, and independent and should have a background in the area of focus.

Candidates must have a master's degree (or equivalent) within microbial ecology, evolutionary biology, molecular ecology or a related discipline. It will be advantageous to have experience in one or more of the following fields; mycology, molecular DNA techniques (PCR, sequencing, cloning, etc.), molecular biology, phylogeny, population genetics, bioinformatics and experimental ecology.

Please contact Assoc. Prof. Håvard Kausrud at the address below for more details.

The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the research training programme at the Faculty of Mathematics and Natural Sciences. The applicants must have obtained undergraduate (cand.mag., i.e. B.Sc. level) and postgraduate (cand.scient. or siv.ing., i.e. M.Sc. level) degrees. This represents approximately five years of full time studies after completion of European Upper Secondary School/International Baccalaureate. For more information see: <http://www.matnat.uio.no/english/research/research.edu/education.html>. Appointment to a research fellowship is conditional upon admission

to the Faculty's research training programme. An approved plan for the research training must be submitted no later than one month after taking up the position, and the admission approved within three months.

See the following URL for further details and guidelines for appointment to research fellowships at the University of Oslo: <http://www.uio.no/admhb/reglhb/personal/tilsettingvitenskapelig/ansettelsesvilkar/-guidelines-researchfellow.xml> The University of Oslo (UiO) wishes to achieve a more equal distribution of scientific employees between the sexes. Female applicants are encouraged to apply.

UiO has an agreement for all employers, aiming to secure rights to research results a.o

Contact Person:

Associate professor Håvard Kausrud, tlf. +47 99697116, e-mail: haavarka@bio.uio.no.

Pay grade: 43 - 48 (NOK 325 600,- - 355 000,- equals ca 41 215,- - 44 937,-) depending on qualifications and seniority).

Application deadline: 30. april 2008

Ref. No.: 2008/2967

Application (including statement about relevance of qualifications), CV (marked Ref. No. 2008/2967), copy of certificates and scientific papers should be sent (in 3 sets) to: Faculty of Mathematics and Natural Sciences, attn. Senior Executive Officer Bente Schjoldager, P. O. Box 1032 Blindern, N-0315 Oslo, Norway. Applicants may be called in for an interview.

Application papers will not be returned.

– Håvard Kausrud Department of Biology University of Oslo P.O.Box 1066 Blindern N-0316 Oslo, Norway

Phone: +47 22854832 (office) +47 99697116 (mob)

Web: <http://biologi.uio.no/meb/db03-staff/-Haavard.html>

UWesternOntario InsectSociogenomics

Graduate Position - Insect Sociogenomics

The lab or Dr Graham Thompson at the University of Western Ontario Canada (<http://www.uwo.ca/-biology/Faculty/thompson/index.htm>) is seeking at least one highly motivated and creative person to pur-

sue graduate research at the MSc or PhD level. The lab is launching a new research programme in the field of insect sociogenomics – the study of how genes and gene networks contribute to variation in social phenotypes.

There are several potential projects available for development, including 1) gene-regulation of termite societies, 2) immunogenetics of termite or honey bee societies, and 3) gene-regulation of selfish egg-laying behaviour, among other related ideas. Applicants would ideally have some experience in population genetic or genomic techniques, be willing to work in the field and at the bench, and be mindful of the genetical theory of social evolution.

For more information on admission to The Department of Biology, the graduate scene, core facilities, and living in London Ontario Canada, follow links from the Biology @ Western homepage <http://www.uwo.ca/biology/> and Graduate homepage <http://www.uwo.ca/biology/graduate/graduate.htm>. Potential applicants can contact me, or otherwise send a CV, an unofficial transcript and a brief statement, together with the names of potential referees, to graham.thompson@uwo.ca

The anticipated start date is September 2008, though May 2008 is possible. The position(s) will remain open until filled.

Graham Thompson

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

fax: 519-661-3935 phone: 519-661-2111 ext 86570 mob: 519 615 6066

<http://www.uwo.ca/biology/people/faculty.htm> graham.thompson@uwo.ca

UZurich MouseSocialSelection

Social selection in house mice

PhD position in Animal Behaviour at the University of Zurich, Switzerland.

A 3-year SNF-funded PhD student position is available in the Animal Behaviour group of the Zoological Institute of the University of Zurich, Switzerland to study the evolution of a cooperative behaviour in wild house mice. In house mice, females rear their litters cooper-

atively, sharing all maternal care of the pups, or alone. Fitness consequences of cooperative care in wild mice are not yet known. The project aims to measure selection on cooperative maternal care, identify environmental influences on trait expression, and unravel the genetic architecture underlying this trait.

We combine laboratory experiments with field work on a free-living population of wild house mice outside of Zurich. We are developing an excellent dataset on social affiliations and lifetime reproduction of individual mice. Currently, we are building a genetic pedigree of the population for use in animal modelling by the PhD student.

The research team includes Dr. Anna Lindholm and Prof. Barbara Koenig at the University of Zurich, and Dr. Luc Janss of the Bioinformatics and Statistical Genetics Group, Aarhus University, Denmark. The University of Zurich offers excellent research facilities and a rich academic community, see <http://www.lifesciencezurich.ch>. We are looking for an enthusiastic, highly motivated student who is interested in social behaviour and quantitative genetics. Experience in handling animals is an asset. A high quality honours or Masters degree or similar in Natural Sciences, with a good background in statistics, is required, as is a driver's license. Yearly salary is 38000 - 44000 SFr. The working language is English.

Applicants should submit a letter summarising motivation, research interests and relevant experience, a short CV (max 2 pages), undergraduate and masters/diploma transcripts, a list of publications (if any), and the names and contact information including e-mail addresses of 2 researchers willing to write a letter of reference, all as one pdf file, to anna.lindholm@zool.uzh.ch. Please write "PhD position" on the subject line.

Review of applications will start on April 15 and will continue until the position has been filled. Ideally, the successful applicant will start in May.

Dr Anna Lindholm Research Associate Animal Behaviour / Verhaltensbiologie

University of Zürich Tel: +41 (0)44 6355276 Institute of Zoology Fax: +41 (0)44 6355490 Winterthurerstrasse 190 CH-8057 Zürich Switzerland Email: anna.lindholm@zool.uzh.ch

UZurich PlantFungalInteractions

Phd Project Can plants make decisions? Can they identify cheats and punish them accordingly? Can they work together to bring down the system? These questions form the centre of an exciting PhD project currently on offer as a collaboration between the University of Zurich and the University of Basel. The work will involve a variety of plant species and their interactions with mycorrhizal fungi: a vital mutualism, crucial to the health and functioning of ecosystems. The project is generously funded by Syngenta and co-supervised by leading experts in their fields. You will benefit from expert advice, state-of-the-art facilities and will take part in ground-breaking experimental work in the plant sciences, including the use of new statistical analyses and genetic techniques (possibly!). You need to have an excellent background in ecology and/or evolutionary biology, some experience in experimental work (particularly with plants if possible) and be keen and enthusiastic. For more information contact Bernhard Schmid (bern-

hard.schmid@uwinst.uzh.ch).

Best wishes,

Bernhard Schmid

DR. BERNHARD SCHMID, PROFESSOR OF ENVIRONMENTAL SCIENCES Institute of Environmental Sciences University of Zurich Winterthurerstr. 190 Tel.: ++41 (0)44 635 5205 CH-8057 Zurich FAX: ++41 (0)44 635 5711 Switzerland <http://www.uzh.ch/uwinst/> New e-mail: Bernhard.Schmid@uwinst.uzh.ch New Journal of Plant Ecology: <http://jpe.oxfordjournals.org/> Recent open access articles: <http://jpe.oxfordjournals.org/cgi/content/full/rtm004?> <http://jpe.oxfordjournals.org/cgi/content/full/rtm006?> [http://www.plosone.org/article/](http://www.plosone.org/article/fetchArticle.action?articleURI=info%3Adoi%2F10.1371%2Fjournal.pone.0000846) <http://www.blackwell-synergy.com/doi/full/10.1111/j.1365-2435.2007.01308.x> <http://www.biomedcentral.com/content/pdf/1471-2180-6-68.pdf> List of publications: <http://hcr3.isiknowledge.com/formViewCharacteristic.cgi?table=Publication&link1=Search&link2=Search%20Results&link3=Biography&id=6220&nav=p1> Bernhard Schmid <bernhard.schmid@uwinst.uzh.ch>

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BardCollegeNY EvolBiology

Visiting Assistant Professor in Evolutionary Biology

The Biology Program at Bard College seeks to fill a position for a Visiting Assistant Professor in Biology for the 2008-2009 academic year. The successful candidate will teach a semester-long introductory course in Evolutionary Biology, develop one or two other topic-based introductory courses, and may develop an upper-level research seminar in his or her area of specialty. The Biology Program emphasizes that students do independent and collaborative research throughout their undergraduate careers, and the successful candidate is also expected to direct undergraduate research. Applicants should hold a PhD in Evolutionary Biology, Ecology, or a related discipline.

Bard College is a highly selective liberal arts college of 1800 students with a strong and growing emphasis on the sciences. This year the Biology Program moved into a new 42,000 foot science center that houses a 10,000 square foot research lab, specialized instrument centers, student project rooms, two model organism facilities, and teaching-research suites. Bard College stresses excellent teaching, and the Biology Program is committed to small class sizes that facilitate extensive interactions between students and faculty, including at the introductory level. Bard College is an equal opportunity employer and welcomes applications from individuals who contribute to its diversity.

Applicants should send a cover letter, CV, statements of teaching philosophy and research interests, and three letters of recommendation by April 11th, 2008 to Human Resources - 2408, PO Box 5000, Annandale-on-Hudson, NY 12504, email to hr@bard.edu or fax to 845-758-7826. AA/EOE

johns@bard.edu johns@bard.edu

Basel BehaviouralEvolution

Field assistants in Behavioural Evolution

Two field assistant positions are available in an international research project on communication and behavioural evolution in nightingales (*Luscinia megarhynchos*).

Fieldwork will be done in April and May 2008 at the Research Station Petite Camargue Alsacienne in France (www.camargue.unibas.ch). The project is run by Dr. Valentin Amrhein (University of Basel, Switzerland) and Prof. Dr. Marc Naguib (Netherlands Institute of Evolution, NIOO-KNAW).

To investigate vocal communication strategies of nightingales, we record songs and conduct playback experiments. The field assistants will also participate in systematic surveys of territory settlement and singing activity, and assist in capturing and banding the birds. Field work will include nocturnal bicycle trips, and field assistants are expected to work on their own at night.

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

Applicants are expected to stay for the entire field season from 7 April to the end of May 2008. The language at the research station will be English.

The positions will be filled as soon as possible. Applications should be in English and should include, in one single pdf or word file, a curriculum vitae and a letter of motivation. Please give names and email addresses of two persons who are willing to write a letter of recommendation, and send applications by email to the following address:

pca.recherche@orange.fr

valentin amrhein <pca.recherche@orange.fr>

BostonU InstrLabDirector

Boston University is hiring a full-time Instructional Laboratory Director to begin in June of 2008. The Director will oversee all administrative, financial and personnel actions related to the teaching laboratories in biology. Teach laboratory sessions in introductory biology and supervise and train teaching fellows and laboratory supervisors to ensure smooth operations of the labs. Develop instructional materials, conduct research and publish in these fields.

We require a Ph.D. in biological sciences, broad knowledge base in ecology, behavior, evolution, molecular biology, cell biology and physiology, some teaching experience at the college level and two to five years of related experience. To apply, please go to BU's website at www.bu.edu/hr <<http://www.bu.edu/hr>> and search for tracking code 4448/B268.

– Melissa B. McElligott, Ph.D. Instructional Laboratories Director Boston University Department of Biology 5 Cummington Street Boston, MA 02215 617-358-1958

CornellU FieldTech WarblerPopulations

Paid Field Technician Positions

The Cornell Lab of Ornithology seeks four biological technicians to conduct field studies of Golden-winged Warblers from early May to 30 June 2008. Two technicians will travel throughout the northern Appalachians (likely PA, NJ, and southern NY) and two will be stationed around the Fort Drum area in upstate NY. The work will focus on surveying Golden-winged Warblers in a variety of habitats to help understand population trends and habitat requirements for this species of conservation concern. Applicants should be highly motivated, have some experience conducting standardized bird surveys, possess a valid drivers license, and be willing to travel extensively (and possibly camp). A salary/stipend, plus expenses will be

provided and likely a field vehicle for the Appalachian positions. This is a great opportunity to gain valuable experience in avian sampling techniques and meet biologists/scientists from academia, state agencies, and conservation organizations.

For more information, please contact Sara Barker at 607-254-2465 or sb65@cornell.edu.

– Rachel Vallender, Ph.D. Post-doctoral Associate

Fuller Evolutionary Biology Program Cornell Lab of Ornithology 159 Sapsucker Woods Rd Ithaca, NY 14850 USA

Office: 607.254.1138 Lab: 607. 254.1128 Fax: 607.254.2486 RF88@cornell.edu

P Save a tree! Don't print this message unless it can't be helped. Pensez à l'environnement avant d'imprimer ce message.

Rachel Vallender <rf88@cornell.edu>

DalhousieU MicrobialMolEvol

DALHOUSIE UNIVERSITY

DEPARTMENT OF BIOCHEMISTRY & MOLECULAR BIOLOGY

ASSISTANT PROFESSOR POSITION

The Department of Biochemistry & Molecular Biology invites applications for a probationary tenure-track position at the rank of Assistant Professor to begin July 1, 2008. The ideal candidate will have expertise in molecular biology or biochemistry with a research emphasis on microbial molecular evolution and/or comparative genomics. Specific research areas of interest include, but are not limited to: molecular biology and evolution of organelles, microbial genome structure and function, biochemical/cellular diversity in prokaryotes and eukaryotes. The candidate must have a research track record that will be highly competitive in attracting external research funding. The successful candidate will join an internationally recognized group of researchers at Dalhousie working on microbial molecular evolution, comparative genomics, bioinformatics and biodiversity. The candidate will have the opportunity to mentor undergraduate honors and graduate students as well as postdoctoral fellows, and be expected to teach undergraduate and graduate courses in molecular biology/biochemistry consistent with her/his background and interest.

The ability to collaborate across disciplines is encouraged. The Department is closely affiliated with the recently established Program in Integrated Microbial Biodiversity (IMB) of the Canadian Institute for Advanced Research (CIFAR) and with a newly created interdisciplinary Centre in Comparative Genomics and Evolutionary Bioinformatics (CGEB) at Dalhousie University. The successful applicant will be nominated as a Scholar in the CIFAR IMB program (information on this program can be found at www2.cifar.ca). More details about the research activities of the Department of Biochemistry and Molecular Biology and the Faculty of Medicine can be found on our web sites: www.biochem.dal.ca and www.medicine.dal.ca.

Applicants must have a Ph.D., at least 2 years of post-doctoral experience and a strong publication record. Please submit curriculum vitae, reprints of several recent publications, one- to two-page statements outlining teaching and research plans, and arrange for three references to be sent under separate cover to:

Dr. D.M. Byers Head, Department of Biochemistry & Molecular Biology Faculty of Medicine Sir Charles Tupper Medical Building Dalhousie University Halifax, NS B3H 1X5.

Closing date for receipt of applications is March 31, 2008. The Academic Planning and Appointments Committee will commence reviewing applications in March.

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

Dalhousie University is an Employment Equity/Affirmative Action employer. The University encourages applications from qualified Aboriginal people, persons with a disability, racially visible persons and women.

– Andrew J. Roger Associate Professor, Fellow CIFAR Program in Integrated Microbial Biodiversity, Dept. of Biochemistry and Molecular Biology, Dalhousie University Rm 8B1, 5850 College St., Halifax, N.S. B3H 1X5 Canada tel:902-494-2620 (office) tel:902-494-2881 (lab) fax:902-494-1355 lab webpage: <http://rogerlab.biochem.dal.ca> How does evolution impact on your life? See: http://evolution.berkeley.edu/evolibrary/search/topicbrowse2.php?topic_idG

Worried about climate change, check out: Check out: <http://www.climatecrisis.net> and/or <http://www.realclimate.org>

Andrew.Roger@Dal.Ca

Dublin SummerResearch

Dear all,

We would be very grateful if you could circulate this reminder to all interested students and colleagues.

CoBiD-UREKA Undergraduate Summer Research Programme 2008 is currently open to applications from undergraduate students completing their 3rd (Junior) year in biological sciences. The deadline for receipt of completed applications is 30 MARCH 2008. We must receive all materials by this date, including application form from student and a reference directly from a member of academic staff in the student's home Institution.

Summer Research in Dublin

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

This summer programme offers research projects and activities for students in organismal biology using biological collections

Research Projects extreme environments | fire ecology | DNA barcoding | freshwater ecology | biocontrol | environmental epigenomics | terrestrial ecology | invasive species | plant evolution and extinction | life history | genomic imprinting

Requirements completion of the third (junior) year of an undergraduate biosciences degree | ability to work independently | strong interest in the project of choice | career goals in organismal biology

Full funding for the 10-week programme will be provided for 10 successful candidates, including assistance with air transportation to and from Dublin, accommodation in Dublin, and a small weekly allowance, as well as project expenses. Prior experience with museum collections is not required - one of the goals of the programme is to expose students to new research skills. The programme is open to all international as well as Irish and EU students.

Term dates: June 16th to August 22nd 2008

For application instructions and more information:

<http://www.ucd.ie/ureka/> Applications must be received by 30 March 2008

Best wishes,

THE UREKA TEAM

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

DukeU ResearchAssoc PrimateCommunication

Job Title: ASSOCIATE IN RESEARCH

Occupational Summary: A full-time research position is immediately available to assist with projects that combine behavioral, chemical, and genetic approaches to study olfactory communication in lemurs and mandrills. The work is to be conducted at Duke University (<http://www.baa.duke.edu/>) and its Lemur Center (<http://lemur.duke.edu/>). Experience in behavioral observation and genotyping is preferred. Experience in analytical chemistry is desired, but on-the-job training is available. The opportunity to develop independent research is also available. The initial appointment is for one year, with a second year of funding conditional on satisfactory performance. Salary will be partly based on previous experience and includes benefits.

Responsibilities: Collect behavioral data on semi free-ranging lemurs using hand-held computer Collect semiochemical data on scent marks, in situ, using portable electronic sensor Download files into databases, maintain data records, use various programs to (a) validate and extract data, and (b) tabulate, calculate, and analyze results Collect biological material from animals and prepare material for various assays Prepare glandular samples from lemurs and mandrills for gas chromatography, mass spectrometry (GCMS) or protein analysis Perform GCMS, maintain data files, identify and align compounds for analysis Prepare blood samples for hormone radioimmunoassay and/or DNA extraction Assist researchers in performing microsatellite, MHC, and sequencing analyses Prepare collection vials, reagents, and solutions; maintain sufficient inventory of laboratory materials and supplies for performance of duties; clean and maintain standard equipment Survey relevant literature and assist in developing new procedures and techniques Assist in the training and review of new personnel Perform other related duties incidental to the work described herein

Qualifications: Work requires a bachelor's degree in biology, zoology, chemistry or related field Experience working with animals and in a laboratory is required The applicant should work well independently or as

part of a team, and should be enthusiastic and motivated

Please email an application to Christine Drea (cdrea@duke.edu), consisting of a CV or resume, a brief statement of research interests, and the names of three people who can be contacted for letters of reference. Evaluation of applicants will begin immediately and will continue until the position is filled. Duke University is an Affirmative Action/Equal Opportunity Employer.

Marylene Boulet <marylene.boulet@duke.edu>

Egypt FieldAssist ReptileSurvey

Field Assistant Wanted

To assist a PhD student surveying reptiles, amphibians and butterflies in Egypt

Mid-May until mid-June 2008 Flights, accommodation and food will be paid for

We are looking for a field assistant to help with surveys of reptile, amphibian and butterfly species in Egypt. These data will be used to ground truth predictions of species distributions made using climate and habitat-based models. Sampling will consist primarily of visual surveys. The visit to Egypt will run (approximately) from 19th May to 23rd June 2008. Flights, accommodation, food and transport in Egypt will all be paid for.

The successful applicant will be a dedicated worker with an interest in evolution and natural history. Because of the nature of the terrain and the hot climate, a high level of fitness is required. The ability to speak some Arabic would be an advantage, although not necessary.

To apply, please send a CV to Tim Newbold (plxtn@nottingham.ac.uk) before 20th April 2008. Any enquiries should be sent to the same address.

For more information on the project, see:

<http://www.nottingham.ac.uk/~plztr/groupsite/conservationecology.html>

Newbold Tim <plxtn@nottingham.ac.uk>

Fairchild Tropical Botanic Garden Curator

FTBG.curator.plant.conservation

Fairchild Tropical Botanic Garden (FTBG) invites applications for the position of Herbarium Curator and Tropical Plant Conservationist at the Center for Tropical Plant Conservation (CTPC).

This position is available immediately. Fairchild Tropical Botanic Garden is a conservation, research and education based botanic garden opened to the public in 1938. Fairchild is an independent not for profit institution with broad community support in south Florida. The garden has over 100 staff including 7 PhDs. The garden maintains one of the world's most comprehensive tropical plant collections with an emphasis on palms, cycads and tropical fruit. The research focus of the Center for Tropical Plant Conservation (CTPC) at Fairchild is on the conservation biology of south Florida and Caribbean plants, evolutionary biogeography and the conservation management of tropical plants and habitats with a special emphasis on palms and cycads.

Fairchild works with partners in over 20 countries with active field programs in the Caribbean, MesoAmerica, Madagascar, South Africa, and East Africa. Working in tandem with the CTPC are highly professional education and tropical horticulture teams. As a public garden with a high profile in the Miami community Fairchild offers unique opportunities to advance the public understanding of tropical conservation and science in general.

Fairchild has a strong and active partnership with Florida International University (FIU), Florida's State research university in Miami. FIU has over 38,000 students and offers more than 200 bachelors, masters and doctoral degrees in 21 colleges and schools. The Department of Biological Sciences of FIU has 39 faculty members, 900 undergraduate majors, and 100 graduate students. Tropical biology and conservation are major themes of the department.

Position background. The CTPC has a major regional herbarium with rich collections from Florida and the Caribbean and specialist collections of palms and cycads. It is an active herbarium with strong partnerships in the USA, the Caribbean and internationally. The FTG Herbarium holds ca. 180,000 specimens with

more than 84,000 on eFTG the first virtualherbarium in the world www.virtualherbarium.org. Position description and required qualifications. The successful candidate will report to the Head of the CTPC. The candidate will be working with a highly experienced herbarium manager and an army of extraordinary volunteers. As a Fairchild staff member he/she will be expected to oversee the management the herbarium, lead conservation research projects (for instance conservation planning in Jamaica) and to develop an externally funded research program that supports excellence in the nexus of systematics and conservation biology, teaching at FIU, and the mentoring of graduate students. We are looking for a candidate with experience in tropical biology and botany, an understanding of the management of a herbarium (including CITES administration) and a passion for the conservation of tropical plants and their habitats. Advancement will be based on papers published, grants and funding obtained and measurable conservation delivery.

The position is a full time contract and the salary is competitive and commensurate with qualifications and experience. Minimum of an M.Sc or ideally a Ph.D. with postdoctoral experience is required that includes grant writing experience and a record of peer reviewed publication. Fluency in a second language (ideally Spanish) will be desirable as is a desire to travel and to make a difference in the world of conservation.

To apply, submit by email or mail/courier a curriculum vitae, statements of research and conservation interests, and have three letters of reference sent to:

Ms Jan Brown, Assistant to the Executive Director, Davis House, Fairchild Tropical Botanic Garden, 10901 Old Cutler Road, Coral Gables, FL 33156-4296.

jbrown@fairchildgarden.org

Barbara A. Whitlock Assistant Professor Department of Biology University of Miami 29 Cox Science Center Coral Gables, Florida 33124 phone: (305) 284-5412 fax: (305) 284-3039 www.bio.miami.edu/whitlock

ImperialCollegeLondon SummerResAssist WildlifeEpidemiology

ImperialCollegeLondon.ShortResearchProject.WildlifeEpidemiology

Summer Research Assistant Based at Imperial College London and the University of Aberdeen, United Kingdom

Temporal and Spatial Dynamics of a Vector-borne Wildlife Disease System

Fixed term: 4 months Start date: 1 May 2008 (slightly flexible) Salary: £1851 per month

We are seeking a graduate or higher level researcher with good quantitative skills to join a 4 month project starting May 2008 to investigate the epidemiology of Louping Ill (LI), a tick-borne wildlife disease affecting northern areas of the United Kingdom. The LI system involves a variety of hosts, including red grouse, mountain hares, sheep and red deer, and is of economic importance to sheep and grouse moor management. This project aims to develop models of the temporal and spatial dynamics of LI transmission between tick vectors and the hosts of the disease, exploring the impact of seasonality and host density on LI epidemiology. The project would be suitable as the placement project for an appropriate Masters course.

The successful applicant will have an interest in ecology and epidemiology along with programming skills (for example in C++, Mathematica or Matlab) and ability to analyse differential equations. The applicant will be based primarily at the Centre for Population Biology, Silwood Park Campus, Imperial College London, and will have opportunities to visit the University of Aberdeen.

Applications (including CV and cover letter) or enquiries should be sent to Dr Penelope Hancock (p.hancock@imperial.ac.uk) or Dr Steve Palmer (s.palmer@abdn.ac.uk).

Websites:

<http://www3.imperial.ac.uk/cpb>
<http://www.aces.ac.uk/projects/>
www3.imperial.ac.uk/people/p.hancock
www.abdn.ac.uk/biologicalsci/staff/details.php?id=-3Ds.palmer&fit

Closing date: 20th March 2008

p.hancock@imperial.ac.uk p.hancock@imperial.ac.uk

Imperial College London

Division of Biology

Faculty of Natural Sciences

Research Associate

Starting Salary: £24,570 per annum

Imperial College is ranked the fifth best university in the world (Times Higher QS World University Rankings 2007)

This is an exciting opportunity for a Research Associate with an interest in evolutionary genetics. The successful candidate will carry out cutting-edge research investigating the molecular evolutionary genetics of colour pattern variation in the mimetic butterfly, *Papilio dardanus*.

The post is funded for 3 years by the Natural Environment Research Council and will be based at the Natural History Museum. The successful candidate will work closely with Professor Vogler and employ advanced genetic, molecular and bioinformatic methodologies to explore the genetic variation in a genomic region corresponding to the classical mimicry locus, H.

Further details of the research group can be obtained from the research group website: <http://www3.imperial.ac.uk/people/a.vogler/research> The successful candidate must possess a PhD or equivalent qualification in evolutionary genetics, molecular evolutionary biology or a closely related discipline; show a proficiency in evolutionary genetics preferable in insects; and have experience of working in a multi-disciplinary context.

Further details and an application form can be obtained from the college employment website: <http://www3.imperial.ac.uk/employment/research> . Completed application forms accompanied by a curriculum vitae and the name and contact details of two referees should be sent to: Prof Alfried Vogler, Imperial College London, SAF Building, Exhibition Road, London, SW7 2AZ, or preferably by email to a.vogler@imperial.ac.uk.

Closing date: 2 April 2008

Valuing diversity and committed to equality of opportunity

“Thomas, Jenny” <j.thomas@imperial.ac.uk>

ImperialCollege ResearchAssociate
EvolutionaryGenetics

IthacaNY PopulationGenetics

Population/Quantitative Geneticist

Employer: Nature Source Genetics, Inc Location: Ithaca, NY Date: March 12, 2008

Nature Source Genetics (<http://naturesourcegenetics.com>) is a computational genetics company dedicated to the development and application of new algorithms designed to harness natural genetic variation in the improvement of plant species. Located in Ithaca, New York, NSG scientists interact with a team of distinguished faculty from Cornell University and other major research institutions to solve problems related to population and quantitative genetics, including detection/measurement of genetic variation, population structure, and optimization of population design for QTL detection/validation. In addition to the computational headquarters in Ithaca, NSG has access to experimental test sites around the world. This position will work with and support a team of scientists working in the areas of computational genomics, statistics and population/quantitative genetics.

We would look to the successful candidate to work with the team of other NSG scientists to help develop and implement new approaches population and quantitative genetics – especially as expanding plant biodiversity and gene discovery. Successful candidate would also have responsibility for overseeing specific projects – including coordinating activities with outside collaborators worldwide.

Qualifications:

- . M.S./Ph.D degree in population genetics, quantitative genetics, or related discipline . Experience in population and/or quantitative genetics . Training/coursework in statistics . Ability to work independently . Strong interpersonal skills and demonstrated ability to effectively communicate with others

Responsibilities

- . Working with the NSG management team and the Scientific Advisory Board members in problems related to population and quantitative genetics, including development and application of tools and algorithms for measuring genetic diversity, population structure, and optimization of population design for QTL detection/validation.

- . Work with the management team to advance projects, including data analysis, reporting to clients, organization of data and progress reports, etc.

- . Interfacing with worldwide clients on questions pertaining to projects

- . Preparing and contributing to scientific reports, pub-

lications and presentations that clearly convey progress and challenges

- . Attending and participating in research planning meetings with other NSG employees, the Scientific Advisory Board, and other scientists (both in academia and the private sector) related to various NSG project

To Apply or Obtain More Information about this Position, Contact:

Dr. Theresa Fulton Director of Operations Nature Source Genetics 95 Brown Road Suite 204; Box 1055 Ithaca, NY 14850 E.mail: tfulton@naturesourcegenetics.com FAX: 607-257-0034

Steve Tanksley <sdt4@cornell.edu>

Montpellier ResAssist ModesOfReproduction

Job Title: Research Assistant

Closing date: 22 March 2008

Salary: 21457 euros per year net, plus travel allowances

Terms & Conditions: Research Staff

Summary

A vacancy now exists for a research assistant to work with Dr. Yannis Michalakis to investigate the evolutionary balance between sexual and asexual reproduction in the ostracod *Eucypris virens* /using molecular genetic approaches. This is a component project of a Marie Curie Research Training Network (see <http://evirens.group.shef.ac.uk/>). The post will be based in Montpellier but the appointee will also work in Sheffield, with Prof. Roger Butlin.

Applicants must have a good grounding in quantitative PCR and some knowledge of evolutionary biology.

The post is full time for 6 or 7 months. Due to funding restrictions, only non-French citizens of the EU or associated states are eligible.

Full post details

Marie Curie Research training network (MRTN) SEX-ASEX – Early Stage Researcher position available in molecular genetics

Researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to apply for a research position in the European Union Marie Curie

Research Training Network SEXASEX, which is coordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. One predoctoral ('Early Stage Researcher') position is vacant, out of a total of 10 positions supported by the network. Criteria of eligibility include: EU citizenship, less than 4 years of research experience (defined as starting when the candidate is awarded a degree that permits entry to a PhD programme, usually an Honours or Masters degree), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. This appointment will be for 6 months.

The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview:

Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (ESR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The network's theoretical and empirical research will apply 13 major approaches, including novel genetic and cytogenetic approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on Euro-

pean excellence and tradition. Please refer to <http://www.naturalsciences.be/EVIRENS/> for more information.

ESR position: /consequences of asexual reproduction on genome size: comparison of //rDNA copy numbers in sexual and asexual /*E. virens*/ ./

Starting date: 1st of April or 1st of May 2008 depending on appointee's availability

Duration: 6 or 7 months

Salary: 21457 net pa plus travel allowances according to the appointee's circumstances

Scientists in charge:

Dr. Yannis Michalakis

Locations: Montpellier, France, with a secondment of up to 2 months to Sheffield, UK (Prof. Roger Butlin).

Places of work: 1) Génétique et Evolution des Maladies Infectieuses, UMR CNRS – IRD 2724, IRD, Montpellier, France 2) University of

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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>

Montpellier ResAssist ModesOfReproduction-Ammended

This position is now open at one of two levels

Job Title: Research Assistant

Closing date: 22 March 2008

Salary: 21457-31330 euros per year net (depending on experience), plus travel allowances

Terms & Conditions: Research Staff

Summary

A vacancy now exists for a research assistant to work with Dr. Yannis Michalakis to investigate the evolutionary balance between sexual and asexual reproduction in the ostracod *Eucypris virens* /using molecular genetic approaches. This is a component project of a Marie Curie Research Training Network (see <http://evirens.group.shef.ac.uk/>). The post will be based

in Montpellier but the appointee will also work in Sheffield, with Prof. Roger Butlin.

Applicants must have a good grounding in quantitative PCR and some knowledge of evolutionary biology.

The post is full time for 6 or 7 months. Due to funding restrictions, only non-French citizens of the EU or associated states are eligible.

Full post details

Marie Curie Research training network (MRTN) SEXASEX – Early Stage Researcher or Experienced Researcher position available in molecular genetics

Researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to apply for a research position in the European Union Marie Curie Research Training Network SEXASEX, which is coordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. The position is open at 2 levels: predoctoral ('Early Stage Researcher') or postdoctoral ('Experienced Researcher'). Criteria of eligibility include: EU citizenship, less than 4 years of research experience for the ESR level (defined as starting when the candidate is awarded a degree that permits entry to a PhD programme, usually an Honours or Masters degree) or less than 10 years research experience after obtaining the degree that gives access to a PhD programme for the ER level (e.g. BSc, MS, Diploma, Honours), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. This appointment will be for 6 or 7 months.

The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview:

Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (ESR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the exten-

sive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The network's theoretical and empirical research will apply 13 major approaches, including novel genetic and cytogenetic approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition. Please refer to <http://evirens.group.shef.ac.uk/index.htm> for more information.

****ESR or ER position**: consequences of asexual reproduction on genome size: comparison of rDNA copy numbers in sexual and asexual *E. virens*/.

****Starting date**: 1st of April or 1st of May 2008 depending on appointee's availability

****Duration**: 6 or 7 months

****Salary**: 21457 (ESR) or 31330 (ER) net pa plus travel allowances

according to the appointee's circumstances

****Scientists in charge**:

Dr. Yannis Michalakis

****Locations**: Montpellier, France, with a secondment of up to 2 months to Sheffield, UK (Prof. Roger Butlin).

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

Phyloinformatics Summer of Code 2008 http://phyloinformatics.net/-Phyloinformatics_Summer_of_Code_2008 *** Please disseminate this announcement widely to appropriate students at your institution ***

The National Evolutionary Synthesis Center (NESCent: <http://www.nescent.org/>) is participating in 2008 for the second year as a mentoring organization in the Google Summer of Code (<http://code.google.com/soc>). Through this program, Google provides undergraduate, masters, and PhD students with a unique opportunity to obtain hands-on experience writing and extending open-source software under the mentorship of experienced developers from around the world.

Our goal in participating is to train future researchers and developers to not only have awareness and understanding of the value of open-source and collaboratively developed software, but also to gain the programming and remote collaboration skills needed to successfully contribute to such projects. Students will receive a stipend from Google, and may work from their home, or home institution, for the duration of the 3 month program. Students will each have one or more dedicated mentors with expertise in phylogenetic methods and open-source software development.

NESCent is particularly targeting students interested in both evolutionary biology and software development. Project ideas (see URL below) range from visualizing phylogenetic data in R, to development of a Mesquite module, web-services for phylogenetic data providers or geophylogeny mashups, implementing phyloXML support, navigating databases of networks, topology queries for PhyloCode registries, to phylogenetic tree mining in a MapReduce framework, and more.

The project ideas are flexible and many can be adjusted in scope to match the skills of the student. If the program sounds interesting to you but you are unsure whether you have the necessary skills, please email the mentors at the address below. We will work with you to find a project that fits your interests and skills.

INQUIRIES: Email any questions, including self-proposed project ideas, to phylosoc@nescent.org.

TO APPLY: Apply on-line at the Google Summer of Code website (<http://code.google.com/soc/2008>), where you will also find GSoC program rules and eligibility requirements. The 1-week application period for students opens on Monday March 24th and runs through Monday, March 31st, 2008.

Hilmar Lapp and Todd Vision US National Evolution-

ary Synthesis Center

====URLs: == 08 NESCent Phyloinformatics Summer of Code: http://phyloinformatics.net/-Phyloinformatics_Summer_of_Code_2008 Eligibility requirements: <http://code.google.com/opensource/gsoc/2008/faqs.html#0.1.eligibility> Stipends: <http://code.google.com/opensource/gsoc/2008/faqs.html#0.1.administrivia> To sign up for quarterly NESCent newsletters: with announcements about upcoming programs at the Center: <http://www.nescent.org/about/contact.php> hlapp@nescent.org

New York Population Genetics

ASSISTANT RESEARCH SCIENTIST

Health Research, Inc., a not-for-profit corp., seeks an Asst. Research Scientist to work in the Vector Biology & Population Genetics Laboratory at the Wadsworth Center in Albany, NY. The incumbent will be responsible for the oversight of the Lab, w/ duties that include extraction, amplification & sequencing of mosquito DNA; management & organization of frozen mosquito collections, freezers & other databases, & preparation of reports. Other related duties as assigned. MINIMUM QUALS: BA/BS in Biology, Public Health, Epidemiology, Statistics, or a related field & 1 yr of relevant experience. 30 grad credit hours leading to an advanced degree may substitute for the required exp. PREFERRED QUALS: Grad degree in a relevant field; background in biology or entomology; exp w/ personal computers & database management; knowledge of the Spanish language would be helpful. Salary is at the rate of: \$36,229 /yr. Excellent benefits including health, paid vacation/holidays, retirement, tuition support, etc. Resume must be received by 3/14/08. Please use code W713TU when responding. Resume can be e-mailed to: HRI-mailin@healthresearch.org with a subject line W713TU, or mailed to Health Research, Inc., Riverview Center, 150 Broadway, Suite 560, Menands, NY 12204-2719 (applicants must include a return address and the reference code W713TU on the envelope). No phone calls or faxes accepted.

www.healthresearch.org/jobs AA/EOE/M/W/D/V

Stacey J. Miller, PHR Human Resource Administrator III Health Research, Inc. Phone: (518) 431-1270 Fax: (518) 431-1234 sjm06@healthresearch.org www.healthresearch.org Riverview Center 150 Broad-

way, Suite 560 Menands, NY 12204-2719

“Stacey J. Miller” <sjm06@healthresearch.org>

NSF EvolBiol ProgramDirectors

ANNOUNCEMENT:

The Division of Environmental Biology (DEB) is searching for three permanent program directors; one in each of three clusters: Ecosystem Science Cluster, Population and Evolutionary Processes Cluster, and Systematic Biology and Biodiversity Inventories Cluster. These individuals will have significant input on future research directions and funding opportunities within DEB and the Directorate for Biological Sciences, and on the proposal review and award process at NSF. The quality of applicants for these positions is therefore of great importance to you, as a researcher in one or more of these areas, as well as it is to us.

We ask for your help in our search by encouraging your well-qualified colleagues to apply. Time is short; the position announcement closes on 4 April 2008. Previous NSF experience is not necessary but applicants must have at least 6 years of research experience past their doctorate degree.

Thank you in advance for helping to ensure that our applicant pool is of the highest quality. <http://jobsearch.usajobs.opm.gov/-getjob.asp?JobId=67754917&AVSDM=2008%2D01%2D25+08%3A32%3A57>

Bette Loiselle Saran Twombly Program Officer, Program Officer, Population and Evolutionary Processes Ecological Biology Tel. 703-292-7207 Tel. 703-292-8133

“Loiselle, Bette A.” <bloisell@nsf.gov>

OhioStateU BioInformatics 2 Programer

Subject: Job: ruby and kml developers at Ohio State University
The Department of Biomedical Informatics at the Ohio State University seeks two programmers to work as part of the team developing the supramap project (supramap.osu.edu) that brings together phy-

logenetics and geography with a special emphasis on infectious disease research. One programmer will concentrate on development of a client and user interface for the project using Ruby on Rails. The user base will be biologists and public health professionals. Another programmer will concentrate on improving the generation of Keyhole Markup Language (KML) files. The source data will be large XML files resulting from phylogenetic analysis. Thus the work will require knowledge of XSLT and KML and a willingness to work with biologists and phylogenetic software they use. For more information please contact Daniel Janies

danjanies@hotmail.com

OhioStateU RubyXML programmers

The Department of Biomedical Informatics at the Ohio State University seeks two programmers to work as part of the team developing the supramap project (supramap.osu.edu) that brings together phylogenetics and geography with a special emphasis on infectious disease research.

One programmer will concentrate on development of a client and user interface for the project using Ruby on Rails. The user base will be biologists and public health professionals.

Another programmer will concentrate on improving the generation of Keyhole Markup Language (KML) files. The source data will be large XML files resulting from phylogenetic analysis. Thus the work will require knowledge of XSLT and KML and a willingness to work with biologists and phylogenetic software they use.

For more information please contact Daniel Janies

danjanies@hotmail.com danjanies@hotmail.com

OregonStateU SystematicEntomology

Harold E. and Leona M. Rice Professorship in Systematic Entomology

Applications are invited for the Rice Professorship in

Systematic Entomology. This is a full-time, 9-month tenured position at the Full Professor level in the Department of Zoology. The holder of the chair is expected to be a midcareer to senior scholar with an international reputation for scholarship and a distinguished record of funding, publication, and teaching in systematic entomology. The Rice Professor will participate in teaching, graduate education, and serve as Director of the Oregon State Arthropod Collection (OSAC), a major research collection with 3 million specimens. The appointment also includes annual discretionary funds of approximately \$100,000 to support the research and teaching programs of the Rice Professor, with approximately one-third to be spent in support of the functions of the OSAC. It is expected that the Rice Professor will continue to be a productive scholar and teacher, participate fully in departmental affairs, contribute to the study of systematic entomology at Oregon State University, and take a leadership role in the local systematics community. The Rice Professor should possess broad disciplinary interests and welcome collaborative research with colleagues across the university and beyond. For additional requirements and to apply see <http://oregonstate.edu/jobs> Posting #0002193. For full consideration apply by 15 July 2008. Direct inquires to Tara Bevandich at bevandit@science.oregonstate.edu or Rice Search Committee Chair, Stevan J. Arnold at arnolds@science.oregonstate.edu.

OSU is an Affirmative Action/Equal Opportunity Employer has a policy of being responsive to dual-career needs.

Tara Bevandich Administrative Assistant Department of Zoology 3029 Cordley Hall Oregon State University Corvallis, OR 97331 Email: bevandit@science.oregonstate.edu Phone: 541-737-5336 Fax: 541-737-0501

Tara Bevandich <bevandit@science.oregonstate.edu>

OxfordU EvolutionaryBiol

Two permanent lectureships are available in the Department of Zoology, University of Oxford, one at the interface of Evolutionary Developmental Biology and Ecology, the other in Quantitative Evolutionary Ecology. Closing date for applications is 4 April 2008. Please see below for more details, or follow the link: <http://www.zoo.ox.ac.uk/news/2008feb/>-

index.htm . Seb Shimeld Department of Zoology University of Oxford sebastian.shimeld@zoo.ox.ac.uk

Department of Zoology UNIVERSITY OF OXFORD Oxford, U.K. TWO UNIVERSITY LECTURESHIPS IN ZOOLOGY:

(1) Development/Ecology and (2) Quantitative Evolutionary Ecology In association with Lady Margaret Hall and Wadham College

The Department of Zoology, Oxford, proposes to appoint two University Lectureships with effect from 1 September 2008 or as soon as possible thereafter. The successful candidates will be offered an Official Fellowship and Tutorship by Lady Margaret Hall (position 1) and Wadham College (position 2), under arrangements described in the further particulars. The combined University and College salary for each post will be on a scale up to £52,628 per annum.

Preference for position 1 will be given to applicants working at the interface of developmental biology and ecology, including evolutionary developmental biology or ecological/evolutionary genomics. Applications for position 1 will also be considered from candidates working at the interface between any two or more of the Department's specialist research fields: behaviour, development, disease, ecology, entomology, evolution and ornithology.

Position 2 is for a quantitative evolutionary ecologist.

The appointees will be required to engage in research, which will contribute to the Department's research reputation; to teach, supervise and examine undergraduate and graduate students; and to contribute to administration in the College and Department.

The appointments are intended to be 'permanent', meaning that on completion of an initial period of appointment (normally five years), a University lecturer is eligible for reappointment until retiring age, subject to the provisions of the Statutes and Regulations of the University. Further particulars, containing details of the application procedure and of the duties, may be obtained from paul.harvey.pa@zoo.ox.ac.uk or peter.holland@zoo.ox.ac.uk. The closing date for applications is Friday 4th April 2008. The University is an Equal Opportunities Employer.

sebastian.shimeld@zoo.ox.ac.uk
sebastian.shimeld@zoo.ox.ac.uk

sebas-

SanDiegoZooSociety Tech MolConservGenetics

A Research Technician opening is immediately available with the the molecular genetics group of Genetics Division at CRES (Conservation and Research for Endangered Species - part of the San Diego Zoo). Applicants must have experience working in a molecular biology lab, with training in nucleic acid preparation (from a variety of source materials) and quantitation required. Skill with PCR, automated sequencing, and microsatellite fragment analysis is necessary. Experience in Mac and/or Windows-based computer programs is required, and knowledge of data analysis programs is preferred. The applicant must have the ability to take direction, work as part of a team, follow through on assignments, and be neat and well organized. The job location is at the Beckman Center for Conservation Research, near Escondido, CA. For more information and to apply, please see: <http://www.sandiegozoo.org/-jobs/index.html> oryder@ucsd.edu oryder@ucsd.edu

Scotland FieldAssistant FishParasiteCoevolution

Field Assistant Wanted, Scottish Outer Hebrides

To assist on an ongoing project on host-parasite coevolution and adaptive radiation in sticklebacks

1st May until 18th May 2008 Travel, accommodation and food will be paid for.

I am looking for a volunteer field assistant to help with surveys of parasite occurrence in stickleback fish populations in Scotland. The work will consist of trapping and dissection of fish from several lochs to record parasite and life history data.

Applicants, who should be living in the U.K., should be outgoing, physically fit, hard working and have a keen interest in evolutionary ecology and natural history. Experience of fish or fish parasites an advantage. Ideal for prospective PhD candidates.

Please send a CV to Andrew MacColl (andrew.maccoll@nottingham.ac.uk) as soon as possible,

and before 14th April 2008.

For more information on the project, see:

<http://www.nottingham.ac.uk/~plztr/groupsite/-parasitesandspeciation.html> Andrew MacColl (andrew.maccoll@nottingham.ac.uk)

Andrew.Maccoll@nottingham.ac.uk

Simula Research Lab

Simula Research Laboratory conducts basic research in the fields of communication technology, software engineering and scientific computing. The research in the Scientific Computing (SC) department is focused on the development of numerical methods, algorithms and software, and large scale biomedical and systems biology oriented simulation studies applying these methods. In recent years, the main application area for computational research studies has been the simulation of the electrical and mechanical activity of the heart. Currently, we plan to extend our computational research to simulations of the evolutionary dynamics of genetic networks controlling the properties of organisms.

The aim of the research project is to study key evolutionary processes such as the adaptation of organisms to their environment, the splitting up of a species into multiple species and the development of multicellular organisms from a single fertilized cells. A key aspect of the research will be to study how the architecture and dynamics of genome organization and gene regulatory network structure influence the properties of organisms and hence how they influence the above mentioned evolutionary processes and how this contrasts with findings from more classical population genetics models.

Our understanding of genome organization and gene regulatory networks has changed dramatically over the last decade. A large part of DNA that was previously considered junk turns out to be functional after all, coding for RNAs that are however not translated into proteins. These RNAs in turn are often involved in regulating the expression of genes, which were previously thought to be exclusively regulated by proteins. Incorporating these new insights into our models is another key aspect of the research project.

Modeling formalisms used will typically be discrete, individual- based, event-based, and often spatially extended and will involve the explicit modeling of the evolution of genes, genomes and gene regulatory net-

works determining the properties of simulated agents. The project will be supervised by a new member of our research group, Dr. Kirsten ten Tusscher (<http://www-bin.f.bio.uu.nl/khwjtuss/>).

Simula offers excellent opportunities for doing high quality research, generous support for travels and equipment, and competitive salary (around 47.000,- Euro/69.000,- USD for a Ph.D. position)

We are looking for candidates who fulfill one or more of the following requirements: - a strong interest in evolutionary biological research - a University degree in computational biology, systems biology, biomedical engineering, artificial life, artificial intelligence, computer science, physics or applied mathematics - experience with computational modeling, simulation and analysis of complex (biological) systems.

The position requires excellent English writing skills and high marks from the BSc and MSc degree. Women are encouraged to apply. For more information contact Joakim Sundnes (sundnes@simula.no) or Kirsten ten Tusscher (tentussc@simula.no). To apply, email a short application letter, curriculum vitae, copies of transcripts and grades, and a publication list to jobs@simula.no. The subject of the email must contain 0830 Scientific Computing.

Application deadline: May 16, 2008

sundnes@simula.no sundnes@simula.no

UCaliforniaLosAngeles ResTech Phylogeography

RESEARCH TECHNICIAN: UCLA ECOL & EVOL BIOLOGY

A technician position is available immediately to assist in projects on landscape genetics, contemporary gene flow, and phylogeography. The technician will perform standard laboratory procedure and data management for research in plant population and conservation genetics. The technician will conduct molecular analyses, including DNA extraction, PCR, genotyping with microsatellite DNA and sequencing, using standard methods and by developing modifications of standard methods. Other duties include: oversee day-to-day management of laboratory including purchase of supplies and equipment; insuring proper operation and maintenance of laboratory equipment; entering and managing electronic data files; working with undergraduate research

assistants; and occasional training of students.

Requirements for the position are a bachelor's degree in biology, botany, genetics, or chemistry, basic computer skills, and laboratory experience with PCR, microsatellites, DNA sequencing, or comparable molecular techniques. Interest in population genetics or molecular ecology will be advantageous.

The position could be filled as a 6-month or 12-month position or on-going position, depending on interest of successful candidate.

Applications will be considered as they arrive. To apply, please email statement of interest and experience, curriculum vitae and names of three references to:

Dr. Victoria Sork, vlork@ucla.edu

Posted by: Victoria Sork UCLA Professor, Dept of Ecol & Evol Biology Professor, Institute of the Environment

Victoria Sork <vlork@ucla.edu>

UGeorgia ResTech PlantEvolution

A full-time Research Technician position is available in the Department of Genetics at the University of Georgia in the laboratory of Dave Moeller. Research in the lab examines a diverse array of problems in plant evolutionary biology and ecology. Current research includes projects on the evolution of species' distributions, the interface of pollination ecology and plant mating system evolution, and ecological genetics of species' responses to climate change. This position may be ideal for a highly motivated person interested in gaining field and laboratory research skills prior to starting graduate school or other work in the life sciences.

The position involves assisting with field research, greenhouse experiments, and molecular genetics in the laboratory. Field research will occur in California during part of the spring and summer months. It is essential that the candidate can spend approximately 4-6 weeks per year in the field conducting research away from home. Conditions for field work can be demanding, including working in hot weather on steep mountain slopes. Responsibilities also include assisting with basic molecular genetics in the laboratory, including PCR, DNA/RNA extraction, gel electrophoresis, cloning, etc. The position also involves caring for plants in growth chambers and the greenhouse as well as lab organization and maintenance.

Candidates are expected to have a Bachelors degree in Biology or a related field. The ideal candidate has a strong work ethic, positive attitude, excellent communication and organization skills, and the desire to acquire new field and laboratory research skills. Experience with both field research and basic molecular biology techniques is highly desired, but not essential.

Please contact me directly (dmoeller@uga.edu) to express interest in the position and with any questions. Formal application must occur through the UGA Human Resources website (posting number: 20080351, www.ugajobsearch.com). Applicants should submit a CV, letter describing research background and interests, and the names of two references. A starting date of May 1 is desired, but flexible. Applications should be submitted as soon as possible; applicants will be reviewed until the position is filled. Salary is commensurate with experience and includes benefits.

The Department of Genetics at UGA (www.genetics.uga.edu) is a dynamic place for research in ecological and evolutionary genetics and has excellent laboratory and greenhouse facilities. The University of Georgia is located in Athens, a diverse city of ~100,000 with easy access to Atlanta and the Appalachian Mountains. Athens has a lively music and arts scene, affordable living, and nearby parks and natural areas.

Dave Moeller Dept. of Genetics Davison Life Sciences University of Georgia Athens, GA 30602 dmoeller@uga.edu (706) 542-5898

dmoeller@uga.edu dmoeller@uga.edu

UHawaii InsectEvolutionaryBiologist

Insect Evolutionary Biologist

Assistant Professor in Entomology, position number 0085510, UHM C of Trop Agr & Human Res, (Manoa), Plant & Environmental Protection Sciences, tenure track, 9 month appointment, to begin January 1, 2009.

Duties: Contribute to an excellent departmental undergraduate program and Entomology graduate program by teaching the following courses: PEPS 250 (World of Insects), General Entomology (PEPS 363 and 363L), yearly; Foundations of Pest Management (PEPS 421), every two years; an appropriate graduate course identified as meeting program needs, such as Insect Phys-

iology, or Insect Identification (taxonomy), every two years; and sharing responsibility periodically for a discussion/seminar and a departmental graduate seminar. Contribute to program assessment efforts. Advise and mentor students.

Develop a successful research program in fields including but not limited to control, ecology, evolution, physiology or behavior of invasive ants / bees or other insect orders. Provide service to the college, university, and community, and perform other faculty duties as required. 60% Instruction and 40% Research.

Minimum qualifications: Earned doctorate with research experience in entomology as evidenced by publications in peer-reviewed journals. Successful experience in instruction at the college level, as evidenced by written or web-based course materials, reports, references, and/or positive student evaluations. Desirable qualifications: Research experience with social hymenoptera or other insect orders as evidenced by publications in peer-reviewed journals; experience in course and/or program development, and assessment; demonstrated success in obtaining extramural funding; evidence of self-improvement in the area of instruction, such as participation in relevant courses, seminars, or other programs. To apply: Send letter of application, curriculum vitae, official transcripts of college training, and have three confidential letters of recommendation sent to Search Committee. Application address: Dr. Ronald Mau, Search Committee Chair, Department of Plant and Environmental Protection Sciences, College of Tropical Agriculture and Human Resources, University of Hawaii at Manoa, 3050 Maile Way, Gilmore 310, Honolulu, HI 96822. Inquiries: Dr. Ronald Mau 808-956-7063 maur@ctahr.hawaii.edu

Date posted: Mar-17-2008 Closing date: Jul-15- 2008

The University of Hawaii is an equal opportunity/affirmative action institution and is committed to a policy of nondiscrimination on the basis of race, sex, age, religion, color, national origin, ancestry, disability, marital status, sexual orientation, status as a protected veteran, National Guard participation, breastfeeding, and arrest/court record (except as permissible under State law). Employment is contingent on satisfying employment eligibility verification requirements of the Immigration Reform and Control Act of 1986; reference checks of previous employers; and for certain positions, criminal history record checks. In accordance with the Jeanne Clery Disclosure of Campus Security Policy and Campus Crime Statistics Act, annual campus crime statistics for the University of Hawaii may be viewed at: <http://ope.ed.gov/security/>, or a paper copy may be obtained upon request from the respective

UH Campus Security or Administrative Services Office.

Dan Rubinoff

Daniel Rubinoff <rubinoff@hawaii.edu>

ULethbridge PopulationBiology

The University of Lethbridge invites applications for a tenure-track (probationary) faculty position in the Department of Biological Sciences at the rank of assistant professor in the area of population biology. Applicants with strength in the areas of population genetics, aquatic or terrestrial ecology, conservation biology, ecosystem management, evolutionary biology or ecology are encouraged to apply. Applicants must have a Ph.D. and demonstrated potential for excellence in teaching and research.

The successful candidate will be expected to build an externally funded research program, supervise graduate students, and will be encouraged to develop collaborations with, and seek funding from, federal and provincial agencies. The Department of Biological Sciences (<http://www.uleth.ca/fas/bio>), with 24 faculty and 47 graduate students, offers an exciting environment with potential for collaborative research in the areas of molecular ecology and evolution, behavioural ecology, aquatic ecosystems, conservation biology, plant systematics, physiological ecology, toxicology and parasitology.

The University of Lethbridge has ready access to a diverse array of prairie and mountain habitats, including many lakes, ponds, and rivers. In addition, the university will soon be opening a new Water and Environmental Sciences building, featuring top-tier aquatic and terrestrial research as well as analytical laboratory facilities. The Department maintains a field research station in the foothills of the Rocky Mountains in southwestern Alberta.

The successful candidate will be expected to participate in teaching at both the junior and senior undergraduate level.

Candidates should submit: a letter of application, a CV, transcripts, a one-page summary of research plans, a statement of teaching interests and teaching philosophy, and reprints of their three most significant publications to Dr. Cam Goater, Chair, Department of Biological Sciences, University of Lethbridge, 4401 University Drive W., Lethbridge, Alberta, Canada T1K 3M4,

preferably electronically via barbara.beckett@uleth.ca. Applicants must also arrange for three letters of reference to be sent electronically. Closing date: April 30, 2008.

The University of Lethbridge offers a competitive salary commensurate with experience and has an excellent benefits plan. The position is open to all qualified applicants, although preference will be given to Canadian citizens and permanent residents of Canada. The University is an inclusive and equitable campus encouraging applications from qualified women and men including persons with disabilities, members of visible minorities and Aboriginal persons.

theresa.burg@uleth.ca

ULyon1 EvolDevoVertebrateMorph

Dear Colleagues,

In 2008, a Professor level position will be available at the University Lyon 1. This position will include research in the Institut de Genomique Fonctionnelle de Lyon at the ENS de Lyon. You can find below a brief summary in French of the research and teaching requirements (teaching should be in French). A more detailed proposal can be found at: http://www.univ-lyon1.fr/-1204632634146/0/fiche___document/ For more information, please do not hesitate to contact Vincent Laudet (Vincent.Laudet@ens-lyon.fr).

Un poste de professeur intitulé "Développement et évolution morphologique des vertébrés" est disponible à l'Université Claude Bernard Lyon 1 pour affectation à l'Institut de Genomique Fonctionnelle de Lyon. Nous recherchons un enseignant-chercheur capable d'animer une équipe de recherche indépendante en interaction entre paléontologie et biologie du développement des vertébrés. Idéalement nous souhaiterions quelqu'un travaillant sur l'évolution des structures minéralisées des vertébrés et en premier lieu la denture

Pascale.Chevret@ens-lyon.fr Pascale.Chevret@ens-lyon.fr

UMunich SystematicEvolutionaryBotany

Prof. Dr. Susanne S. Renner Chair, Systematic Botany, University of Munich Research: <http://www.umsl.edu/~biosrenn/> Associate lecturer position in Systematic and Evolutionary Botany Ludwig Maximilians University of Munich

The Institute of Systematic Botany of the University of Munich is seeking a botanist with an interest in evolutionary research questions. Competence in general biostatistical methods and knowledge of the Central European flora are an advantage. The successful candidate will have basic teaching obligations and is expected to develop an extramurally funded research program, as well as collaborating with other staff-members in research projects.

We (<http://www.botanik.biologie.uni-muenchen.de/botsyst/home.html>) are actively involved in systematic, molecular phylogenetic, biogeographical, evolutionary, and floristic research. Facilities include an excellent library, an herbarium of almost 3 million specimens, cultivation facilities, and a botanical garden with some 14000 living species.

The position is available from 1 July 2008, and applicants should submit a CV, including a summary of research interests, a listing of publications, and the names of three potential referees to Susanne Renner (renner@lrz.uni-muenchen.de) by 13 April 2008.

Contact person: Susanne Renner (<http://www.umsl.edu/~biosrenn/>)

Susanne Renner <renner@lrz.uni-muenchen.de>

UNewBrunswick ResTech ForestGenomics

Research Technician

Canada Research Chair in Forest and Conservation Genomics and Biotechnology Faculty of Forestry and Environmental Management University of New Brunswick, Fredericton

A full-time position of Research Technician is available immediately in the Forest Genetics and Genomics Lab at the University of New Brunswick, Fredericton. The Research Technician will be a member of an active and well-funded research group of Dr. Om Rajora, consisting of Ph.D., master and undergraduate students, postdoctoral fellows and research assistants, working on various aspects of molecular, population, conservation and evolutionary genetics; structural, functional and conservation genomics; and biotechnology of forest trees. The Forest Genetics and Genomics Lab has state-of-the-art molecular genetic and genomics facilities, including automated DNA sequencers, robotic systems. The position is currently funded for three years and may likely continue. The salary will commensurate with qualifications and experience of the successful candidate.

Duties and Responsibilities The Research technician is expected to contribute significantly to the Canada Research Chair research program. The main duties and responsibilities of the position are as follows. - Manage and maintain the lab infrastructure to ensure proper functioning, operation and equitable access of the equipment. - Develop, improve, optimize and/or use molecular biology, genetics and genomics technologies to ensure efficient and timely completion of the research program. -Conduct research work on various components of genomics, biotechnology, and molecular, population and conservation genetics research projects as directed by Dr. Om Rajora to facilitate achievement of the research program milestones. -Train students, postdoctoral fellows, research assistants and other researchers in the use of equipment and research technologies. - Develop and implement lab policies in consultation with Dr. Om Rajora. - Procure equipment, consumables and other supplies required for the research program. - Prepare lab reports as requested by the Project Principal Investigator from time to time.

Qualifications - A B.Sc. or M.Sc. degree in molecular biology, genetics, biochemistry or related field or equivalent qualifications, preferably with lab experience in plant molecular biology and genomics. In exceptional cases, people with a Ph.D. degree who wish to further their career by gaining experience as a technician may be considered. - Adequate theoretical background and lab experience in molecular biology, genomics and genetics, preferably in a plant system. Proficiency in common molecular biology techniques, such as DNA/RNA isolation and purification, PCR, RT-PCR, genotyping, cloning, transformation, sequencing, etc. - Excellent English writing, communication, interpersonal, organizational, management and leadership skills, and motivation and dedication to research work. - Ability to

solve complex problems where analysis of situations or data requires an evaluation of intangible variables. - Ability to work in a highly independent and self-directed as well as team-work environment.

Application Please send your application to Prof. Om Rajora via e-mail (Om.Rajora@unb.ca), consisting of a complete CV; letter of application outlining how your qualifications and experience fit the position; statement of research interests; and names, addresses (e-mail and postal) and telephone numbers of at least three referees. Evaluation of the applications will commence on March 31, 2008 and will continue until the position is filled.

Om P. Rajora, Ph.D. Professor and Senior Canada Research Chair in Forest and Conservation Genomics and Biotechnology Faculty of Forestry and Environmental Management P.O. Box 44555, 28 Dineen Drive, University of New Brunswick Fredericton, NB E3B 6C2 Canada

E-mail: Om.Rajora@unb.ca Phone: (506) 458-7477
Fax: (506) 453-3538

orajora@unb.ca

UniAndes Colombia Evolutionary Parasitologist

UNIVERSIDAD DE LOS ANDES

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 Parasitology. Applicants must have a Ph.D. degree, preferably with postdoctoral research and teaching experience. Researchers with experience in Molecular Biology and Tropical Parasitology are especially encouraged to apply.

The successful candidate is expected to teach and 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 December 15, 2008 to:

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

bio@uniandes.edu.co

samadrin@uniandes.edu.co samadrin@uniandes.edu.co

UniAndes Colombia PopulationGenetics

UNIVERSIDAD DE LOS ANDES

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 Population Genetics and Biostatistics. Applicants must have a Ph.D. degree, preferably with postdoctoral research and teaching experience. Researchers with experience in the quantitative analysis of molecular data in the context of evolutionary studies are especially welcome.

The successful candidate is expected to teach introductory and advanced courses in biostatistics, 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 May 2, 2008 to:

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

samadrin@uniandes.edu.co samadrin@uniandes.edu.co

UNottingham FrozenArkProject

Applications are invited for this post in the Institute of Genetics and School of Biology at the University of Nottingham, UK. The successful candidate will be expected to conduct a research programme of international quality, to direct the major initiative in conservation genetics, and to teach within the School of Biology. Direction of the Frozen Ark Project will be the main administrative task, and the person appointed will be spared other such duties within the School and Institute.

Applications will be considered from candidates who

work in the area of genetics and conservation and whose research strengthens existing areas within the Institute and School.

Information about research in the Institute of Genetics is available at: <http://www.nottingham.ac.uk/-genetics> Further information about the School of Biology is available at: <http://www.nottingham.ac.uk/-biology> and about the Frozen Ark at: <http://www.frozenark.org> Salary will be within the professional scale, minimum £51,095 per annum.

Informal enquiries may be addressed to Professor J D Brook, tel: 0115 8230345, Email: David.Brook@nottingham.ac.uk or to Professor Bryan Clarke, tel: 01223 245293, Email: bryan.clarke@nottingham.ac.uk.

For more details and/or to apply on-line please access: <http://jobs.nottingham.ac.uk/JK25526>. If you are unable to apply on-line please contact the Human Resources Department, at the University of Nottingham, tel: 0115 951 3262 or fax: 0115 951 5205. Please quote ref. JK/25526. Closing date: 18 April 2008.

This post is open until filled review of applications from 18 April 2008 onwards.

bryan.clarke@nottingham.ac.uk
bryan.clarke@nottingham.ac.uk

UParis11 EvolBiol

Application Deadline: March 30, 2008

Dear Colleagues,

In 2008, a Professor level position will be available at the University Paris-Sud 11 (Orsay). This position will include research in the Evolution, Genomes and Speciation laboratory at CNRS (Centre National de la Recherche Scientifique) in Gif-sur-Yvette. You can find a description of our main research interests on our laboratory website (<http://www.legs.cnrs-gif.fr/>).

We are looking for a highly motivated colleague that will be interested in contributing to the building of a local Evolution network. An absolute requirement of the position is teaching of and research in Evolution.

The central theme of the teaching will be evolution at Licence (BSc), Master and Doctorate (LMD) level. This will include Population Genetics, Molecular Evolution, Evo-Devo, and Animal Biology. In addition, new teaching units will be developed. In terms of re-

search, the main topics developed will focus on the relationships between genotype and phenotype. More precisely, this relationship will be investigated through the structural and functional plasticity of genomes and their variability within and between species. This includes several non-exclusive domains of investigation such as micro Evo-Devo, Populations Genetics, Epigenetics and Gene networks. The applicant will work in one of these areas using arthropods as biological model(s).

For more information, do not hesitate to contact Pierre CAPY (pierre.capy@legs.cnrs-gif.fr <<mailto:pierre.capy@legs.cnrs-gif.fr>>).

Sincerely, Pierre Capy

pierre.capy@legs.cnrs-gif.fr pierre.capy@legs.cnrs-gif.fr

UPuertoRico AnimalBehaviorPopulationEvolution

The following message is the revised, official version of an earlier post from March 16, 2008.

Position Vacancy in Animal Behavior and/or Population Evolution

The Department of Biology, University of Puerto Rico, Mayagüez (UPRM, www.uprm.edu/biology) invites applications for a Tenure-track Position as Assistant Professor in Animal Behavior and/or Animal Population Evolution to begin August 2008 or until position is filled. A Ph.D. degree is required, post doctoral experience desired. Candidates must demonstrate teaching skills for undergraduate courses in Animal Behavior, Evolution and General Biology and graduate courses in Population Ecology and Behavioral Ecology as well as the ability to design and develop courses in area of specialty. The successful candidate will be expected to develop an active research program along with his/her teaching duties. Research collaboration with other faculty from Agricultural Sciences and Engineering as well as both undergraduate and graduate students is desirable. External funds, when obtained, will allow eligibility for release time and/or additional compensation during the academic year and/or summer. UPRM is a Land-Grant, Sea-Grant, and Space-Grant institution; interaction with faculty and researchers in these fields is encouraged.

Puerto Rico represents a suitable setting to develop research in tropical systems, and the University of Puerto

Rico stimulates collaboration with active faculty and students in a wide range of the Biological Sciences and Biotechnology. Benefits include health insurance, relocation costs (if applicable), and tuition waivers in the UPR system for immediate family members. Knowledge of English and Spanish or a willingness to learn is desirable. Please send Curriculum Vitae, statements of research interests and teaching philosophy, and contact information for three references (by e-mail with hard-copy to follow) by April 14, 2008 to Dr. Lucy Bunkley-Williams, Director, (lwilliams@uprm.edu) Department of Biology, University of Puerto Rico, Mayagüez Campus, P.O. Box 9012, Mayagüez, Puerto Rico 00681-9012. The University of Puerto Rico is an Equal Opportunity Employer.

Approved by the State Elections Commission (#CEE-C-08-025 submitted December 12, 2007). This advertisement is required by the General Rules of the University of Puerto Rico (#6479) (Certification No. 90 Series 2001-02 of the Board of Trustees)

Posted by Nico Franz <http://academic.uprm.edu/~franz/> Antes ahora y siempre COLEGIO University of Puerto Rico at Mayaguez <http://www.uprm.edu>

URochester SummerResearch

Undergraduate Summer Research Fellowships

Summer Research Training Fellowships are available to study the molecular ecology of endosymbiotic bacteria in insects at the University of Rochester. The fellowships will include travel expenses, a stipend, and housing for 8 weeks. The summer research training program will span June to August 2008 (dates are flexible). Interest in one of the following areas; entomology, microbiology, evolution or ecology is required and some experience in PCR is desirable. During the fellowship you will learn the methods involved in identification of insect hosts, screening, molecular typing of endosymbiotic bacteria (genus Wolbachia), and analysis of data relating to variation, global distribution and host associations of these endosymbionts.

More information is available at:

<http://troi.cc.rochester.edu/~wolb/FIBR/education.html> For any additional questions regarding this Summer Training Program contact:

Rachel Edwards at redward2@mail.rochester.edu

mclark11@mail.rochester.edu

mclark11@mail.rochester.edu

WoodsHole ResAssist GenomeEvol

Full-time Research Assistant position - genome evolution of bacterial endosymbionts Marine Biological Lab, Woods Hole, Mass.

The MBL seeks a highly motivated individual to join Jennifer Wernegreen's lab as a full time research assistant beginning this summer (2008). The successful applicant will contribute to our projects exploring mechanisms and outcomes of genome evolution in bacterial endosymbionts. Specific projects examine functional genomics and population dynamics of endosymbionts within ant hosts. In addition, we're using computational approaches to explore genome variation across diverse host-associated bacteria. Our lab is part of the MBL's Josephine Bay Paul Center in Woods Hole, a collaborative research group centering on microbial diversity, molecular evolution, and comparative genomics (<http://jbpc.mbl.edu/>).

Responsibilities: This position is ideal for someone interested in genomics, evolution, bioinformatics, symbiosis, and/or microbiology. Responsibilities will include high throughput sequencing using ABI and pyrosequencing (454) technologies, DNA and RNA extractions, standard and quantitative PCR, in situ hybridization, pulsed field gel electrophoresis, microscopy, assisting with field collection and rearing of ants, and general lab maintenance (ordering, etc.). Opportunities for data analysis will include DNA sequence alignment, phylogenetic analysis, design of PCR and sequencing primers, and extensive use of molecular databases. Experience with any or all of the above is desirable. Please see <http://jbpc.mbl.edu/labs-wernegreen.html> for a description of our projects, and contact Jen Wernegreen (jwernegreen@mbbl.edu) with any questions.

Qualifications: This position requires a B.A., B.S., or M.S. in biology or a related field and prior experience in an active research lab. It is essential that applicants have a genuine drive to perform basic research and prior experience with molecular techniques, ideally in a research setting. We also prefer a working knowledge of UNIX/LINUX operating systems and PERL, and computer programming skills. This position requires excellent written, verbal, and interpersonal skills, exceptional organization skills, attention to detail, a superb

work ethic, and an enthusiastic, determined approach to research. Position level and salary will depend upon education and experience.

To apply: Please prepare the following: (i) a cover letter describing your motivation for applying, prior research experience, and specific experience with the job responsibilities listed above; (ii) your CV; (iii) names and contact information for three references, including at least one supervisor or advisor who can comment on your independent research skills; and (iv) transcript of your undergraduate and (when applicable) graduate course work. Please contact Jen (jwernegreen@mbl.edu) for instructions on how to submit these items.

Applications will be considered until position is filled. However, for full consideration, please apply by April 7.

Jennifer Wernegreen <jwernegreen@mbl.edu>

WoodsHole ResAssist Symbiont Viruses

POSITION: Research Assistant II/III Symbiont Viruses

A full-time Research Assistant II/III position is available in the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution at the Marine Biological Laboratory. This position is part of an evolutionary genomics research program and will involve interconnections among molecular biology, symbiosis, virology, genomics, evolutionary biology, and phylogenetics. Questions can be addressed to sbordenstein@mbl.edu and additional information about the Bordenstein lab can be found at: <http://jbpc.mbl.edu/labs-bordenstein.html> Wolbachia are one of the most common group of intracellular inherited bacteria on the planet and span the spectrum of symbiotic associations from parasitism in arthropods, to mutualism in nematodes, and pathogenesis in humans. The bacteria have gained increasing interest for their potential roles in evolutionary processes of invertebrates, arthropod vector control, and human filarial diseases. Primary research projects will focus on the genome evolution and function of Wolbachia viruses. Responsibilities include molecular biology activities such as purification and enrichment of viruses from insect symbionts, isolation of viral DNA, qPCR, genomic library

construction, DNA sequencing, bioinformatics, and genetic database searching. Skills in some of these duties are required and should be highlighted in the cover letter. Basic Qualifications: Bachelor's or Master's degree and training in Microbiology, Molecular Biology, Evolution, Genetics, or a related field. The exact position will depend upon education and previous experience. Preferred Qualifications: Training in some molecular biology techniques preferred, including cloning and sequencing, virus purification, sequence alignments, phylogenetics, or genomics. Familiarity with computational skills, GenBank, Mac OS, Windows, and Linux/Unix a plus. The successful applicant is expected to have good team skills, but work with a high level of independence under broad supervision. Candidates with interest and experience in Molecular Biology, Virology, Parasitology, Evolution, Genetics, or Comparative Genomics may find this position particularly rewarding. Position is available until a suitable candidate is identified. Candidates outside the New England area are encouraged to apply. The position includes generous benefits and coauthorship on scientific publications. Physical Requirements Able to lift 20 lbs. Apply online at mbl.simplehire.com An Equal Opportunity Employer

Marian Padenski Human Resources Assistant Marine Biological Laboratory 7 MBL St. Woods Hole, MA 02543 phone: 508.289.7422 mpadenski@mbl.edu

Human Resources <humanres@mbl.edu>

WoodsHole Summer AntBacterialSymbiosis

REU- bacterial symbiosis

The Marine Biological Laboratory in Woods Hole, MA invites undergraduates to apply for a summer REU position. The student will explore the evolution and functional significance of an antibacterial symbiosis within the lab of Jen Wernegreen (<<http://jbpc.mbl.edu/labs-wernegreen.html>><http://jbpc.mbl.edu/labs-wernegreen.html>). The 10-week position will include housing at the MBL, travel, and a summer stipend. The position is contingent upon funding from the NSF.

Applications are due March 15. For details of the project and an online application, please see:

< <http://www.mbl.edu/hr/employment.html>

><http://www.mbl.edu/hr/employment.html>

Click Search MBL jobs >> Seasonal/Temporary >> Research Experience for Undergraduates- insect endosymbionts

Please contact Jen Wernegreen (jwernegreen@mbl.edu)

with any questions.

Marian Padenski Human Resources Assistant Marine Biological Laboratory 7 MBL St. Woods Hole, MA 02543 phone: 508.289.7422 mpadenski@mbl.edu

Human Resources <humanres@mbl.edu>

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Alan Forrest <aforrest@rjb.csic.es>

AFLP ABI

Dear EvolDir members,

I have got two questions concerning AFLP analyses on an ABI 3130xl Genetic Analyzer:

1. Currently we do a sephadex purification of the PCR products before running them on the sequencer. ABI doesn't recommend such a purification. Does anyone know if the purification does any difference to the results? Do you gain much weaker signals after purification, do you even lose fragments, or are the peaks better detectable due to less noise?

2. The injection volume we use is 2 μ l multiplexed PCR products, 0.25 μ l ROX and 7.75 μ l Hi-Di formamide, so a total volume of 10 μ l per sample. ABI recommends to use at least 12 μ l, or even 20 μ l, which simply means adding more Hi-Di to the sample. They argue that having a larger volume would prevent loss of fragments due to evaporation. As the signals we detect are rather weak, we wonder what would be best to increase peak size, having a larger volume and/or extending injection time (now 12 seconds). I am very grateful for any ideas how to get better signals...

Thanks a lot in advance!

Simone

Simone Steffen

Institut für Spezielle Botanik und Botanischer Garten
Bentzelweg 9a 55099 Mainz Germany

phone: +49 6131 3922624 fax: +49 6131 3923524 mail:
ssteffen@uni-mainz.de

Antirrhineae leaf samples

Does anyone out there have vouchered leaf material of *Pseudorontium cyathiferum* (syn: *Antirrhinum cyathiferum*)? The 2 ITS and 1 trnL sequences on GenBank give very contrasting placements in a phylogeny of tribe Antirrhineae, and we would like to confirm these with our own sequences, as well as new sequences for extra chloroplast and nuclear markers. Thanks in anticipation. Dr Alan Forrest Real Jardin Botanico de Madrid

Ant preservation in silica gel

Hi, I wonder if anyone has experience in drying/storing ants using silica gel for DNA analysis. Thanks, Alejandro

Alejandro.Nettel-Hernanz@leec.univ-paris13.fr

Applied Biosystems Veritis thermalcycler problems

Dear colleagues,

I have recently purchased the new model of Applied thermalcycler (Veritis), but several programs that used to amplify well in our other thermalcyclers (Eppendorf) simply does not work well (or do not work at all) on the Veritis.

We even realized that at least in one case, the thermalcycler actually does not follow the times specified in the programs (It had to stay 30 minutes at 37 degrees but if continues for a while at that temperature).

A colleague told me that the problems may be related with the faster ramp times capabilities of the Veritis.

Does any of you have similar problems (and solutions)? You may reply to edutars@icb.ufmg.br, and I will send a list of helpful comments.

I would like to have the customers perspective before to contact the Applied technical support.

Thanks Eduardo

– Eduardo Tarazona-Santos Professor Adjunto Instituto de Ciencias Biologicas Universidade Federal de Minas Gerais Telephone: ++55 31 34092572 e-mail: edutars@icb.ufmg.br

apache@mail.icb.ufmg.br

Assignment with triploid fish

Dear EvolDir members,

Currently I do population assignments (9 μ sat) with fish captured in different rivers by sportive fishermen.

I have 8 potential source-populations (nP) composed of pisciculture and wild population strains, but one of them is triploid. Also, among fish captured by fishermen, a small proportion is triploid too. As population assignment with triploid individuals is not possible, I have two problems:

1) to convert my triploid source-population in a diploid one (because that pisciculture also produced diploid fish from the same strain, which could then be found in nature, but it is not possible for me to obtain those 2N fish). To do it, I randomly resampled 2 loci out of the 3 possible loci for each individual and then created 10 populations of diploid fish. Fst between those populations were really low and the population with the smallest Fst was chosen for the assignment analyses. Was it OK to do it?

2) to convert my triploid fish of unknown origin in diploid ones. Should I use the same method?

Thanks a lot in advance!

Isabel

Isabel Thibault, PhD candidate Biology Department Laval University, Quebec Quebec, Canada, G1V 0A6 phone: 418-656-2131 #7862 fax: 418-656-2339 mail: isabel.thibault.2@ulaval.ca

Bottleneck detection

Dear members,

Recently we assessed whether a genetic bottleneck had occurred in Sheko cattle population (currently classified as being endangered) using the BOTTLENECK (Cornuet and Luikart 1996 Genetics 144:2001-2014). However for our paper the reviewer pointed out that this method is unlikely to detect a genetic signal, as only much smaller bottlenecks are likely to show this effect.

Furthermore, this method does not always detect even quite small, recent bottlenecks.

So my question is does any one out there have an idea of a better and much more powerful method than BOTTLENECK that can detect a genetic signal?

Thanking you in advance.

Mwacharo J.M. Doctoral Candidate Tokyo University of Agriculture

mwacharo@gmail.com

CallforEuropean PopGenetics Research Consortia ConGen 2

Call for ConGen European Research Consortia

The ESF Research Networking Programme on “Integrating Population Genetics and Conservation Biology: merging theoretical, experimental and applied approaches” (ConGen) aims at providing a venue for concerted action in the field of conservation genetics combining and integrating theoretical, experimental and applied approaches. The Programme, which runs until November 2009, pursues these objectives by training young scientists through travel, exchange grants and courses, and by organising workshops.

To ensure long-standing collaborative research in the field of conservation genetics beyond November 2009, the Steering Committee (SC) has decided to promote and stimulate the establishment of European Research Consortia that successfully can apply for research funding from different granting organisations like the EU. To this end, the SC has decided to provide funding to organise an initiating discussion meeting between prospective collaborating researchers. ConGen is offering a maximum of 7500 EUR for such a 2-3-day meeting. We expect collaboration between researchers from at least four different European countries. The Call is open for all researchers working within or having affiliations to institutions eligible for support by, or which are part of, agencies that are Member of the ESF. However, some preferences may be given to consortia which include a significant number of, or are chaired by, researchers from ConGen contributing countries (<http://www.congen.biz> or <http://www.esf.org/congen>). The Consortium itself should be novel, inviting participation of scientists / laboratories that so far had only limited cooperation.

Application Procedure

Applications should be submitted online at http://www2.esf.org/asp/form/scmeetings/sc_form.asp?id=82, and should include:

- (i) a clear description of the long-term aims of the consortium and the research questions addressed (1 A4 page),
- (ii) prospects about the possibility of getting further funding in a general way
- (iii) name and affiliation of all participants of the consortium including a short CV providing expertise and five recent relevant publications of each participants
- (iv) the name of the researcher leading the consortium (Chair) responsible for the application
- (v) and a calculation of the costs of the meeting.

After the meeting it is expected that the coordinators of the funded Consortia should write a summary of the discussions of the meeting and outline funding prospects of the Consortium, or alternatively, a sketch for proposal(s) to be submitted to funding agencies.

Deadline

The deadline for submitting applications online is 1 April 2008.

Contact

Professor Kuke Bijlsma (r.bijlsma@rug.nl) Chair of the ConGen Programme

Ms. Céline Seewald (cseewald@esf.org) ESF Administrator

Celine Seewald <cseewald@esf.org>

Canadian basic research threatened

Dear Canadian EvoDir members,

As you may be aware, the conservative government has released the details of its budget as it pertains to scientific research. Following on their closure of the National Science Advisor post, they have decided to funnel large sums to a small number of individuals working in particular applied areas. The implications for basic research are not ambiguous. I refer you to news reports by Science and Nature about the impact of this administration on Canadian science, and I encourage you to inform your colleagues about these recent developments.

<http://sciencenow.sciencemag.org/cgi/content/full/2008/226/1> <http://www.nature.com/nature/journal/v451/n7181/full/451866a.html> Best wishes,

- Ryan Gregory

Dr. T. Ryan Gregory Assistant Professor Department of Integrative Biology University of Guelph 50 Stone Rd. E. Guelph, Ontario N1G 2W1 CANADA

<http://www.genomesize.com/gregorylab/> rgregory@uoguelph.ca rgregory@uoguelph.ca

ChicagoBotanicGarden SummerResearch

National Science Foundation Research Experiences for Undergraduates Plant Biology & Conservation: From Genes to Ecosystems

The Chicago Botanic Garden (CBG) and Northwestern University (NU) collaborate to host a 10-week summer research experience in Plant Biology & Conservation.

Our program exposes interns to a rich research environment in a small, friendly institution (CBG), as well as access to world-class facilities (NU). REU interns experience all aspects of plant biology and conservation research starting with the experimental design, data collection and analysis, through to presenting the results in a symposium at the end of the internship. Interns also participate in field trips, workshops, and lectures. REU interns are paired with CBG and NU scientists to participate in research fields including:

Molecular Ecology Soil Biology & Biogeochemistry
Quantitative Genetics Environmental Horticulture Systematics and Evolution Restoration Ecology

Program Dates: 26th May - 1st August, 2008
Application deadline: Friday March 14, 2008
For more information and application details, visit <http://labs.corpus-callosum.com/cbg/> Nyree Zerega Director of Graduate Program Plant Biology and Conservation Northwestern University Chicago Botanic Garden <http://www.plantbiology.northwestern.edu> nzerega@chicagobotanic.org nzerega@chicagobotanic.org

Course on Genetic software

Hi all:

I am a PhD student working in my thesis about quantitative genetic in aquaculture, actually I am start to full the data base for calculate heritability and genetic correlations. For these reasons I am looking for a practical course about genetic softwares packages (VCE, dfreml, ASREML or other). I appreciate if you can give me some information about some course. Thanks in advance. Regards Rodrigo Badilla

Atte. Rodrigo Badilla. Biologo Marino. Programa de Doctorado en Acuicultura. Laboratorio de Genetica Marina. IUSA, UPGC. Las Palmas, Gran Canaria. España. movil:+34 606237167 www.grupoinvestigacionacuicultura.org rodrigo.badilla@gmail.com

Data for Haldanes rule

Dear all,

I am working on compiling studies / datasets of hybridization that report the results of backcrosses between taxa that show Haldane's rule. I am looking for a specific type of data, but I am still surprised over how few studies I have been able to find so far and suspect that I am missing quite a few studies. If you are aware of any studies fulfilling the below criteria, or if you know of anyone that might know, I would greatly appreciate some help with my quest. Please reply or respond to me directly at: Goran.Arnqvist@ebc.uu.se These are the criteria that need to be fulfilled for useful data sets: 1. Crosses between the two taxa in question should show some degree of Haldane's rule (for fertility, viability or both). 2. All possible reciprocal backcrosses should be reported, such that both types of homogametic F1 hybrids [female hybrids in XY taxa; male hybrids in ZW taxa] are backcrossed to the heterogametic sex of both parental species [males in XY taxa; females in ZW taxa]. This yields four types of backcrosses. 3. The study should then report measures of fertility or viability for offspring of the heterogametic sex [males in XY taxa; females in ZW taxa] from these four types of backcrosses.

I would be very grateful for any pointers that you could provide,

/Göran

Prof. Göran Arnqvist Animal Ecology Department of Ecology and Evolution Evolutionary Biology Cen-

tre University of Uppsala Norbyvägen 18d SE - 752 36 Uppsala Sweden

Email: Goran.Arnqvist@ebc.uu.se Phone: +46-(0)18-471 2645 Cell phone: +46-(0)70-2935032 Fax: +46-(0)18-471 6484 Homepage with PDF downloads and more at: <http://www.ebc.uu.se/-zoeko/GoranA/GA.html> goran.arnqvist@ebc.uu.se

Double AFLP bands

Dear colleagues

I moved some time ago to a new research institute and had to change to the ABI AFLP core kit for performing AFLPs. Rather expensive, but handy as this provides a master mix for PCRs to be mixed just with primers and DNA (R-L, however, is still performed in the classical way).

Shortly, I get most of the time double peaks for all fragments present in the gel. They are 1bp different in size, so they seem to be a result of incomplete addition of the extra nucleotide to the final strand. I found out in Vos (1995) paper that such problems might appear from too low concentration of dNTPs, but as nobody knows how much dNTPs is in the secret ABI kit, this surely isn't very useful for a scientist. I used previously GoldTaq and RedTaq and never had this problem. However, I must mention that I also changed the study organism, so I can't exclude different components in my extractions. Lately I was the only one doing AFLPs in the lab, so unfortunately I can't check if anybody else using this kit has similar problems.

The problem appears in classical AFLPs, but also in its variant MSAP (where two different pairs of restriction enzymes are used separately, i.e., in my case the isoschizomers HpaII and MspI in combination with EcoRI).

Does anybody have any clue what can cause the double pattern?

Thanks a lot Ovidiu

Ovidiu Paun, PhD Molecular Systematics Section, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3DS United Kingdom Tel: 020 8332 5378 Fax: 020 8332 5310 O.Paun@kew.org<<mailto:O.Paun@kew.org>> opaun@networld.at<<mailto:opaun@networld.at>>

Ovidiu Paun <O.Paun@kew.org>

Drosophila Song Equipment

Hi All,

I'm looking for a microphone or a device for recording and amplifying the songs (the insectavox) of *Drosophila*. Does anyone know any information about it? What software should I use to record the songs?

Thank you very much.

Dr Richard Bailey Evolutionary Biology Centre (EBC) Uppsala University, SWEDEN Email: Richard.Bailey[AT]ebc.uu.se Phone: +46 18 471 2662

Gao xiang <gaoxiang.xiao@gmail.com>

ESEB2009 call for symposia

Call for symposia

ESEB-members are invited to propose subjects for symposia during the XII Congress of ESEB. Proposals should include the following:

1. Title
2. A short description of the subject area and motivation why the symposium is of interest to Evolutionary Biology.
3. A tentative list of possible invited speakers.
4. Names and addresses of the organisers including their affiliation and e-mail address.

Symposia proposals should be sent to the following e-mail address no later than May 20, 2008: eseb2009@unito.it Information about the Congress and Turin will be available soon at: <http://www.eseb2009.it> The organizers M. Cristina Lorenzi and Gabriella Sella

The 12th Congress of The European Society for Evolutionary Biology < <http://www.eseb.org> > will be held in Turin, Italy, August 24-29, 2009. The structure of the congress is similar to previous meetings, each day starting with a plenary keynote speaker, followed by parallel symposia. About 25 symposia will be accepted. A symposium will typically consist of two-three invited talks and 8-10 contributed talks. The congress will cover the field of evolutionary biology in a wide sense, but with emphasis on processes and mechanisms of evolutionary phenomena.

lutionary phenomena.

eseb 2009 <eseb2009@unito.it>

Estimating divergence times

Dear EvolDir members,

I'm studying the phylogeography of a sea urchin species by sequencing the entire mitochondrial gene Cyt b. Assignment analysis with BAPS revealed the presence of three sympatric clusters with maximum statistical support ($P=1$). To make some considerations about the origin and spread of the clusters I'd like to estimate the divergence time among the three clusters. I would greatly appreciate if someone could suggest me the way and the software to proceed in this estimation?

Michele Barbieri Ph.D. student Università di Pisa Dipartimento di Biologia Unità di Biologia Marina ed Ecologia Via A. Volta 6, 56126, Pisa - Italy (I) tel: +39 050 2211407 fax: +39 050 2211410 mbarbieri@biologia.unipi.it

Michele Barbieri <mbarbieri@biologia.unipi.it>

Estimating divergence times answers

Dear EvolDir members, I'm studying the phylogeography of a sea urchin species by sequencing the entire mitochondrial gene Cyt b. Assignment analysis with BAPS revealed the presence of three sympatric clusters with maximum statistical support ($P=1$). To make some considerations about the origin and spread of the clusters I'd like to estimate the divergence time among the three clusters. I would greatly appreciate if someone could suggest me the way and the software to proceed in this estimation?

Answers:

- Hi Michele, would suggest MDiv. Please could I have the summary of replies? thanks and good luck, Ute

- use BEAST (rambaut & drummond et al) Mark Schultz Charles Darwin University C/- Arafura Timor Research Facility PO Box 41775 Casuarina NT 0811 Australia Ph: +61 (0)8 8920 9292 Fax: +61 (0)8 8920 9222

- Ciao Michele, ho letto il tuo post su evoldir; io lavoro a ferrara e mi sono (e talvolta ancora) occupato di tempi di divergenza, barcodig e cose del genere; di solito quando faccio datazioni molecolari uso Beast (gli autori sono Drummond e Rambaut beast.bio.ed.ac.uk/Main_Page); altrimenti puoi provare con MrBayes (anche se è più complicato gestire l'output) oppure con multidivtime (del gruppo di Thorne <<http://statgen.ncsu.edu/thorne-multidivtime.html>> o r8s (di Sanderson <http://ginger.ucdavis.edu/r8s/>)) ma usando questi ultimi due approcci devi avere già un albero sensato che rappresenti le relazioni tra le tue sequenze e in generale implementano relaxed clock models (mentre con mrbayes e beast puo mettere l'orologio "strict"). Oppure puoi semplicemente calcolare le distanze tra gruppi con Mega e avere una idea di massima della situazione. Spero di esserti stato utile e se hai bisogno di altre informazioni scrivimi pure. Ciao, Stefano

- Hi Michele, Without knowing much about your data, I'd suggest IMA (by Nielsen and Hey) and/or BEAST (Drummond et al). Are the clusters very different? Just by stochastic processes you could have the appearance of clades while the population is actually panmictic. In my thesis work I used MDIV, which is like IMA but simpler, and BEAST to look at divergences among frogs. see <http://www.biomedcentral.com/1471-2148-7/247/abstract> good luck, Kathryn

Kathryn R. Elmer, Ph.D. Humboldt Postdoctoral Fellow Evolutionary Biology (LS Meyer) Dept. of Biology University of Konstanz D-78457 Konstanz Germany phone: +49 (0) 75 31 88 37 10 (from abroad, no (0)) fax: +49 (0) 75 31 88 30 18 e-mail: kathryn.elmer@uni-konstanz.de website: <http://www.evolutionsbiologie.uni-konstanz.de/~kathryn/> - You really need to have an external marker, like a biogeographic event. MtDNA evolution rates can vary quite a lot and can be very different between relatively closely related lineages. Certainly this is true in insects, which I work in; perhaps you should look into whether urchins might be more consistent. However, I would certainly not assume that a rate obtained for a distant group will apply to yours. Karl
Karl Magnacca
Postdoctoral Researcher Department of Zoology Trinity College, Dublin 2 Ireland

- ciao Michele riguardo alla tua richiesta su evoldir i programmi piu' usati per divergence time siano MrBayes e Beast. mrbayes e' facile da usare, mentre Beast fornisce molte piu' opzione, ma e' piu' difficile da usare. consiglio anche Tracer per analizzare gli output di entrambi i programmi. pero' se i tuoi cluster sono interni alla specie (cioe' stiamo parlando della stessa specie) allora un approccio cladistico e' impossibile perche' ce' orizzontal transfer. In quel caso, a detta di un mio collega che studia divergence time, non ce' niente da fare. inoltre lui sottolinea che avresti cmq bisogno di un grosso numero di sostituzioni nucleotidiche, diciamo un centinaio per ramo, ma dubito che cytb per organismi cosi correlati proti un segnale di questo tipo. quindi non lo sappiamo. ciao e in bocca al lupo.

- Hi Michele, The program r8s (Sanderson, 2002 MBE 19:101; Sanderson, 2003, Bioinformatics 19:301) will allow you to do this based on adding another sequence into your phylogeny for which the divergence time is known. You then constrain the node that the div time is known for (fossil records are the best source of this sort of data) and the remainder of the node ages are calculated for you Good luck -mark chapman

Mark A. Chapman mchapman@plantbio.uga.edu My webpage: <http://markachapman.googlepages.com/>

— / —

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>

Estimating founder population size

Dear EvolDir members

I am attempting to estimate founder population size for a recently introduced population (c. seven years/max 10 generations) of *Anolis* using microsatellite data. Standard estimates of effective population size are likely to be inappropriate in this case since mutation rate cannot be accurately estimated due to the recent nature of the introduction.

I have come across a paper (Rasner et al 2004, Molecular Ecology) that attempts to answer the question using the number of alleles (n) within the most variable locus in the introduced population as an absolute minimum estimate of the founder population size. (Eight generations were assumed to have passed between founding and sampling). The paper then uses simulation to re-sample a specified number of 'founder individuals' from the native population 1000 times and calculates the proportion of times that at least this number (n) of alleles

are captured in the samples. The smallest number of founders consistent with the data was taken to be the number that gave a probability > 0.05 of capturing n observed alleles (Rasner et al 2004).

My questions are

first, does anyone know of a method for estimating founder population size using microsatellite data in such a recently founded population?

second, is there a program in the public domain that can handle a simulation such as that described above? It is presumably relatively easy to write such a program, unfortunately it is not my expertise!

Many thanks for your anticipated help on this problem, Jacqui Eales Doctoral candidate, Bangor University, Wales, UK

bsp030@bangor.ac.uk

European source N-phenacylthiazolium bromide

Dear colleagues,

Would anyone of you know about a European chemical manufacturer that would sell N-phenacylthiazolium bromide (PTB)? To date, I was only able to find this product in N America.

Thank you, and best regards,

Philippe Gaubert.

Philippe Gaubert UR IRD 131 - UMS MNHN 403 Département Milieux et Peuplements Aquatiques Muséum National d'Histoire Naturelle 43, rue Cuvier 75005 Paris FRANCE Tel. (33)1 40 79 31 68 / Fax. (33)1 40 79 37 71 Email: gaubert@mnhn.fr

* Zootaxa website: <http://www.mapress.com/zootaxa/> gaubert@mnhn.fr

EvolApplications journal

Dear fellow evolutionary biologists,

We are pleased to announce the official launch of the

highly anticipated evolution journal, Evolutionary Applications. The journal is currently freely available worldwide at:

< <http://www.evolutionaryapplications.com>
>www.evolutionaryapplications.com

Evolutionary Applications publishes papers that utilize concepts from evolutionary biology to address biological questions of health, social and economic relevance. Papers are expected to employ evolutionary concepts or methods to make contributions to areas such as (but not limited to): agriculture, aquaculture, biomedicine, biotechnology, conservation biology, disease biology, fisheries and wildlife management and invasion biology. Theoretical, empirical, synthesis or perspective papers are welcome.

We look forward to receiving your papers.

Sincerely,

Louis Bernatchez, Editor in Chief Michelle Tseng, Managing Editor

Associate Editors: Troy Day, George Gilchrist, Jessica Hellmann, Carol Lee, Isabelle Olivieri, Craig Primmer, Thomas Smith, Pete Thrall

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Louis Bernatchez

Titulaire de la Chaire de recherche du Canada en Génomique et Conservation des Ressources Aquatiques

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Tél: 418 656-3402 Fax: 418 656-2043 Courriel: Louis.Bernatchez@bio.ulaval.ca Web: <http://www.bio.ulaval.ca/louisbernatchez/>

Louis.Bernatchez@bio.ulaval.ca

Evolutionary Bioinformatics Journal

Dear colleagues

I am pleased to announce that the open-access jour-

nal, Evolutionary Bioinformatics, has been accepted for coverage in several Thomson Scientific databases including Science Citation Index Expanded (SciSearch) and Journal Citation Reports/Science Edition. These databases will be familiar to many readers as sources of information on later citations of earlier articles and related information. The journal also now appears in several Current Contents databases, which are rapid alerting services.

EBO is the official journal of New Zealand's Bioinformatics Institute, which is based at the University of Auckland. The Editor-in-Chief, Dr Mark Pagel, heads a notable Editorial Board. The journal is published by Libertas Academica, and submissions are accepted for the journal on an on-going basis. All articles published are immediately available to all internet users without restriction and articles attract substantial readership.

For further information on EBO, please visit www.la-press.com. Allen Rodrigo Associate Editor, Evolutionary Bioinformatics Director, The Bioinformatics Institute

Allen Rodrigo <a.rodrido@auckland.ac.nz>

Evolution of *Ceratocapnos claviculata*

Dear members of Evoldir.

I am a Ph D student at the University of Giessen and I have just started my research on the range expansion of *Ceratocapnos claviculata* (for details see <http://www.uni-giessen.de/fbr09/landschaft/>). I am searching for vegetation relevés from Great Britain containing the species, because I intend to compare the ecological requirements of the species in the native region (Western Europe) with those in the newly established ranges in Brandenburg (Eastern Germany) and South Sweden.

Furthermore I am going to analyze the genetic diversity of the species within this project. For these genetic analyses I would need freshly collected, dried plant tissues from many sites across the species range. It would be a great help to me if you could collect plant tissue (see attachment for sample instructions) of the species from your region. In case that you can not help me, it would be nice if you could refer me to somebody else who could collect material. Thank you very much in advance!

Kind regards,

Nicole Voss

– Nicole Voß

Professur für Landschaftsökologie und Landschaftsplanung Justus-Liebig-Universität Gießen Heinrich-Buff-Ring 26-32 35392 Gießen

Tel.: +49-(0)641-99-37188 Fax: +49-(0)641-99-37169

E-mail: nicole.voss@umwelt.uni-giessen.de

<http://www.uni-giessen.de/fbr09/landschaft/>

Nicole.Voss@umwelt.uni-giessen.de

GCG seqlab petition

Hi all -

I apologize for my multiple cross-group postings but I feel the importance and urgency of this message warrant it.

As many of you are aware, last summer Accelrys announced that they would be discontinuing support for GCG and SeqLab this upcoming June. That situation dismayed me and others and I wanted to do something about it. I contacted Steven Smith, one of the original authors of SeqLab, and discussed the situation with him. He volunteered to contact Accelrys in an attempt to minimally get SeqLab's license and code released to him. I gave Steve several months to try to persuade the company. Accelrys was not very cooperative. Therefore, I set about creating a petition in an attempt to add some leverage. I've contacted a few of you earlier regarding this initiative and appreciate your support. Anyway, I have created and posted that petition. It's at:

<http://www.petitiononline.com/gcg/petition.html>

And a nicely formatted PDF version is available in my own Web space:

http://bio.fsu.edu/~stevet/Accelrys_petition.pdf

I would very much appreciate you adding your name to this petition, if you agree with our sentiment. Thank you for your time!

Cheers - Steve

Steven M. Thompson stevet@bio.fsu.edu <http://bio.fsu.edu/~stevet/cv.html> FSU SCS / BioInfo 4U

Florida State University School of Computational Science

1st floor DIRAC 150G Tallahassee, Florida 32306-4120

850-644-4490

2538 Winnwood Circle Valdosta, Georgia 31601-7953
229-249-9751

Steve Thompson <stevet@bio.fsu.edu>

Genetic data simulation

Dear all

I'm looking for a simulation software for genetic data that allows:

- input genotypic data - perform random mating simulation for several generations

Easypop doesn't allow to input data file. I'm grateful to all for any help.

Daniele Porretta

Dep. Gen. and Mol. Biol. University of Rome "La Sapienza" Via dei Sardi 70 00185 Italy phone/Fax: +340649917820 email: daniele.porretta@uniroma1.it

Daniele.Porretta@uniroma1.it

Daniele.Porretta@uniroma1.it

Genotype data for graduate students

Hi all,

I am looking for genotype data (microsatellites), with family structure known. I need this just to make simulations for graduate students with pedigree reconstruction software. I need to have at least 8 markers. It doesn't matter species or additional information about it, only genotype data and a known family structure. If you have such data and you are willing to share them, I will appreciate. Thanks in advance
Regards Rodrigo
rodrigo.badilla@gmail.com

Atte. Rodrigo Badilla. Biologo Marino. Programa de Doctorado en Acuicultura. Laboratorio de Genética Marina. IUSA, UPLGC. Las Palmas, Gran Canaria. España. movil:+34 606237167 www.grupoinvestigacionacuicultura.org rodrigo.badilla@gmail.com

HighMolWeight DNA 2

Dear EvolDir I made an error in my previous posting on the extraction of high molecular weight DNA, which has helpfully been corrected by Dr Trina Roberts! Please see message below, and my apologies for any misleading that I have caused yours sincerely Tom Gilbert

Begin forwarded message:

> From: Trina Roberts <trina.roberts@uaf.edu> >
> Hi Dr. Gilbert, > > I might be misinterpreting your (3) below, but... unless I'm > completely wrong, the old Genra PureGene (now 5' ArchivePure) is > not a silica/chaotropic salt method. It uses an SDS/Tris/EDTA/ > Proteinase K digestion, protein precipitation with ammonium acetate, > and alcohol precipitation. It is basically a "salting out" method, > which essentially makes it a modification of the NaCl-based method > reported by Aljanabi and Martinez, if I'm remembering all this > correctly. > > We've had great results from the basic PureGene animal tissue > protocol (on mammals) and an assortment of variations to it that > seem to increase yield, but we're not particularly worried about big > fragments or so I can't say whether we are recovering them (or > shearing them). > > -Trina > > > Trina E. Roberts > Postdoctoral fellow > University of Alaska Museum > University of Alaska Fairbanks > 907 Yukon Drive > Fairbanks, AK 99775-6960 > (907) 474-1195 > trina.roberts@uaf.edu
mtpgilbert@gmail.com

HighMolWeight DNA answers

Hi evolDir

I posted a comment last month asking for opinions on the recovery of high molecular weight DNA from tissues. Thanks very much to all who replied, and in particular Scott McCairns, Eric Parent, Diana Wolf and Tasha Belfiore. There is not much variation in the answers, which is a good sign. The following summary may be of use to readers:

(1) The good old phenol:chloroform method never appears to disappoint. So that is one option. Can be cou-

pled with ethanol or isopropanol precipitation for extra purity. Intriguingly however, the reason I wrote this posting originally is that we were getting a lot of degradation in our samples that were P:C purified. I now speculate that we must just have very crappy tissue, or some nasty nuclease contamination in our buffers.

(2) A second option is the method reported by Aljanabi and Martinez, *Nucleic Acids Research* 25:4692-4693 (1997). Apparently can be of great use on a number of tissues. I have the pdf for anyone who would like it.

(3) Lastly some useful info derived from Qiagen. Qiagen state that their filter based kits (and by inference other people's filter based kits) shear the DNA more than alcohol precipitation and spin methods. They recommend therefore the Gentra puregen kit that they sell. For USA users, these are sold by Fisher under the name Archivepure. As the method is based on a silica solution (as far as I can tell), I suspect one could also use the original protocol published by Boom et al (*Rapid and Simple Method for Purification of Nucleic Acids*, *J Clin Microbiology* 28:495-503 (1990)). Again I have the pdf if anyone wants it.

Well thanks again to the respondents, and good luck to anyone out there after the big fragments.

Tom Gilbert

Dr Tom Gilbert Lektor/Associate Professor Institute for Biology University of Copenhagen Denmark

mtpgilbert@gmail.com

High throughput plant DNA extraction

Please reply to m.stift@bio.gla.ac.uk

Dear members,

For a project estimating outcrossing rates in wild populations of *Arabidopsis lyrata*, we need to do a vast amount of DNA extractions from dried leaves (up to 5000 samples). We used to do our extractions with a FastDNA kit, but for thousands of samples this is still taking too much time (max. 48 on one day).

Is anyone in the community aware of companies that could do this for us? Any other tips would be helpful as well.

Thanks a lot, Marc Stift and Barbara Mable.

Marc Stift Division of Environmental & Evolution-

ary Biology Graham Kerr Building Molecular Ecology Group (Room 314c) Graham Kerr Building University of Glasgow Glasgow G12 8QQ, SCOTLAND Office: +44 (0)141 330 5346 m.stift@bio.gla.ac.uk

Hintelmann Award for Zoological Systematics

10TH R. J. H. HINTELMANN SCIENTIFIC AWARD FOR ZOOLOGICAL SYSTEMATICS

Established by Mrs. Elisabeth Hintelmann in memory of her husband Robert J. H. Hintelmann

For outstanding achievements in zoological systematics, phylogenetics, faunistics or zoogeography the association "Freunde der Zoologischen Staatssammlung M \ddot{A} nchen e.V." has the pleasure to announce the 8th R.J.H. Hintelmann Scientific Award. The prize has the value of Euro 5,000.- and its target group are young post-graduate scientists. The price was awarded annually since the year 2000 (see in the internet: <http://www.zsm.mwn.de/events/wiss-preise.htm>).

This prize is awarded not only in appreciation of the previous scientific performance of the applicant, but the prize-winner will also be given the opportunity to continue his/her research work in coordination with the Zoologische Staatssammlung M \ddot{A} nchen (ZSM). This may be carried out either by visiting the ZSM or by being provided with ZSM materials for work elsewhere. The 10th R.J.H. Hintelmann Scientific Award will be presented in January, 16th, 2009 during a ceremony at the ZSM in Munich, where the prize-winner has to provide a short lecture on his/her research topics.

Nominations may name any young post-graduate scientist with outstanding performance in the fields mentioned above. The pertaining proposal or application should provide an account of the candidate's scientific achievement. In addition, curriculum vitae, list of publications, and selected reprints (not more than five) have to be submitted (please submit in printed as well as digital form, e.g. on CD-Rom). The submitted documents remain with the awarding association.

Candidates may be nominated by any zoologist; self-nomination and repetitive application in several years are also possible. The prize-holder is elected on absolute majority basis by a jury appointed by the executive committee of the "Freunde der Zoologischen Staatssammlung e.V."

Depending on the quality of applications the association reserves the right to withhold the award in any given year.

Please send applications or nominations until July 15th 2008 to the following address:

Freunde der Zoologischen Staatssammlung München
e.V. R. J. H. Hintelmann-Wissenschaftspreis
Münchenhausenstrasse 21 D-81247 München,
Germany

For further information please contact: schoen-
itzer@zsm.mwn.de Munich, February, 2008

jmpadial@yahoo.com

Incomplete lineage sorting and hybridization

Dear all,

Are there any methods that can specifically distinguish between incomplete lineages sorting from introgressive hybridization for sequence data. I'm studying two sister species that are well separated in microsatellites, allozymes, morphology and ecology but share all common haplotypes in one mitochondrial gene and two nuclear introns (that also lack a deep divergence between any haplotypes). MDiv gives maximum likelihood estimates of M (mNe) up to 2 in some populations and because of this divergence time estimates are uncertain (non-zero ends on the posterior probability distributions). Due to the high estimates of M we would like to argue that indeed the sharing of haplotypes is mainly due to introgression. Nevertheless reviewers to the manuscript argue that this still could be due to incomplete lineage sorting and claim that test specifically designed to distinguish between these two scenarios do exist (without mentioning which). I haven't been able to find such a test in the literature so I ask for your help.

Thank you in advance.

Petri Kemppainen, PhD student Tjärnö Marine Biological Laboratory, 45296, Strömstad, Sweden Tel: +46 526 686 83 Fax: +46 526 686 07 Mob: +46 709 360 124

petri.kemppainen@tmbl.gu.se
petri.kemppainen@tmbl.gu.se

Incomplete lineage sorting and hybridization answers

Hi all,

I recently posted a question about incomplete lineage sorting and hybridization and I will here forward all the relevant and excellent answers (thanks a lot!!) I received. I was glad to see that this is a topic that many of you are thinking about.

Original post: Dear all,

Are there any methods that can specifically distinguish between incomplete lineages sorting from introgressive hybridization for sequence data. I'm studying two sister species that are well separated in microsatellites, allozymes, morphology and ecology but share all common haplotypes in one mitochondrial gene and two nuclear introns (that also lack a deep divergence between any haplotypes). MDiv gives maximum likelihood estimates of M (mNe) up to 2 in some populations and because of this divergence time estimates are uncertain (non-zero ends on the posterior probability distributions). Due to the high estimates of M we would like to argue that indeed the sharing of haplotypes is mainly due to introgression. Nevertheless reviewers to the manuscript argue that this still could be due to incomplete lineage sorting and claim that test specifically designed to distinguish between these two scenarios do exist (without mentioning which). I haven't been able to find such a test in the literature so I ask for your help.

Thank you in advance.

Answers:

Dear Petri,

Your reviewer is wrong. The IM and Mdiv packages designed to implement the models described by Nielsen and Wakeley (2001) and by Hey and Nielsen (2004) are specifically designed to address exactly this question. Do you have non-zero tails at both ends of your TDIV distribution? The right tail in your TDIV posterior will always be non-zero for analyses of a single locus data, no matter what your estimate of M is; this is shown in the original Nielsen and Wakeley paper. If you analyzed several of your data sets together using IM instead of

MDIV, this non-zero tail in Tdiv MIGHT go away.

As far as demonstrating introgression rather than lineage sorting, you could use the posterior distribution of M to calculate the probability that it is different from some benchmark. In a paper I published in *Molecular Ecology* (see refs below), I summed under the curve of the posterior distribution to show that I could reject the hypothesis that M was greater than or equal to 1; there is a boundary condition at zero so I couldn't calculate the probability that M was actually different than zero, but I was able to reject panmixia. Depending on the shape of your posterior distribution you MAY be able to reject the hypothesis that M is less than one.

If you look at the IM discussion board: <http://groups.google.com/group/Isolation-with-Migration>, you can find a recent exchange I had with Jody Hey about using this procedure to test demographic hypotheses:

http://groups.google.com/group/Isolation-with-Migration/browse_thread/thread/64dd7f6187960c1f

Hey, J., and R. Nielsen. 2004. Multilocus Methods for Estimating Population Sizes, Migration Rates and Divergence Time, With Applications to the Divergence of *Drosophila pseudoobscura* and *D. persimilis*. *Genetics* 167:747-760.

Nielsen, R., and J. Wakeley. 2001. Distinguishing migration from isolation: a Markov Chain Monte Carlo approach. *Genetics* 158: 885-896.

Smith, C. I., and B. D. Farrell. 2005. Phylogeography of the longhorn cactus beetle *Moneilema appressum* Leconte (Coleoptera: Cerambycidae): Was the differentiation of the Madrean sky-islands driven by Pleistocene climate changes? *Mol Ecol* 14:3049-3065.

(Petris comment: this is what I will first and foremost do for my data! thanks a lot Chris!)

Hi Petri,

There are a couple of recent papers that talk about identifying introgression as inconsistent alleles from particular genes with respect to (most) other genes. They do this using IM or IMA, a program that will estimate divergence times and ancestral population sizes under a coalescent model (which will account for incomplete lineage sorting). The latter also includes a parameter for secondary gene flow following divergence. The logic is that if a set of genes or alleles gives a significantly more recent divergence time estimation than the combined dataset, or the dataset without those alleles, they are likely to have been introduced due to introgression. Jody Hey, who co-authored these programs,

has a google discussion group as well. The papers are below. I'd be interested in any other suggestions you get. Good luck!

Peters et al. 2007. *Evolution* 61(8): 1992-2006
Carling & Brumfield. 2008. *Genetics* 178: 363-377.

Hi Petri,

Check out my paper attached. The method has its problems but might be ok in some situations. Also, you should check out the models of

— / —

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

Insect Microsat Library Development

Dear EvolDir

Has anybody out-sourced the development of (insect) microsatellite primers. Any advice on laboratories that provide this service would be appreciated.

Kind regards,

Michael McLeish South African National Biodiversity Institute Kirstenbosch Research Centre Private Bag X7 Claremont, 7735 Cape Town South Africa Tel: +27-(0)21 799 8860 Fax: +27-(0)21 797 6903

Mcleish@sanbi.org

Insect Microsat Library Development answers

Thanks to those that replied to my query. Nearly half of the responses were from those keen to learn of any helpful replies. Here are the 6 responses that indicated a facility that would undertake microsatellite library development.

1. I've been using the GIS company (<http://www.genetic-id-services.com/index.htm>) to develop li-

baries of microsatellites in 2 bat species and was very happy with the results. This company also developed microsatellites for many species of insects (<http://www.genetic-id-services.com/species.htm>) so it might interest you.

All the best,
Sebastien.

2. Ecogenics are not cheap, but they have always delivered what was

requested: <http://www.ecogenics.ch/>

Best, Christoph

3. I am a graduate student in the Richard Stouthamer lab at the University of California, Riverside. We outsourced microsatellite development to a company called GIS in Chatsworth, California. They are good quality primers and come with a potential library of over 100 markers. I worked with microsatellites (for a fish) from this company before and mapped close to 130 markers on the genome. If you have the money (\$10000 US); it might be worth it.

Good luck,

James

4. We can develop the markers for you if you want here at the GT Genome Center. Let me know if you are interested.

Seifu Seyoum, PhD GT Genome Center Georgia Institute of Technology 130 Ferst Drive Atlanta GA 30332

5. Regarding your inquiry on Evodir, I have very recently approached a Swiss company to get a quotation for developing a microsatellite library for some hoverflies. I'm attaching (reattached) their generalized pricelist FYI, which includes different options depending on how far you would like them to go with primer development and tests of polymorphism. I cannot give you any advice on the quality of their service since I haven't yet decided whether to use them. I would be interested in any other options, so if you don't mind forwarding other replies to me after collating them I would be very grateful!

Best wishes,

Luc

6. I had Ecogenics in Switzerland develop microsatellites for the comma butterfly *Polygonia c-album*. Butterflies are tricky, but they did it without problem. And for much less than it would have cost me to hire someone to (try) to do it!

Cheers

Soren

Thanks again to all that replied. Cheers,

Michael

Michael McLeish South African National Biodiversity Institute Kirstenbosch Research Centre Private Bag X7 Claremont, 7735 Cape Town South Africa Tel: +27-(0)21 799 8860 Fax: +27-(0)21 797 6903

Mcleish@sanbi.org

Inverse PCR

Does anyone have experience with inverse PCR, and would like to share their knowledge? I keep getting stuck at the ligation step, and feel like I've tried everything I can think of to correct the problem. I know it's a notoriously tricky procedure, but I know others have mastered it....

If you have any suggestions please reply off list. Thanks!

Rachel RF88@cornell.edu

– Rachel Vallender, Ph.D. Post-doctoral Associate

Fuller Evolutionary Biology Program Cornell Lab of Ornithology 159 Sapsucker Woods Rd Ithaca, NY 14850 USA

Office: 607.254.1138 Lab: 607. 254.1128 Fax: 607.254.2486 RF88@cornell.edu

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rf88@cornell.edu

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This inaugural conference on infectious disease dynamics will be comprised of keynote presentations by invited speakers supplemented by contributed oral and poster papers together with interactive round tables and mini presentations on the following themes:

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Eddie Holmes Center for Infectious Disease Dynamics, Department of Biology, The Pennsylvania State University, Mueller Laboratory, University Park, PA 16802. USA. Tel: (814) 863 4689 Fax: (814) 865 9131 <http://www.bio.psu.edu/home/> http://www.cidd.psu.edu/people/bio_holmes.html Eddie Holmes <ech15@psu.edu>

Microsporidian Mosquito DNA extraction

Dear members

I'm working with the microsporidian *Vavraia culicis*, in the mosquito host, *Anopheles gambiae* and I would like to know if anyone has a reliable method of extracting DNA from parasite and host together. Likewise, if anyone can recommend a fixed-copy target gene for qPCR for either or both species I would be most appreciative. Any help on this would be great as I'm new to molecular biology! Please contact me at nayna@vyaspatel.co.uk.

Many thanks,

Nayna.

e.harrison06@imperial.ac.uk

e.harrison06@imperial.ac.uk

Molluskan DNA extraction

Dear all

Hello, I am a masters student working on mitochondrial DNA analysis of several gastropod species of the genus *Conus**, in the Faculty of Science of the University of Lisbon. I am e-mailing you to ask for some advice regarding some technical problems I've been facing. My work focuses on the analysis and comparison of mitochondrial and morphological data, in order to understand the correlation between genetic and morphological traits.

Although having successfully amplified DNA fragments

of some of the samples, I continue to face some difficulties in the amplification process. I am aware that molluscan tissues are very difficult to work on, due to its richness in mucopolysaccharides, and have, therefore, tried several DNA extraction kits and the phenol:chloroform:isoamyl alcohol method. To enhance the yield, I tried using liquid nitrogen to grind the tissues (before the enzymatic action) and also tried purifying the samples after the extractions were done but was unsuccessful for most of the samples. I also tried diluting the extractions to 1:10 and 1:100 and, again, the success rate remained minimal. There seems to be some inhibition but so far haven't quite understood what is affecting the PCR.

Up until now, very few samples were amplified and the best extraction and amplification procedures are yet to be defined. The optimal conditions seem to be variable for each specimen.

Do you have any suggestion on the best approach to a case like this?

Thank you in advance! Best regards, Carla Pereira

shortysquab@gmail.com

Molluskan DNA extraction 2

Dear All,

I would like to start by thanking all for the replies so far! It was of great use!

Although I had already tried most of the appointed suggestions, my last resort (and probably the best approach) will be the CTAB extraction method.

Nevertheless, any further information or suggestion will be greatly welcomed!

My best regards, Carla Pereira

shortysquab@gmail.com

NESCent ComparativeMethodsInR

The National Evolutionary Synthesis Center (NESCent) is pleased to announce the launch of www.r-phylo.org, a community resource for people inter-

ested in using and developing phylogenetic comparative methods in R. The wiki currently contains information on analyses and packages available in R and provides step-by-step tutorials for those just getting started. There is also a mailing list, to sign up for it go to <https://stat.ethz.ch/mailman/listinfo/r-sig-phylo>. We strongly encourage new users, experienced users and developers to both use and modify this resource to create a thriving comparative methods in R community.

Samantha Price Postdoctoral Fellow National Evolutionary Synthesis Center (NESCent) 2024 W. Main Street Suite A200 Erwin Mills Building Durham, NC 27705 USA

sprice at nescent dot org sprice at duke dot edu

NESCent programming

Phyloinformatics Summer of Code 2008 http://phyloinformatics.net/-Phyloinformatics_Summer_of_Code_2008 *** Please disseminate this announcement widely to appropriate students at your institution ***

The National Evolutionary Synthesis Center (NESCent: <http://www.nescent.org/>) is participating in 2008 for the second year as a mentoring organization in the Google Summer of Code (<http://code.google.com/soc>). Through this program, Google provides undergraduate, masters, and PhD students with a unique opportunity to obtain hands-on experience writing and extending open-source software under the mentorship of experienced developers from around the world.

Our goal in participating is to train future researchers and developers to not only have awareness and understanding of the value of open-source and collaboratively developed software, but also to gain the programming and remote collaboration skills needed to successfully contribute to such projects. Students will receive a stipend from Google, and may work from their home, or home institution, for the duration of the 3 month program. Students will each have one or more dedicated mentors with expertise in phylogenetic methods and open-source software development.

NESCent is particularly targeting students interested in both evolutionary biology and software development. Project ideas (see URL below) range from visualizing phylogenetic data in R, to development of a Mesquite

module, web-services for phylogenetic data providers or geophylogeny mashups, implementing phyloXML support, navigating databases of networks, topology queries for PhyloCode registries, to phylogenetic tree mining in a MapReduce framework, and more.

The project ideas are flexible and many can be adjusted in scope to match the skills of the student. If the program sounds interesting to you but you are unsure whether you have the necessary skills, please email the mentors at the address below. We will work with you to find a project that fits your interests and skills.

INQUIRIES: Email any questions, including self-proposed project ideas, to phylosoc {at} nescent {dot} org.

TO APPLY: Apply on-line at the Google Summer of Code website (<http://code.google.com/soc/2008>), where you will also find GSoC program rules and eligibility requirements. The 1-week application period for students opens on Monday March 24th and runs through Monday, March 31st, 2008.

Hilmar Lapp and Todd Vision US National Evolutionary Synthesis Center

====URLs: ====2008 NESCent Phyloinformatics Summer of Code: http://phyloinformatics.net/-Phyloinformatics_Summer_of_Code_2008 Eligibility requirements: http://code.google.com/opensource/-gsoc/2008/faqs.html#0.1_eligibility Stipends: http://code.google.com/opensource/-gsoc/2008/-faqs.html#0.1_administrivia

To sign up for quarterly NESCent newsletters: with announcements about upcoming programs at the Center: <http://www.nescent.org/about/contact.php> -

Hilmar Lapp :- Durham, NC :- informatics.nescent.org

Hilmar Lapp <hlapp@nescent.org>

NESCent survey

Dear colleagues,

Together with a consortium of journals and scientific societies in evolutionary biology and related disciplines, NESCent and the MRC are studying attitudes and practices in data sharing among evolutionary biologists. We are inviting all evoldir readers (including students, postdocs, educators and senior researchers) to help in this effort by completing a short survey: [http://](http://datadryad.org/survey/)

datadryad.org/survey/. We estimate that the survey will take less than 20 minutes of your time. Your responses are critical for guiding the design of the next generation of supplemental data archives for evolutionary biology. In addition, the first fifty respondents will be eligible for a drawing for a new 4GB iPod nano. Responses must be received by April 16th, 2008.

We thank you in advance for your participation, and look forward to seeing your responses.

Todd Vision Associate Director for Informatics, U.S. National Evolutionary Synthesis Center (NESCent) <http://www.nescent.org> Jane Greenberg Director, Metadata Research Center (MRC) School of Information and Library Science University of North Carolina at Chapel Hill <http://www.ils.unc.edu/mrc/> tjv@bio.unc.edu tjv@bio.unc.edu

No mtDNA divergence

Dear all,

I have a data set from two sister species of marine gastropods that occur sympatrically throughout the whole distribution range (NE Atlantic). They are well separated in allozymes (Nei's $D=2.5$), mikrosatellites (no abiquities detected among 320 individuals from very distant populations in assignment tests), morphology and ecology. Still no deep divergence in cytochrome b can be found and all common haplotypes are shared between the species. Although extensive mitochondrial introgressions can be common in local populations, only few examples exist where this is the case in the whole distribution range. In addition, the examples I have found are in species that are endemic to restricted geographic areas in contrast to my species that are distributed throughout the whole NE Atlantic.

I therefore call for any additional examples with a lack of mitochondrial divergence in species that are well separated in nuclear DNA and morphology. I am mostly interested in examples where the species also have large distribution ranges.

Thank you in advance,

/Petri

Petri Kemppainen,

PhD student

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Primer dye

Dear members of evoldir,

Currently we are using a Spectrumedix 24-capillary sequencer. In order to increase the dye set we are using, we are looking for more dyes that work on this system. At the moment we are successfully using (increasing emitting wavelength): FAM (abi), VIC (abi), NED (abi), TAMRA, PET (abi), ROX and LIZ (abi)

We are specifically looking for dyes with an emitting wavelength above that of PET and ROX (600nm) but lower than LIZ (unknown, 650?). I would be thankful if you would share any good (or bad) experiences or other information on dyes you are using.

Suggestions welcome to koen.degelas@inbo.be
<mailto:koen.degelas@inbo.be>

Thanks

Koen De Gelas

Research Institute for Nature and Forest (INBO)

Belgium

Koen.DEGELAS@INBO.BE

Koen.DEGELAS@INBO.BE

Program for FStatistics

Dear EvolDir Members,

Does anyone know of a program that can calculate F statistics (eg. Fst) from microsatellite allele frequency data (with or without expected heterozygosity) in the absence of individual genotype data?

Thanks,

Hania

Hania Lada Postgraduate Research Associate School of

Roomate for Evolution Symposia

Hi,

I am a PhD student who planned to attend the 2008 evolution meeting in Minneapolis, Minnesota. I just booked a double dormitory room for June 20th to 23rd since there is no single dormitory room available now. I am wondering if someone want to share. Please email me back by yuguoqin2001@gmail.com if you would like to.

– Guoqin Yu Schaal Lab EEPB program Washington University in St. Louis St. Louis, MO. 63130 <http://www.biology.wustl.edu/faculty/schaal/-website/Homepage.htm> Phone (Lab): 314-935-6815 Cell phone:314-302-3532

yuguoqin2001@gmail.com

Same mitochondrial genome different nuclear genomes

Dear all,

I have just come across a strange phenomenon that I'm finding difficult to explain. I have designed microsatellite primers for an Australian limpet species (genus Siphonaria). COI sequences of all specimens are nearly identical, with <1% sequence divergence and no distinct phylogroups. DNA combind from 3 specimens was used for the enrichment.

With some of these primers, I'm getting good amplification in about 90% of the specimens, and other primers amplify product only in the remaining 10%, with no cross-amplification. It's as though we have two different species here whose microsatellite flanking regions are so different that primers designed for the one species do not anneal to the flanking region of the other. This seems highly unlikely given that there are no obvious morphological differences and no mtDNA differentiation.

Extraction method (CTAB) and DNA concentration (50 ng/ul) are the same for all samples.

Has anyone come across something like this before?

Thanks, Peter Teske Macquarie University Sydney

Dr Peter R. Teske Postdoctoral Researcher Molecular Ecology Lab Dept. of Biological Sciences, E8C Macquarie University Sydney, NSW 2109 Australia Phone: +61 2 9850 9251 Fax: +61 2 9850 8245 E-mail: Peter.Teske@bio.mq.edu.au Website: <http://www.bio.mq.edu.au/molecularecology/people.htm> Publications: http://www.ru.ac.za/academic/departments/botany_research/peter/ Peter.Teske@bio.mq.edu.au

Same mitochondrial genome different nuclear genomes answers

Dear list members,

My query about different nuclear genomes but the same mitochondrial genome in Australian limpets got an overwhelming number of responses, so rather than reply to everyone in person, I've included a list of suggestions below.

The following explanations were suggested: contamination, convergent evolution, mitochondrial capture, highly variable flanking regions (more variable than mtDNA), heteroplasmy, primer annealing sites located on transposable elements present in only a portion of the population (resulting in sequence lengths too large to amplify), and accidental amplification of a parasite.

The explanation that I found most convincing was "mitochondrial capture", where hybridization has resulted in the introgression of mtDNA haplotypes from one species to another. This seems to be quite common in a wide variety of taxa, including mammals, birds and frogs, and it seems very likely that there would be hybridization between local and introduced species in the vicinity of Sydney harbour. There is in fact a recent paper in Molecular Ecology dealing with this that I completely overlooked (because of the bad habit of ignoring most papers that don't deal with marine biology): Good et al. 2008, Ancient hybridization and mitochondrial capture between two species of chipmunks. Mol Ecol 17:1313-1327.

What convinced me was that we're finding this strict segregation in our limpets either the one set of primers

work, or the other. One recent development is that we seem to have found our first non-hybrid specimen it is morphologically slightly different, the same microsat primers work for it than in the 10% of the samples, but at the mitochondrial level it seems to be so different that the COI gene has repeatedly failed to amplify using the Folmer primers. I've now amplified it using some alternative COI primers and am also sequencing some nuclear introns to see if the patterns we're getting from the microsats hold up.

Thanks to everyone for their suggestions, and I hope those of you who told me that they've run into the same problem can now test whether they've got a case of mitochondrial capture in their species. The lesson here seems to be that hybrid zones and places where lots of aliens are likely to have established themselves are better avoided when selecting samples for designing microsat libraries. But it seems that what started off as a bit of a disaster has now turned into an interesting challenge.

Best wishes, Peter

Dr Peter R. Teske Postdoctoral Researcher Molecular Ecology Lab Dept. of Biological Sciences, E8C Macquarie University Sydney, NSW 2109 Australia Phone: +61 2 9850 9251 Fax: +61 2 9850 8245 E-mail: Peter.Teske@bio.mq.edu.au Website: <http://www.bio.mq.edu.au/molecularecology/people.htm> Publications: http://www.ru.ac.za/academic/departments/botany_research/peter/

Scott Williamson

Dear friends and colleagues,

I am saddened to inform you that Scott Williamson passed away last Friday, March 14, 2008. As many of you know, Scott and his family fought a heroic battle against an inoperable brain tumor that was diagnosed about a year ago. He is survived by his wife, Shannon, young daughters Emma and Claire, and parents, Brad and Carol.

A graduate of University of Kansas, Scott was an immensely talented theoretical population geneticist who did his Ph. D. work under Maria Orive. He was a post-doc with me and Rasmus Nielsen from 2003 through 2006, and had started as an assistant professor in our department shortly before his diagnosis. His area of expertise was in using diffusion models for inference of se-

lection and demography in population genetic data. He will be fondly remembered by all who worked with him for his brilliance, humble nature, and kindness of spirit. I feel immensely grateful for the time Scott spent in my group. I learned much from him, and he was an incredibly giving collaborator and scientist. A man of many talents, Scott loved the outdoors, cycling, and population genetics. He was also a devoted husband and wonderful father. We, his friends, will miss him, and the evolutionary genetics community has lost a great mind.

I am also including a beautiful obituary that Scott's sister has written and will appear in the Ithaca Journal tomorrow. The obituary gives details of memorial services which will take place this weekend and of a college fund that has been established for the girls.

Please feel free to forward this email to those who knew Scott.

Carlos D. Bustamante

Obituary for Scott Williamson

This week, we revel in the coming of spring and reflect on the well-lived life of Scott Williamson, 32. Scott had an intense appreciation of the natural world, and he and his wife, Shannon, and their daughters, Emma and Claire, loved to explore nature's woodlands, sea shores, mountains, and prairies. It is with heavy hearts that we pay tribute to Scott who passed away on Friday, March 14 after a courageous battle with glioblastoma.

Scott and his family lived in Trumansburg, NY where he was a rising star in the field of population genetics and an assistant professor at Cornell University. In the last year, Scott's ground-breaking work in evolutionary biology was featured in the New York Times and listed in the "Top 100 Science Stories of 2007" by Discover magazine. Although Scott was an incredibly talented and gifted researcher, he gracefully balanced his career with an intense commitment to family and an appreciation of life's simple pleasures such as walking in the woods, decorating special cakes for his daughters' birthdays, crafting exquisite furniture, making wooden toys, building a backyard play cottage, watching for birds, growing vegetables in his garden, playing in the ocean, listening to bluegrass music, looking for salamanders, canoeing with his family, and baking his special key lime pie. Scott embodied kindness, humor, and humility, and his very presence made everyone around him a better person.

Although Scott cherished the forests, mountains, and glacier-fed lakes of New York, he had a deep love for his native state of Kansas, home to his surviving grandparents J Fred Williamson and Lois Patton; parents,

Brad and Carol Williamson, in-laws Fran and Cheryl Herrick, and sister, Erica Reynolds. Scott spent many of his last days enjoying walks in the prairies, woodlands, and sandstone canyons of Kansas. If Scott were with us today, he would rejoice in the tiny green shoots of Dutchman's breeches, trout lilies, and toothwort peeking out of the blanket of last autumn's leaves and acorns, and look for the five-petaled, white flowers of false rue anemone. These spring wildflowers—aptly named ephemerals—last only through the spring before the foliage of the more dominant oaks, hickories, and sycamores develop into the woodland canopy and hoard the sunlight. The physical world, much like the wildflowers, is only ephemeral. But Scott's influence on our world and our love for him is forever.

In honor of Scott, a visitation with friends and family will be held on Friday, March 21 from 4 p.m. to 6 p.m. at Penwell-Gabel, 14275 Blackbob Road, Olathe, KS (<http://www.penwellgabel.com>). A Tribute to All Things Scott will be held on Saturday, March 22 from 1 p.m. at the Church of the Resurrection, Chapel, 13720 Roe Avenue, Leawood, KS 66224 (<http://www.cor.org>) with a reception to follow. And the First Annual Everybody-Loves-Scott Event will be on Saturday evening at the Prairie Center, 26235 West 135th Street, Olathe KS 66061. The campfire will start at 6 p.m.- dress warm, and bring your binoculars. To honor Scott's wishes that his daughters both be able to fulfill their dreams, a college fund has been established for Emma and Claire

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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>

Softare TreeRot BugFix

Our sincere apologies for the inconvenience, but thanks to additional reports from users, we've identified and fixed some additional bugs in TreeRot version 3 (one of which was inadvertently introduced during that last fix) . If you use the program for determining decay indices (Bremer support) and/or partitioned support, please trash your current version of the program and download it one more time.

Thanks, Mike

<http://people.bu.edu/msoren/TreeRot.html> Michael Sorenson Associate Professor Department of Biology Boston University 5 Cummington St. Boston, MA 02215

(617) 353-6983 FAX: (617) 353-6340

msoren@bu.edu msoren@bu.edu

Software APE

I am pleased to announce that ape's web pages are back on-line with a new URI:

<http://ape.mpl.ird.fr/> All sections have been updated; a new document with the API to ape's C code is now included (see the development section).

Many thanks to Régis Hocdé and Yves Pournin at IRD in Montpellier for technical assistance.

Emmanuel Paradis – Institut de Recherche pour le Développement UR175 CAVIAR France

Emmanuel.Paradis@mpl.ird.fr
manuel.Paradis@mpl.ird.fr

Em-

Software GeoPhyloBuilder bug fix

We wish to announce the release of GeoPhyloBuilder v1.0.2 for ArcGIS 9.2 that creates geophylogenies from input evolutionary trees and associated distribution data. This version fixes the bug that resulted in branches crossing the -180/+180 meridian (line of longitude). It also implements line densification so branches curve when projected into different coordinate systems. Download from http://www.nescent.org/informatics/download.php?software_id=3 We also invite student applications for the following NESCent Google Summer of Code project.

*Freeing Geophylobuilder: Implementing an Internet-Based Java Client (GeoPhyloBuilder-J) *

Geophylobuilder for ArcGIS (https://www.nescent.org/wg_EvoViz/GeoPhyloBuilder) (Kidd and Liu, 2008) creates geophylogenies from input evolutionary trees and associated distribution data. Geophylogenies are spatiotemporally georeferenced phylogenies (Kidd, submitted) although the the same

data structure can also be used to represent reticulate spatiotemporal relationships between any type of geographical entities including, islands, continents, watersheds and areas of endemism. /Geophylobuilder for ArcGIS /was developed in .Net using the ESRI ArcObjects COM library hence an (expensive) software license is required. Two online services already provide services to create geophylogenies, the CIPRIES tree server (<http://www.treebase.org/gettrees/>) and SupraMap (<http://supramap.osu.edu/supramap>). Both these services support the creation of simple geophylogenies in KML format from a tree file and associated tip point. SupraMap is further restricted by requiring data to be in POY4 format with an apomorphy list.

Many Thanks David Kidd and Xianhua Liu

Phyloinformatics Summer of Code 2008
<http://phyloinformatics.net/-Phyloinformatics.Summer.of.Code.2008> *** Please disseminate this announcement widely to appropriate students at your institution ***

The National Evolutionary Synthesis Center (NESCent: <http://www.nescent.org/>) is participating in 2008 for the second year as a mentoring organization in the Google Summer of Code (<http://code.google.com/-soc>). Through this program, Google provides undergraduate, masters, and PhD students with a unique opportunity to obtain hands-on experience writing and extending open-source software under the mentorship of experienced developers from around the world.

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NESCent is particularly targeting students interested in both evolutionary biology and software development. Project ideas (see URL below) range from visualizing phylogenetic data in R, to development of a Mesquite module, web-services for phylogenetic data providers or geophylogeny mashups, implementing phyloXML support, navigating databases of networks, topology queries for PhyloCode registries, to phylogenetic tree mining in a MapReduce framework, and more.

The project ideas are flexible and many can be ad-

justed in scope to match the skills of the student. If the program sounds interesting to you but you are unsure whether you have the necessary skills, please email the mentors at the address below. We will work with you to find a project that fits your interests and skills.

INQUIRIES: Email any questions, including self-proposed project ideas, to `phylosoc@nescent.org`.

TO APPLY: Apply on-line at the Google Summer of Code website (<http://code.google.com/soc/2008>), where you will also find GSoC program rules and eligibility requirements. The 1-week application period for students opens on Monday March 24th and runs through Monday, March 31st, 2008.

Hilmar Lapp and Todd Vision US National Evolutionary Synthesis Center

====URLs: == 08 NESCent Phyloinformatics Summer of Code: http://phyloinformatics.net/-Phyloinformatics_Summer_of_Code_2008 Eligibility requirements:

— / —

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>

Software IDEA

Dear Colleagues,

Version 2.4.2 of IDEA (Interactive Display for Evolutionary Analyses) has now been released (<http://ideanalyses.sourceforge.net/>). IDEA provides a graphic user interface (GUI) to launch some of the most common PAML analyses, and to view and explore the results.

IDEA is a “stand alone” program with features that include: - a GUI to launch PAML’s `codeml` and `baseml`; - integration with PHYLIP for optional tree reconstruction; - analyses run with multiple starting omega values, and automatic merging of results; - likelihood ratio tests of nested models; - a GUI to view and explore results of `codeml` pairwise analyses or of `codeml` analyses using sites models; - a graphic display of the *.rst output file, to visualize selective pressure along a protein-coding gene; - taking advantage of a computer grid, if one is available, to run multiple datasets.

New to this IDEA release: - Mac OS X and 64-bit Linux are supported, in addition to Unix/Linux 32-bit - PAML 4 is supported - increased memory efficiency

Best regards, Joana

Joana C. Silva, Ph.D. Assistant Professor

University of Maryland School of Medicine Institute for Genome Sciences & Dept Microbiology and Immunology 685 W. Baltimore St., HSF-I Rm 130 Baltimore, MD 21201

`jcsilva@som.umaryland.edu`

Ph:410.706.6721

Fax:410.706.6777

Software IDEA update

Dear Colleagues.

An updated version of IDEA (Interactive Display for Evolutionary Analyses), v2.4.3, was released two days ago and should replace the version released two weeks ago. A bug present in the previous version, which prevented the graphic display of the rst file from being seen, has been corrected.

*** If you have downloaded IDEA in the last two weeks, please make sure it is v_2.4.3, available at <http://ideanalyses.sourceforge.net/main.html> ***

Briefly, IDEA is a “stand alone” program with features that include: - a GUI to launch PAML’s `codeml` and `baseml`; - integration with PHYLIP for optional tree reconstruction; - analyses run with multiple starting omega values, and automatic merging of results; - likelihood ratio tests of nested models; - a GUI to view and explore results of `codeml` pairwise analyses or of `codeml` analyses using sites models; - a graphic display of the rst output file, to visualize selective pressure along a protein-coding gene; - taking advantage of a computer grid, if one is available, to run multiple datasets.

Cheers, Joana

Joana C. Silva, Ph.D. Assistant Professor

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jc-

silva@som.umaryland.edu

Software MANTiS

Dear all,

For those interested into comparative genomics in a phylogenetic framework, MANTiS has been recently updated and is available for download at www.mantisdb.org. Among others, we implemented a much better gene information window and a completely new view for over- or under-representation of gene expression anatomical systems.

MANTiS is an application system that: -builds a relational database integrating, in an explicit phylogenetic framework, all Ensembl genes, corresponding PANTHER molecular functions and biological processes, as well as GNF, e-genetics, and HMDEG expression data; -makes extensive use of the Ensembl ortholog/paralog prediction pipeline for identifying gene duplication events; and -implements a dynamical programming approach for the mapping of gene gains, duplications, and losses on the phylogenetic tree.

Through a user-friendly interface, MANTiS allows the user to identify:

1. Gains and losses on specific branches of the tree,
2. Genome content of ancestral nodes,
3. Statistically over- or under-represented molecular functions, biological processes, and gene expression anatomical systems,
- and 4. Tissue specificity of gained, duplicated, and lost genes.

Finally, the entire set of information available in MANTiS can be exploited further using an advanced system of queries by which gene identity, mapping, and function parameters can be combined using logical operators.

The original paper is open-access and available in the journal *Bioinformatics* <http://bioinformatics.oxfordjournals.org/cgi/content/full/24/2/151> as well as on the MANTiS website (www.mantisdb.org).

Reference: MANTiS: a phylogenetic framework for multi-species genome comparisons Tzika A.C., Helaers R., Van de Peer Y. & M.C. Milinkovitch *Bioinformatics* 2008 24(2):151-157

Michel C. Milinkovitch, Laboratory of Evolutionary genetics, Inst. of Molecular Biology & Medicine, Univer-

sité Libre de Bruxelles (ULB), cp 300, Rue Jeener & Brachet, 12, B-6041 Gosselies, Belgium.

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e-mail: mcmilink@ulb.ac.be www.ulb.ac.be/sciences/ueg "Michel C. Milinkovitch" <mcmilink@ulb.ac.be>

Software OrthoMaM Version2

Dear EvolDir members,

We have just released OrthoMaM version 2: a major update of our database of orthologous single-copy nuclear exons for mammalian phylogenetics.

It can be queried from a new dedicated webserver:

<http://www.orthomam.univ-montp2.fr/> The new version 2 is based on the Ensembl release v48 and now includes 23 taxa and 4155 candidate markers.

Major changes from the initial version include:

- Requests on 23 taxa (instead of 12). The 11 new taxa are bushbaby, mouse lemur, tree shrew, Guinea pig, ground squirrel, pika, cat, little brown bat, hedgehog, shrew, and platypus.
- Sequence alignment using a combination of MAFFT and TransAlign - Amino-acid alignments can be visualized and downloaded

We expect the OrthoMaM database to be useful for further resolving the phylogenetic tree of placental mammals at different taxonomic levels and for better understanding the evolutionary dynamics of their genomes.

The PDF describing the database is freely available from BMC Evolutionary Biology:

<http://www.biomedcentral.com/1471-2148/7/241> OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics Vincent Ranwez, Frederic Delsuc, Sylvie Ranwez, Khalid Belkhir, Marie-Ka Tilak and Emmanuel JP Douzery *BMC Evolutionary Biology* 2007, 7:241 (doi:10.1186/1471-2148-7-241)

We hope this will be of use to members of the community.

Frederic Delsuc and co-authors

–

Frédéric DELSUC (Chargé de Recherches CNRS) Laboratoire de Paléontologie, Phylogénie et Paléobiologie - CC064 Institut des Sciences de l'Evolution - UMR5554-

CNRS Université Montpellier II Place Eugène Bataillon 34095 Montpellier Cedex 05 France Tel: (+33) 4 67 14 39 64 FAX: (+33) 4 67 14 36 10 Email: Frederic.Delsuc@univ-montp2.fr Webpage: <http://frederic.delsuc.neuf.fr>

Software PGETtoolbox

Hello all,

PGETtoolbox has recently been updated and the source code is now available for download.

Abstract: "PGETtoolbox is a Matlab-based open-sourced software package for data analysis in population genetics. The main features of this software are as follows: 1) capability for handling both DNA sequence polymorphisms and single nucleotide polymorphisms (SNPs), which include genotype and haplotype data; 2) exhaustive population genetic analyses and neutrality tests based on the coalescent theory; 3) extendibility and scalability for complex and large genome-wide datasets; 4) simple yet effective graphic user interfaces and sophisticated visualization of data and results."

The software can be obtained from:

<http://bioinformatics.org/pgettoolbox> Reference: Cai JJ. PGETtoolbox: A Matlab Toolbox for Population Genetics and Evolution. *J Hered.* 2008 Feb 29; PMID: 18310616

Best regards,

James J. Cai Stanford University Department of Biology Herrin Hall, Petrov Lab, room 352 Stanford, CA 94305 USA

e-mail: jamescai@stanford.edu phone: 1-650-736-2249 fax: 1-650-723-6132

jamescai@stanford.edu jamescai@stanford.edu

SouthAfrica Volunteer MammalBehavior

Volunteer needed as field assistants for the project:

Socio-Evolution of small Mammals in the Succulent Karoo of South Africa

>From April 2008 onwards

Project: We study the reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students with a BSC/Vordiplom or equivalent are preferred as candidates. Applicants must have an interest in working in the field and with animals. Whereas the research is mainly non-invasive, this is no job for extreme animal right persons (we take tissue and blood samples). Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5-6 days a week. Applicants must be able to manage extreme temperatures (below 0 at night, sometimes over 40C during days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

Work of field assistants: Trapping and marking of mice and rats; radio-tracking to determine home ranges and nest sites; direct behavioral observations in the field; experiments and observations with captive specimen under natural weather conditions; maintenance and cleaning of the research station.

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 750 (around 80 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 2000 or 200 Euro/month). Including extras, you should expect costs of about 350 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: Currently we are looking for a volunteer from April 2008. Field assistants are expected to stay at least 2 months, but longer periods of up to

6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@zool.uzh.ch.

More information under www.strippedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin Research Assistant, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

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

visit <http://www.strippedmouse.com> Carsten Schradin <carsten.schradin@zool.uzh.ch>

Understanding how these different understandings of species difference function and to what ends helps us to raise serious questions about one of the least interrogated bases for the domination of both human and non-human animals in Western culture. This edited collection calls for papers across multiple disciplines (biological and social science, political and philosophical theory and practice, as well as imaginative work) to better understand species difference and how it functions in particular fields of inquiry.

Interested authors should provide 200 word abstracts and a 100 word biography to Vincent J. Guihan vguihan@connect.carleton.ca and/or Sinead Collins (s.collins@ed.ac.uk) by April 15, 2008 for consideration.

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

s.collins@ed.ac.uk

SpeciesDifferences Call for papers

CFP: Animal Bodies of Knowledge: Understandings of Species Difference Across Disciplines

Over the twentieth century, a number of key works of cultural theory, social and biological science have effectively exposed and challenged domination on the basis of race, gender, class, age, and national difference, as social and discursive constructs that suit the needs of the political status quo. But what about species differences? For the hundreds of thoughtful essays, books, collections on race, gender, nationality, age and other bases for domination, the academy has been reluctant to raise similar questions about what we presuppose to be the differences, real or imagined, between human and non-human animals. Although the scientific and philosophical discussion of species difference has its roots in ancient Western thought, over the course of the last 150 years or so, this discussion has produced separate bodies of conflicting but also recapitulating knowledge across the sciences, the humanities and in creative/imaginative work. At the same time, different modes of interrogating what it means to be human as opposed to what it means to be an animal have become increasingly estranged from each other, such that thinkers from a given discipline (biology, philosophy, political science) run the risk of ignoring prevalent ideas or important advances in other disciplines.

SSB 3rdWorld Scholarships

SSB is pleased to announce the availability of scholarships for scholars from developing countries to attend workshops and courses in systematics, or to visit a lab engaged in systematic research for training. The emphasis of this program is the transfer of knowledge to the scholar's home country. Therefore, applicants should currently be in their home country or have definite plans to return in the near future. Courses such as the The Summer Institute in Statistical Genetics, Molecular Evolution Workshop at Woods Hole, and Applied Phylogenetics Workshop at Bodega Bay are examples of courses that are appropriate for this funding. This scholarship can also be used to fund a short term visit to a laboratory for training in systematic techniques and analyses. It is the applicants responsibility to arrange lab visits or admission to a class before applying for this fund. Support for attending a course will be contingent on admission to the course through the normal admissions process. This grant does not support travel to conferences and meetings. Requests for support may be in any amount up to \$3,000.

Please see the website (<http://systbio.org/?q=node/25>) for details regarding submission requirements.

Applications should be sent to SSB Award Committee, at ssb_apps_mailbox@cornell.edu.

Application deadline is March 31, 2008

Grant and Fellowship Application Committee Society of Systematic Biologists <http://systbio.org/> ssb_apps-mailbox@cornell.edu ssb_apps-mailbox@cornell.edu

SSB ErnstMayr award competition

Ernst Mayr Award Announcement

The Society of Systematic Biologists announces the award competition for The Ernst Mayr Award given to the presenter of the outstanding student paper in the field of systematics at the annual meetings of the Society of Systematic Biologists. The award consists of \$1000 and a set of available back issues of Systematic Biology.

Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to: <http://systbio.org/?q=node>). Previous Mayr award winners are not eligible.

Applicants should 1) submit their titles for the SSB Meeting in Minneapolis, Minnesota and indicate at the time of submission that their talk is a potential competitor for the SSB Ernst Mayr Award; 2) submit a 400-word abstract of their talk to the SSB awards committee.

Please see the SSB website for more details on submission requirements. <http://systbio.org/?q=node/10> Application deadline is 1 April 2008 (same deadline for title submissions for the conference).

Grant and Fellowship Application Committee Society of Systematic Biologists <http://systbio.org/> ssb_apps-mailbox@cornell.edu ssb_apps-mailbox@cornell.edu

SSB Graduate Student Research Awards

The Society of Systematic Biologists (SSB) announces the 2008 annual Graduate Student Research Award competition. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary

data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbio.org/>). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards will range between \$1,000 and \$2000 and approximately six awards will be made.

Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2008.

For more information, please see the SSB Student Awards (<http://systbio.org/?q=node/22>)

Grant and Fellowship Application Committee Society of Systematic Biologists <http://systbio.org/> ssb_apps-mailbox@cornell.edu ssb_apps-mailbox@cornell.edu

SSB Mini PEET award

SSB Mini PEET award competition:

Society of Systematic Biologists (SSB) is pleased to announce the availability of awards to enhance the transfer of taxonomic expertise, modeled after the PEET program at NSF. Unlike the NSF PEET program, awards will not be limited to taxonomically understudied taxa; the primary purpose of this program is to pass on taxonomic expertise in general. The awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group. This would support the PEET goal of passing on taxonomic expertise before it is lost. Activities can include a trip to the taxonomist's laboratory, or pay for the taxonomist to visit the applicant's laboratory for a period of time. Requests for support may be in any amount up to \$3,000.

A complete application includes a brief description of the project, justification of the importance of the taxon,

an itemized budget, the applicant's CV, and a letter of support from the taxonomic expert. If the applicant is a student or post-doc, please also include a letter of recommendation. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbio.org/?q=node/6>). The narrative part of the application should be no more than two pages long, not including the curriculum vitae and letters of support.

Requests should be sent to the SSB Award Committee, (ssb_apps-mailbox@cornell.edu). E-mail submissions are required, and applicants are encouraged to use pdf format for all documents. In the subject line of the email, please indicate the SSB award category.

Please see the SSB website for details of this award and complete submission requirements (<http://systbio.org/?q=node/26>).

Application deadline is March 31, 2008

SSB Applications <ssb_apps@cornell.edu>

SSE TravelAwards

2008 SSE INTERNATIONAL TRAVEL AWARDS FOR YOUNG SCHOLARS

The Society for the Study of Evolution announces the establishment of travel awards intended to foster communication between evolutionary biologists from different countries, with particular emphasis on young scholars at an early stage of their career.

SSE will sponsor two types of travel awards for young scientists: 1. Travel awards to non-USA/Canada young scientists living outside the USA to support attendance at the annual SSE meeting; 2. Travel awards for young USA/Canada or non-USA/Canada scientists living in the USA or Canada to attend non-SSE evolution meetings outside the country where they study or reside.

Description of the awards: 1. Support of up to \$700 toward travel and living expenses (15 awards total). 2. Registration fees (the award will not cover late registration fees). 3. Membership in SSE including an electronic membership to Evolution for 1 year.

Application guidelines:

1. Applications can be presented by young (<35 years old) scientists at various stages of their professional career. Applicants from North America, Europe, Aus-

tralia or New Zealand should be SSE members. 2. Applicants may apply several times, but if successful, they are not eligible for a second award for a period of 5 years. 3. Applicants cannot apply for other SSE sponsored travel awards in the same year, but they can seek support from other sources. 4. The applicant should submit a CV and a one page cover letter explaining: a. Why the chosen meeting is important for the development of their career. b. How they are going to find additional funds to support their expenses. c. A support letter from their advisor or mentor. 5. Proposals should be submitted to the chair of the SSE International Committee (Dr. Gisella Caccone at adalgisa.caccone@yale.edu) by April 15th 2008. 6. Winners will be notified in early May 2008.

Decision process: 1. Proposals will be evaluated by the chair of the International Committee (Adalgisa Cacccone), the non-North American VP (Stuart West), and a council member chosen by the chair of the International Committee (Axel Meyer). 2. Awards will be presented to the winners at the relevant society's annual meeting. 3. Preference will be given to young scholars presenting a paper or poster on which they are sole or first authors.

For Dr. Dale Clayton clayton@biology.utah.edu Secretary, Society for the Study of Evolution

Carey Madsen careymadsen@bioscience.utah.edu Executive Secretary Department of Biology University of Utah 257 So. 1400 E. Room 308 ASB Salt Lake City, UT 84112-0840

Tel 801-585-1791 Fax 801-581-2174

Carey Madsen <careymadsen@biology.utah.edu>

Too many haplotypes per individual

Dear all,

I am sequencing an intron to arginine kinase in a marine gastropod. Through cloning I have, on several occasions, managed to consequently sequence more than two (but typically not more than 4) haplotypes from one individual (even after re-extraction of template DNA). Immediately I suspected gene duplication but the haplotypes do not differ from each other by more than a few mutations (the sequence is only about 300 bp long) and gene duplications for this gene are not known from other invertebrates. One explanation might be a very recent gene duplication, but could there be other ex-

planations as well?

One additional nuclear intron (calmodulin) does not show this phenomenon.

Thank you in advance, Petri

Petri Kempainen, PhD student Tjärnö Marine Biological Laboratory, 45296, Strömstad, Sweden Tel: +46 526 686 83 Fax: +46 526 686 07 Mob: +46 709 360 124

petri.kempainen@tmbl.gu.se

petri.kempainen@tmbl.gu.se

URochester SummerResFellowships

Undergraduate Summer Research Fellowships

Summer Research Training Fellowships are available to study the molecular evolution of endosymbiotic bacteria in insects at the University of Rochester. The fellowships will include travel expenses, a stipend, and housing for 8 weeks. The summer research training program will span June to August 2008 (dates are flexible). Interest in one of the following areas; entomology, microbiology, evolution or ecology is required and some experience in PCR is desirable. During the fellowship you will learn the methods involved in identification of insect hosts, screening, molecular typing of endosymbiotic bacteria (genus *Wolbachia*), and analysis of data relating to variation, global distribution and host associations of these endosymbionts.

More information is available at:

<http://troi.cc.rochester.edu/~wolb/FIBR/-education.html> For any additional questions regarding this Summer Training Program contact:

Rachel Edwards at redward2@mail.rochester.edu

Michael Clark <mclark11@mail.rochester.edu>

WoodsHole MBL REU AntSymbionts

Attn: students interested in ants, symbiosis, or both.

REU - Ant-bacterial symbiosis

We seek a very motivated undergraduate student to join

us this summer as we explore an ant-bacterial symbiosis. Working within Jennifer Wernegreen's lab at the MBL, the student will contribute to our ongoing evolutionary and functional studies of an obligate mutualism between bacteria and ants of the tribe Camponitini.

This 10-week REU (Research Experience for Undergraduates) position includes housing in Woods Hole, travel, and a summer stipend. The position is contingent upon funding from the NSF.

Project details: The REU student will help us explore how bacterial symbiont densities and gene expression patterns fluctuate within ants, according to the diet quality and nutritional demands experienced by the host. You'll contribute to diverse aspects of this study, by collecting local ant species, maintaining ants in the lab, performing diet experiments, and using molecular approaches (DNA and RNA extractions, quantitative PCR) to measure symbiont densities and gene expression within ant hosts. You'll be involved in data analysis throughout the project and will present a synthesis of results at the end of the summer. Please see <http://jbpc.mbl.edu/labs-wernegreen.html> for more information about system and publications relating to the project.

Qualifications: REU positions are funded by the NSF and are only open to U.S. citizens or permanent residents who are currently enrolled in an undergraduate institution and have not graduated prior to starting the position (sorry, no graduating seniors). Essential qualifications include: attention to detail, exceptional organizational and communication skills, ability to work independently in the field and lab, excellent analytical and laboratory skills, a genuine drive to perform basic research, and enthusiasm for field work under conditions in which mosquitoes, ticks and poison ivy are quite common. Prior research is essential, ideally involving insect maintenance and/or molecular techniques. The project is best suited for a student interested in symbiosis, insect nutritional physiology, evolution and ecology, functional genomics, or related fields.

If interested, please contact Jennifer Wernegreen directly (jwernegreen@mbledu) for details of how to apply. In general, the application is simply a CV, statement of interest, unofficial transcript, and contact info for references.

Applications will be reviewed March 21, 2008.

Jennifer Wernegreen <jwernegreen@mbledu>

YouTube SelfishGeneticElements

Dear EvolDir readers,

as assignments in a course on genetic conflicts, a bunch of enthusiastic master students have produced video material on selfish genetic elements which is made available on Youtube. You can find the videos here:

<http://youtube.com/user/Genesinconflict> There are movies on B-chromosomes, transposable elements, selfish sex chromosomes and meiotic drive.

We hope you will enjoy them! Comments and remarks of any sort are very welcome. You can drop me an email, add comments to the movies on youtube, or even “better”, webcam your remarks to youtube!

All the best, Tom Van Dooren and Ken Kraaijeveld
Institute of Biology Leiden Netherlands

t.j.m.van.dooren@biology.leidenuniv.nl

PostDocs

Bristol StatisticalGenetics Bacteria	85	UCollegeCork ArabidopsisVariation	97
BrownU PlantMolSystematics	85	UGreifswald StemCellBioinformatics	97
ColoradoStateU EvolutionaryGenetics	86	UIDaho PlasmidHostRangeEvolution	98
EmoryU HostParasiteInteractions	86	UKonstanz MolEvolGenomics	98
Harvard ComparativeMethods EvolutionaryAnthropology	87	ULausanne PlantReproductiveEvolution	99
ImperialCollegeLondon SpeciationGenomics	87	ULyon BacterialEndosymbionts	99
Kanagawa Japan PopulationGenetics	88	UManchester YeastBioinformatics	100
LeidenU Bioinformatics ViralRNA	88	UMemphis BioinformaticsComputationalGenomics	101
Lisbon Genomics	88	UNebraska PopulationBiology	102
LosAngeles GeneticHistory	89	UNebraska ViralEvolution	102
MaxPlanckInst Jena MolEvol	89	UNewBrunswick PopulationGenetics	102
Montpellier ModelingPlantPathogens	90	UOregon MetagenomicInformatics	103
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OxfordU StatisticalGenetics	92	UPenn Microbe Evolution	106
Paris 1year PopulationModeling	92	UPierreMarieCurie AntEvol	106
Paris 1year PopulationModelling	93	UWisconsinMadison PlantEvolution TrophicInteractions	106
SanDiegoZooSociety Mammalian Phylogenetics	94	UWyoming EvolutionaryStructuralBioinformatics	107
StonyBrookU DrosophilaEvolutionaryGenetics	95	UWyoming SalmonComparativeGenomics	107
TulaneU EvolutionHawaiianFish	95	Valencia ComparativeGenomics	108
UArizona EvolabilityTheory	95	Vienna Zebrafish EvolutionaryBiol	108
UArizona MulticellularityEvol	96	WilliamMaryCollege Biomath	108
UBritishColumbia ComparativeGenomics	96		
UCaliforniaSantaBarbara Phylogenetics	96		

Bristol StatisticalGenetics Bacteria

A thirty-month position is available immediately to join a Wellcome Trust funded international multidisciplinary collaboration to develop computationally intensive statistical methodology to analyze bacterial evolution.

New sequencing technology allows complete genome sequences to be determined for hundreds or even thousands of bacteria from the same species. The aim of the project is to develop tools to analyze this new data in order to understand how bacteria evolve and to relate genetic variation to important bacterial phenotypes such as drug-resistance and pathogenicity. The project builds on existing software (ClonalFrame and Mauve) and involves both statisticians (Peter Green) and statistical geneticists (Daniel Falush, Xavier Didelot and Aaron Darling) and will involve interacting with various producers of bacterial sequence data including Julian Parkhill at the Sanger Institute.

You will develop statistical tools to (1) characterise the origins of DNA imports and the pattern of DNA exchange in bacteria, and (2) understand the fitness interactions between different adaptations to particular environments. The post would suit either statisticians who wish to move into statistical genetics, or biologists with a strong quantitative aptitude who wish to learn cutting-edge statistical methodology. Advantageous qualifications include: (1) knowledge of MCMC or similar techniques, (2) good programming skills, (3) a good publication record, (4) knowledge or interest in evolutionary genetics.

The statistics group in Bristol is one of the very strongest in the UK. There are currently 17 faculty, 8 postdocs and 25 graduate research students, with interests ranging across core methodology and key application areas. The group is involved in many interdisciplinary collaborations, across the University and outside, and there is much activity in cognate groups including the Centres for Complexity Science and for Multilevel Modelling, the Department of Social Medicine, AI in Engineering, and the Heilbronn Institute.

Contact Daniel Falush (d.falush@ucc.ie) or see <https://www.bris.ac.uk/boris/jobs/ads?ID=71705> for further details:

“Falush, Daniel” <D.Falush@ucc.ie>

BrownU PlantMolSystematics

A post-doctoral research position is available in the Edwards lab in the Ecology and Evolutionary Biology Department at Brown University. We are looking for an enthusiastic botanist with expertise in molecular systematics. The successful candidate will take the lead in ongoing phylogenetic studies of the Portulacineae, an enigmatic group of plants that includes the cacti, the Anacampserotae, the Didiereaceae, and various lineages of old “Portulacaceae”. Molecular labwork will include both ‘traditional’ directed-PCR approaches as well as collection and analysis of EST data from selected taxa. There is also wide-open opportunity and encouragement for additional research into character/ecological evolution in the group. Good bioinformatics skills are not essential but a definite plus. There is guaranteed funding for one year, with negotiable extension. We are aiming for a starting date of summer/fall 2008, but can be very flexible for the right person.

Brown University is located in Providence, RI. Providence has recently been dubbed the “Renaissance City” and is a thriving community. Also home to the Rhode Island School of Design, it has an active and creative arts and music scene. It also houses the Johnson and Wales Culinary Institute, and J&W alumni provide the city with a truly ridiculous number of great restaurants. All in all, Providence is a wonderful place to live.

Please send a CV and names/contact info for three references to erika.edwards@brown.edu . Brown is an equal opportunity employer.

Erika J. Edwards Department of Ecology and Evolutionary Biology Brown University 80 Waterman St Box G-W Providence, RI 02912

office: 401.863.2081 lab: 401.863.6275 fax: 401.863.2166

email: erika_edwards@brown.edu

lab website: http://www.brown.edu/Research/-Edwards_Lab/index.php erika.edwards@brown.edu

ColoradoStateU EvolutionaryGenetics

Postdoc in Evolutionary Genetics at Colorado State University

A postdoctoral position in evolutionary genetics and evolutionary ecology is available in the lab of Dr. Amy Angert at Colorado State University. The successful candidate will use molecular markers to study the effects of gene flow on adaptive divergence between populations and the evolution of geographic range limits. Candidate must have completed his/her Ph.D. or have a scheduled defense date. A strong background in genetics or evolution is required. Experience extracting and amplifying DNA from plant tissue and analyzing microsatellite data is preferred. The successful candidate will be expected to interact with incoming graduate and undergraduate students in a growing lab group.

The Department of Biology at Colorado State University is an interdisciplinary group with a strong and growing group of ecologists and evolutionary biologists. In addition to the Department of Biology in the College of Natural Sciences, CSU has four other colleges dedicated to life science research: Applied Human Sciences, Agricultural Sciences, Veterinary Medicine & Biomedical Sciences, and the Warner College of Natural Resources. In addition, the Centers for Disease Control and Prevention, the United States Department of Agriculture, and the United States Geological Survey have active laboratories in Fort Collins. Fort Collins is a city of approximately 120,000 people located one hour north of Denver at the base of the Rocky Mountains.

To apply, please submit the following materials as a single pdf file: (1) CV, (2) one-page statement of research interests, (3) up to three recent publications, and (4) contact information for three referees to: angert@mail.colostate.edu. Review of applications will begin immediately and continue until the position is filled. The position is available immediately, and start date is negotiable. For more information, please contact me by email at angert@mail.colostate.edu.

--- Amy L. Angert Assistant Professor Department of Biology Colorado State University Fort Collins, CO 80523 Ph: (970) 491-5947 Fx: (970) 491-0649 Email: angert@mail.colostate.edu

Amy.Angert@colostate.edu

EmoryU HostParasiteInteractions

Insect-Pathogen Postdoctoral Position Emory University, Atlanta, GA USA Laboratory of Dr. Nicole Gerardo

There is funding available for one postdoctoral researcher in the laboratory of Dr. Nicole Gerardo. Our lab's focus is on the evolutionary ecology of microbial host-parasite interactions.

We combine molecular genetics, phylogenetics and experimentation to study pathogens associated with diverse insect systems. Our research is centered on understanding how insect hosts adapt to defend against pathogens and how pathogens then adapt to overcome these host defenses. We also study how mutualistic microbes may play a role in defending their hosts against pathogens. Initial projects will focus largely on the interactions of aphids, their bacterial symbionts and microbial pathogens, though there may be opportunities to work on fungus-growing ants and other systems as well. For more information, go to www.biology.emory.edu/research/Gerardo/-Gerardohome.html . The lab is part of Emory's Population Biology, Ecology and Evolution program, which has a strong focus on host-parasite interactions and disease ecology. For more information on the program and the researchers at Emory, go to: www.biomed.emory.edu/PROGRAM_SITES/PBEE/ Candidates should have a background in host-parasite interactions or symbioses, as well as an interest in research combining experimental and molecular approaches to understanding the interaction of insects and their microbial communities. Background in experimental biology of insects and or microbes, molecular ecology, and/or bioinformatics strongly preferred. Postdocs must have strong communication skills and be willing to help with lab maintenance and training of undergraduate students. If interested, please send a CV, along with a brief statement of interests and experiences in the above-mentioned areas, to Nicole Gerardo by May 15, 2008. Candidates must be able to start the position no later than December 2008.

Dr. Nicole Gerardo Emory University Department of Biology nicole.gerardo@emory.edu

Harvard Comparative Methods Evolutionary Anthropology

Postdoctoral Researcher: Comparative Methods in Evolutionary Anthropology

Department of Anthropology (Biological Wing) at Harvard University

A postdoctoral research position is available to assist with projects that use phylogeny-based comparative methods to address questions in evolutionary anthropology. Research activities will potentially include applying phylogenetic methods to cross-species, cross-cultural and linguistics data, developing new databases for comparative studies, and building a website to disseminate comparative databases and methods for evolutionary anthropologists. Specific research topics will be determined based on the interests of the successful candidate.

The research will take place in the Department of Anthropology (Biological Wing) at Harvard University, with an anticipated start date of September 2008. The initial appointment is for one year, with a second year of funding available conditional on satisfactory performance. Salary will be based on previous experience and includes benefits.

The position requires an independent, enthusiastic and innovative researcher with an interest in applying comparative approaches to real-world questions. Competitive individuals will have previous experience in one or more of the following areas: phylogenetic comparative methods, analysis of geographic data, reconstruction of phylogeny, bioinformatics, and programming experience (especially, but not limited to, R). Applicants from diverse fields are invited to apply, including researchers from biological sciences, anthropology, and linguistics.

Please email an application to Charles Nunn (nunn@eva.mpg.de) consisting of a CV, statement of research interests and qualifications, and the names of three people who can be contacted for letters of reference. Evaluation of applicants will begin on March 31 and will continue until the position is filled.

Harvard University is an Affirmative Action/Equal Opportunity Employer.

Charles L. Nunn website: www.eva.mpg.de/primat/-staff/charles_nunn/index.htm mammal parasites:

www.mammalparasites.org phylogeny of sleep: www.bu.edu/phylogeny/index.html Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig, Germany email: nunn@eva.mpg.de tel.: ++49 (0) 341 3550 204 fax: ++49 (0) 341 3550 299

and

Department of Integrative Biology University of California Berkeley, CA USA tel.: ++1 510 643 2579

Effective July 1, 2008:

Department of Anthropology (Biological Wing) Harvard University 11 Divinity Avenue Cambridge MA 02138

nunn@eva.mpg.de nunn@eva.mpg.de

Imperial College London Speciation Genomics

POSTDOC IN SPECIATION GENOMICS AT IMPERIAL COLLEGE LONDON

Department of Life Sciences

Faculty of Natural Sciences

Research Associate

Salary: GBP 24,570 - GBP 31,240 per annum

Imperial College is ranked the fifth best university in the world (Times Higher QS World University Rankings 2007).

This is an exciting opportunity for a Research Associate with an interest in Speciation Genomics. The successful candidate will carry out cutting edge research investigating the mechanisms of ecological speciation in two sympatric palms endemic of Lord Howe Island, Australia (Nature 441:210, 2006), conducting AFLP genome scans, BAC probing, DNA sequences and coalescence analyses.

The successful candidate will have practical experience in population genetics and/or genomics and strong interests in evolutionary biology.

The post is funded for 3 years by the Natural Environment Research Council and will be based at Silwood Park Campus. The successful candidate will work closely with Dr Vincent Savolainen and his research group, in collaboration with Prof Roger Butlin (Univ. of Sheffield) and Dr Bill Baker (Royal Botanic Gardens Kew).

Further details of the research group can be obtained from the research group website: <http://www3.imperial.ac.uk/people/v.savolainen> Application Form, Job Description and Person Specification available at:

<http://www3.imperial.ac.uk/employment/research/ns2008059jt> Completed application forms accompanied by a curriculum vitae and the name and contact details of two referees should be sent to: Diana Anderson, Imperial College, Silwood Park Campus, Buckhurst Road, Ascot, Berkshire, SL5 7PY or by email to d.anderson@imperial.ac.uk

Closing date: 7 April 2008

Valuing diversity and committed to equality of opportunity

Dr Vincent Savolainen Reader in Ecology and Evolutionary Biology Imperial College London, and Royal Botanic Gardens, Kew Silwood Park Campus Buckhurst Road, Ascot, Berkshire, SL5 7PY, UK Tel +44 (0)20 7594 2374 Fax +44 (0)20 7594 2339 Email v.savolainen@imperial.ac.uk or v.savolainen@kew.org Web <http://www3.imperial.ac.uk/people/v.savolainen> 'Think before you print'

v.savolainen@imperial.ac.uk

Kanagawa Japan PopulationGenetics

POSTDOCTORAL POSITION IN POPULATION GENETICS AND GENOME EVOLUTION

A POSTDOCTORAL POSITION is available in the laboratory of Hideki Innan (<http://www.sendou.soken.ac.jp/esb/innan/InnanLab/Index.En.html>) at the Graduate University for Advanced Studies in Japan. The successful candidate will be expected to work on projects in theoretical population genetics and genome data analysis. We are looking for a motivated individual with a strong background in population genetics and/or computational genomics. Some programming experience are required.

The initial appointment is for one year, and an extension will be considered conditional on satisfactory performance. The start date is flexible but the position is available immediately.

To apply, please send me a CV and a brief statement of research interests and background. Applications will

be accepted until the position is filled.

HIDEKI INNAN

Graduate University for Advanced Studies School of Advanced Sciences Kamiyamaguchi 1560-39 Hayama, Kanagawa 240-0193, Japan Phone: +81-46-858-1600 Fax: +81-46-858-1544 E-mail: innan_hideki@soken.ac.jp

innan_hideki@soken.ac.jp

LeidenU Bioinformatics ViralRNA

BIOINFORMATICS POSTDOCTORAL POSITION - VIRUS RNA STRUCTURE RESEARCH

A postdoctoral position is available at the Leiden Institute of Biology, Leiden University, The Netherlands. A motivated candidate will work on theoretical analysis of influenza virus RNA structures. The position is in the framework of EU project funded for 2 years. The candidate is expected to search/predict/study the conserved RNA structures in influenza virus genome, study evolution of found RNA structures and the potential effects of RNA folding on virus replication and adaptation. This bioinformatic research will be performed in very close collaboration with experimental research on RNA structure at the Leiden Institute of Chemistry.

Contact: dr. Alexander P. Gulyaev, Section Theoretical Biology, Leiden Institute of Biology, Leiden University, Kaiserstraat 63, 2311 GP Leiden, The Netherlands. tel. +31 (0)71 5274814 email a.p.gulyaev@biology.leidenuniv.nl

[Patsy Haccou <p.haccou@biology.leidenuniv.nl>](mailto:p.haccou@biology.leidenuniv.nl)

Lisbon Genomics

Would you be so kind to include in the EvolDir website, a job announcement for a 5-Years Post-Doctoral Position in Environmental Genomics, at the Centre for Environmental Biology of Lisbon, Portugal? The announcement may be found at: <http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=8804> Thank you in advance. With kind

regards Claudia Oliveira Centre for Environmental Biology

Centro de Biologia Ambiental <cdambiental@fc.ul.pt>

“Carlos D. Bustamante” <cdb28@cornell.edu>

LosAngeles GeneticHistory

Postdoctoral Fellowship in Genetic History. In conjunction with its Mellon Seminar on Genetics and History (for more information see <http://www.sscnet.ucla.edu/historyandgenetics/>), the Department of History at UCLA offers a postdoctoral fellowship in Genetic History for the academic year 2008-09. We desire a scholar with a disciplinary grounding in history, anthropology, linguistics, archeology, population genetics or biostatistics experienced in the use of genetic data for historical scholarship and interested in interdisciplinary collaboration. Duties will include the co-organization of an interdisciplinary faculty seminar and the teaching of one course. The Fellowship carries a salary of \$45,000 plus benefits, a one time moving allowance of \$1,500, and a \$1,000 research budget. Applications should send a resume, description of two possible course offerings, and three letters of reference by April 15, 2008 to Professor Patrick Geary, Department of History, UCLA, Los Angeles CA 90095-1473. For more information contact Professor Geary at geary@ucla.edu. UCLA is an AA/EOE. All qualified applicants are encouraged to apply, including minorities and women.

On Mar 6, 2008, at 1:28 AM, Soraya de Chadarevian wrote:

> Dear Colleagues >> Please find attached the announcement for the Mellon Foundation > postdoctoral fellowship in Genetic History for 2008/9. Please pass > it on to any of your students who might be interested. We have > posted the announcement an the website of the American Historical > Association. We would be grateful for other suggestions where to > post it. > Many thanks you for your cooperation >> Soraya and Pat >> Soraya de Chadarevian > Professor > UCLA Department of History and > Center for Society and Genetics > Los Angeles, CA >> <Postdoctoral Fellowship in Genetic History.doc>

Carlos D. Bustamante Assistant Professor, Biological Statistics and Computational Biology 101 Biotechnology Building Ithaca, NY 14853 cdb28@cornell.edu office: (607) 255-1640 fax: (607) 255-4698 dept: (607) 255-5488 cell: (607) 280-3233

MaxPlanckInst Jena MolEvol

Molecular/Evolutionary Biologist (PostDoctoral position) at the Max Planck Institute for Chemical Ecology/Department of Entomology

A Postdoctoral position is available in the Department of Entomology (Director: Prof. David G. Heckel) at the Max-Planck-Institute for Chemical Ecology in Jena/Germany (http://www.ice.mpg.de/hec/home/home_en.htm?mp=134). The institute is international in character, with English the daily scientific language. We aim at establishing herbivore model systems of economic importance to study physiological, molecular, evolutionary and genetic adaptations to host plant compounds and insecticides in the field. We are interested in identifying large-scale physiological changes of Lepidopteran larvae exposed to plant secondary metabolites with custom microarrays to identify toxin-induced genes, general detoxification mechanisms and a correlation of plant-derived factors with specific insect counterdefenses (e.g. detoxification, coping with oxidative stress) in several Lepidoptera. Identification and verification of candidate genes by heterologous expression, biochemical characterizations, evolutionary analysis within and between species will be followed by manipulation of these in insects (transformation and RNAi). Candidates should have the following: A PhD in genetics, genomics, biochemistry or a related field. Drive and motivation to solve difficult scientific problems. Good communication/interpersonal skills, good experimental skills and thorough experience in molecular biology or evolutionary biology. A background in the application of bioinformatic methods to genome studies and/or microarray analysis or biochemistry would be a competitive advantage. E-mail inquiries are welcome to Heiko Vogel (hvogel@ice.mpg.de) <<mailto:hvogel@ice.mpg.de>>. Applications (preferably by e-mail) should include cover letter, CV, names and contact info for 2 references, pdf's of two most significant publications or manuscripts. Review will begin February 2008, and will continue until the position is filled.

Dr. Heiko Vogel Max Planck Institute for Chemical Ecology Department of Entomology Hans-Knoell-Strasse 8 D-07745 Jena Germany Phone: (+49) 3641-571512 Fax: (+49) 3641-571502 e-mail: hvogel@ice.mpg.de <<mailto:hvogel@ice.mpg.de>>

Heiko Vogel <hvogel@ice.mpg.de>

Montpellier ModelingPlantPathogens

18-month POSTDOCTORAL POSITION Modelling the demo-genetics of emergent fungal plant pathogen species.

A postdoctoral position is available to work with Virginie Ravigné, Jean Carlier (UMR BGPI - CIRAD, Montpellier, France) and Marie-Laure Loustau (INRA Bordeaux, France) in the context of a project funded by the ANR (French national research agency) Biodiversity programme (Project EMERFUNDIS - Understanding the emergence of fungal plant diseases: a step towards the assessment of global change risks).

Its overall aim is to identify the factors that contribute to the emergence of fungal plant diseases in crop and natural systems and to categorize known pathogens and agro-ecosystems according to their risk of disease emergence under the effects of human-induced global changes such as global warming, increase in pathogen introductions and agro-ecosystem management.

So far, plant theoretical epidemiology has much improved our understanding of spatio-temporal population dynamics processes of disease spread, with much effort in linking theory and empirical data. Theoretical tools for understanding the factors that drive plant disease emergence are far less developed. It is now obvious that the adaptive potential of pathogens is a major determinant in disease outbreaks and is influenced by factors such as propagule introduction rate, inoculum size, and population genetics. The post-doctoral researcher will thus develop a simulation tool to model the population dynamics and genetics of fungal pathogens clearly integrating into the simplest framework, key-characteristics of diseases (e.g., mating system) and ecosystem properties (e.g., hosts distribution and variability). He/She will then conduct a sensitivity analysis to look for matches between putative successful pathogen strategies and candidate vulnerable agro-ecosystems. He/She will also be able to participate in the building and analysis of a large database gathering relevant information about all pathogens known to cause emergent fungal plant diseases.

The theoretical approach developed by the postdoc is central to the ANR Biodiversity Project EMER-

FUNDIS that gathers 8 French teams working in the field of phytopathology. The post-doc will thus be part of a dynamic network of researchers with numerous opportunities to establish collaborations.

Requirements for the position include (1) a proven record of research; (2) a PhD in biology, mathematics, statistics, or related area; (3) excellent skills in scientific programming (C/C++, or Delphi). The ideal candidate should be well acquainted with demo-genetics simulations.

Applications are welcome from candidates in any country. Screening of applicants will begin March 6, 2008. Starting date: April, 2008. Highly motivated applicants are encouraged to email a statement of research interests, CV, and contact details for three references to Jean Carlier (Jean.Carlier@cirad.fr).

Virginie Ravigné Chercheuse CIRAD

Département BIOS UMR Biologie et Génétique des Interactions Plantes-Parasites TA A 54 / K - Campus International de Baillarguet - Bureau 114 34398 Montpellier Cedex 5 France Tel : + 33 4 99 62 48 10 Fax : + 33 4 99 62 48 48 Mail : Virginie.Ravigne@cirad.fr

Virginie Ravigné <Virginie.Ravigne@cirad.fr>

NetherlandsInstEcol BirdPopulations

The Netherlands Institute of Ecology (NIOO) is a top research institute of the Royal Netherlands Academy of Arts and Sciences (KNAW). NIOO- KNAW focuses on excellent fundamental, strategic research into individual organisms, populations, ecological communities and ecosystems. More than 240 staff are employed at three centres as well as the head office. The Centre for Limnology (CL) in Nieuwersluis focuses its research on freshwater ecology. The Centre for Marine and Estuarine Ecology (CEME) in Yerseke deals with ecosystems in brackish and salt water and emphasis at the Centre for Terrestrial Ecology (CTE) in Heteren is put on land-based ecology.

The Vogeltrekstation ??? Centre for Avian Migration and Demography is part of the Netherlands Institute of Ecology (NIOO), and jointly led by NIOO, SOVON Dutch Centre for Field ornithology and the Ringers Association. Vogeltrekstation (VT), founded in 1911, coordinates all ringing activities of wild birds

in the Netherlands by issuing permits and metal bird-rings to individual ringers (both volunteer and professional), by processing and storing all ringing and recovery data and by running a number of standardized ringing projects. The extensive databank allows detailed analyses of birds' survival rates, breeding success and movements. VT stimulates the use of ringing data by initializing collaborations with research institutes and universities as well as conducting her own research.

The Vogeltrekstation and NIOO are looking for a POST-DOCTORAL RESEARCHER (m/f) Vacancy number CTE-VT-08408

Project description Animal movement, i.e. migration and dispersal, is an important process both from an evolutionary ecological point of view as well as in more applied approaches. The analysis of ringing data of individual birds is a potentially powerful tool to address questions about the rate of dispersal and the distribution of animals at different times of the year. However, the distribution of observed recoveries is strongly affected by the spatio-temporal distribution of observers. One way to correct for this bias is to build State space models that combine ring recoveries with ringing totals and an index of relative abundance from census data, or with data on the distribution of suitable habitat. Another way is to use multistate mark recovery models (in particular M-surge), using separate stages for breeding and wintering.

We are looking for a Post-doctoral researcher who will address the question dealing with bias due to observer distribution in the analysis of ringing data (CTE-VT-08408) using and developing further the approaches described above or similar methods. At NIOO the natal dispersal and seasonal migration will be analysed using extensive data on white stork, little owl, barn owl as well as a suite of other species. The project is funded by the Royal Netherlands Academy of Sciences. Requirements

We are looking for a highly motivated, enthusiastic and creative person with a PhD in biology, and an excellent publication record. Experience with capture-recapture theory and multi-state capture-recapture / recovery analyses and fluency in English are prerequisites. Experience with Geo Information Systems (GIS) is a bonus.

Appointment This position involves a temporary appointment for a period of 2 years.

Salary Depending on training and work experience, the maximum gross monthly salary coming with a full-time appointment will amount to ??? 3678,00 scale

10, Collective Agreement for Dutch Universities (CAO-Nederlandse Universiteiten), excluding 8% holiday pay and a year-end bonus. We offer an extensive package of fringe benefits.

Location The work location will be at NIOO-CTE, Heteren, the Netherlands.

Information Additional information about vacancy is available upon request from Dr. H.P. van der Jeugd (tel. 026-4791233, e-mail: h.vanderjeugd@nioo.knaw.nl) or Prof. Dr. A. van Noordwijk (tel. 026-4791258, e-mail: a.vannoordwijk@nioo.knaw.nl). Information on the Netherlands Institute of Ecology (NIOO), can be found at <http://www.nioo.knaw.nl> Applications Please send your application before 10 april 2008 including complete curriculum vitae, referees and the vacancy number to Prof. Dr J.A. van Veen, Centre Director CTE, NIOO-Centre for Terrestrial Ecology, P.O. Box 40, 6666 ZG Heteren, The Netherlands or by e-mail g.giesen@nioo.knaw.nl

“Jeugd, Henk van der”
<H.vanderJeugd@nioo.knaw.nl>

NorwegianU FungalMolecularEvolution

A three year postdoctoral position in molecular ecology is available at the Norwegian University of Life Sciences (UMB).

Project title: Endophytic fungi in boreal forest bryophytes

Project description: We seek a candidate for a three year full time postdoctoral position in a project focusing on biodiversity of endophytic fungi and their functional role in boreal forest bryophytes. A main aspect is to analyze the diversity and composition of fungal endophytes in boreal mosses using molecular techniques. The project integrates molecular, chemical, mycological and ecological competences, and is based on collaboration between three universities, i.e. the Norwegian University of Life Sciences, the University of Oslo, and the University of British Columbia.

For more information about the position go to: <http://www.jobbnorge.no/visstilling2.aspx?stillid=-46630&lang=EN> havard.kauserud@bio.uio.no
havard.kauserud@bio.uio.no

OxfordU StatisticalGenetics

UNIVERSITY OF OXFORD

WELLCOME TRUST CENTRE FOR HUMAN GENETICS

5 x Post Doctoral Research Scientists in Statistical Genetics GRADE 8: SALARY £33,779 - £40,335 or depending on qualifications and experience GRADE 7: £26,666 - £32,796 with an appropriate change of duties

An exciting opportunity has arisen for 5 post doctoral scientists in statistical genetics to work on one of two cutting-edge projects in human genetics.

Genome-wide association studies (GWAS) have revolutionised our understanding of the genetics of common human diseases. The Wellcome Trust Case Control Consortium (WTCCC), chaired by Professor Peter Donnelly, was the largest of the first generation of these studies. Together with subsequent collaborations and follow-up, it has led to the discovery of over 50 genetic variants associated with common diseases. Science picked this field as its "Research Breakthrough" of 2007, and the WTCCC study won several awards: from The Lancet (Research Paper of the Year); Scientific American (Research Leader of the Year); The American Heart Association (Top Research Advance of the Year); and was one of Nature's "Editor's Picks" for 2007.

Posts 1 and 2 relate to the second phase of the WTCCC, a major extension of the original study, which includes association studies for copy number variation in eight diseases, and resequencing and fine-mapping of associated loci across 13 diseases. The postholders will work in a collaboration between the Donnelly, Holmes, McVean, Marchini, and Myers groups. Posts 3-5 relate to a major new consortium funded by the Wellcome Trust for GWAS for 15 diseases. They will be based in the Donnelly group, which will take primary responsibility for methods development and analysis for these new studies, with extensive collaborations with the groups above.

The postholders will gain a unique insight and experience in the design and analysis of GWAS and high-throughput genetic epidemiological studies. Alongside the scientific investigation the postholders will be given the opportunity and encouragement to follow indepen-

dent research lines and methods development, with support from the PIs, in the context of statistical genetics.

Genetics is one of the most exciting and challenging application areas in modern statistics. These posts present a good opportunity for statisticians interested in moving into this field, as well researchers already working in statistical genetics and related areas. The Wellcome Trust Centre for Human Genetics is at the forefront of this field, and the successful applicants would join perhaps the leading international research grouping in the area, with a focus both on the development of new methods and their application. All the posts will allow considerable individual involvement and responsibility for the research undertaken.

Candidates should have a strong background in modern statistics and its application. An existing background in the application of statistics in genetics would be an advantage, but candidates wishing to move into the genetics field are also encouraged to apply. Good computational skills are essential, and for several of the posts candidates should be able to program in a low level language such as C or C++. Candidates should have a doctorate or equivalent experience in quantitative genetics, statistics, or a closely related discipline. Posts 1 and 2 are available for 2-3 years and posts 3-5 for 3 years in the first instance. All posts are funded by the Wellcome Trust.

A detailed job description quoting reference H5-08-18-PD is available from the Personnel Administrator, (email: personnel@well.ox.ac.uk, tel: +44 1865 287508 or from our web page www.well.ox.ac.uk/vacancies). Applications, in the form of a full and detailed CV together with the names and addresses of two referees, should be sent to the Personnel Administrator at the Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford, OX3 7BN, or by email to personnel@well.ox.ac.uk, or fax to +44 1865 287516. Please quote the reference number on your application. The closing date for applications is March 7, 2008.

donnelly@stats.ox.ac.uk donnelly@stats.ox.ac.uk

Paris 1year PopulationModeling

Physiologically structured population models for viability analysis One Post-doctoral position 2008-2009 available at the Ecology-Evolution Laboratory (CNRS, UMR 7625) at the Ecole Normale Supérieure (CERES-ERTI) in Paris.

Applications are invited for a one-year postdoctoral position funded by R2DS (<http://www.r2ds.centre-cired.fr/>) to investigate the dynamics of small populations with plastic life histories using physiologically structured populations models.

Population persistence is notably conditioned by the degree of individual variation in reproductive success, which depends on variation in any part of the life cycle. Yet, the majority of studies that examined population extinction have tended to ignore life history variation and plasticity. Here, we wish to use life history models to inform the dynamics of small populations and ask how plasticity in life history traits influences extinction dynamics. Many aspects of life history can interact with population dynamics and the project concentrates on three of them, namely growth, maturation and survival.

The post-doc will explore this issue by developing models that account for variation in life history traits using the theory of physiologically structured populations (PSP). This theory takes into account that physiological development (e.g. growth, maturation) depends on the current state of the environment (e.g., temperature, food and predator densities). In turn, the influence of the population on the environment closes a feedback loop between environment, population and life history. The theory of PSP models is thus particularly well-suited to study the interaction between population dynamics and plastic life history. Small populations are subject to stochastic fluctuation in abundance. The project aims to study the feedback of this variability on life history and the consequences for extinction dynamics. The models will be parameterized with estimates from field and experimental studies undertaken with the common lizard, a species with strong thermal and food plasticity in life history traits.

The post-doc will be based at the Ecology-Evolution Laboratory (CNRS, UMR 7625) at the Ecole Normale Supérieure (CERES-ERTI) in Paris, where the applicant will work with David Claessen and Jean-François Le Galliard. This post-doc project is part of a research network on the dynamics of small populations funded by ANR from 2008 to 2012 and will therefore interact with a larger group of researchers. The post can start on September 1st or October 1st 2008 and will run for one year with a possible one year extension by applying to extended funding from the R2DS network in spring 2009. Gross salary will be 2500 per month. The starting date can be postponed in exceptional circumstances.

References: Claessen, D. (2005). Alternative life-history pathways and the elasticity of stochastic matrix

models. *American Naturalist* 165: E27-E35. Le Galliard, J.-F., Fitze, P. S., Ferrière, R. and J. Clobert. 2005. Sex ratio bias, male aggression, and population collapse in lizards. *Proceedings of the National Academy of Sciences USA* 102(50):18231-18236. Claessen, D; Van Oss, C; de Roos, AM; Persson, L. 2002. The impact of size-dependent predation on population dynamics and individual life history. *Ecology* 83 (6): 1660-1675.

Candidate profile There are no nationality restrictions and the successful candidate will: (1) Possess a doctoral degree in ecology and/or mathematics, dating no more than 2 years before 1 October 2008, though the last condition may be negotiated in exceptional circumstances. (2) Not have worked in the hosting lab, nor have prepared his thesis within the hosting lab, except for a return after a period of absence of at least one year. (3) Have strong competence in modeling, with an interest in population dynamics, viability analyses and conservation biology and knowledge of C programming or closely related languages. (4) Have personal qualities needed for group work and inter-disciplinary study.

Contact Application: Chantal Cuisinier, tel.: +33 1 44 27 36 89, email: Chantal.Cuisinier@snv.jussieu.fr, postal address is CNRS UMR 7625, Université Paris 6, 7 Quai St Bernard, 75005 Paris Research project: David Claessen, tel.: +33 1 44 32 27 21, email: david.claessen@ens.fr

How to apply 1 Applicants have until April 30 2008 to send a completed application form available at <http://jf.legalliard.free.fr/> to the Application contact point. 2 The lab director and a local jury will select one candidate from the application forms and contact the candidates from May 31 2008. 3 The regional office of the CNRS will be responsible for drawing up the contract.

galliard@biologie.ens.fr galliard@biologie.ens.fr

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lations with plastic life histories using physiologically structured populations models.

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The post-doc will explore this issue by developing models that account for variation in life history traits using the theory of physiologically structured populations (PSP). This theory takes into account that physiological development (e.g. growth, maturation) depends on the current state of the environment (e.g., temperature, food and predator densities). In turn, the influence of the population on the environment closes a feedback loop between environment, population and life history. The theory of PSP models is thus particularly well-suited to study the interaction between population dynamics and plastic life history. Small populations are subject to stochastic fluctuation in abundance. The project aims to study the feedback of this variability on life history and the consequences for extinction dynamics. The models will be parameterized with estimates from field and experimental studies undertaken with the common lizard, a species with strong thermal and food plasticity in life history traits.

The post-doc will be based at the Ecology-Evolution Laboratory (CNRS, UMR 7625) at the Ecole Normale Supérieure (CERES-ERTI) in Paris, where the applicant will work with David Claessen and Jean-François Galliard. This post-doc project is part of a research network on the dynamics of small populations funded by ANR from 2008 to 2012 and will therefore interact with a larger group of researchers. The post can start on September 1st or October 1st 2008 and will run for one year with a possible one year extension by applying to extended funding from the R2DS network in spring 2009. Gross salary will be 2500 per month. The starting date can be postponed in exceptional circumstances.

References: Claessen, D. (2005). Alternative life-history pathways and the elasticity of stochastic matrix models. *American Naturalist* 165: E27-E35. Le Galliard, J.-F., Fitze, P. S., Ferrière, R. and J. Clobert. 2005. Sex ratio bias, male aggression, and popu-

lation collapse in lizards. *Proceedings of the National Academy of Sciences USA* 102(50):18231-18236. Claessen, D; Van Oss, C; de Roos, AM; Persson, L. 2002. The impact of size-dependent predation on population dynamics and individual life history. *Ecology* 83 (6): 1660-1675.

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Contact Application: Chantal Cuisinier, tel.: +33 1 44 27 36 89, email: Chantal.Cuisinier@snv.jussieu.fr, postal address is CNRS UMR 7625, Université Paris 6, 7 Quai St Bernard, 75005 Paris Research project: David Claessen, tel.: +33 1 44 32 27 21, email: david.claessen@ens.fr

How to apply 1 Applicants have until April 30 2008 to send a completed application form available at <http://jf.legalliard.free.fr/> to the Application contact point. 2 The lab director and a local jury will select one candidate from the application forms and contact the candidates from May 31 2008. 3 The regional office of the CNRS will be responsible for drawing up the contract.

galliard <galliard@biologie.ens.fr>

SanDiegoZooSociety Mammalian Phylogenetics

A postdoctoral position funded by a collaborative NSF research award under the Assembling the Tree of Life competition is immediately available. Conserved primer sequences will be used to generate large data sets of orthologous sequences from diverse mammalian taxa to combine with morphological data for assembling a comprehensive mammalian phylogeny. A Ph.D. is required. Extensive experience in generating DNA sequence data and phylogenetic analysis of aligned data sets is highly desirable. This position is multi-year. For

further information and application procedures, please see: <http://www.sandiegozoo.org/jobs/index.html>

oryder@ucsd.edu oryder@ucsd.edu

StonyBrookU DrosophilaEvolutionaryGenetics

Post-Doc Opportunity in Drosophila Evolutionary Genetics

A Post-doctoral research associate position is anticipated to become available working in NIH-funded research in the laboratory of Dr. John R. True, Dept. of Ecology and Evolution, Stony Brook University. The successful candidate will be involved in molecular marker assisted quantitative trait locus mapping of morphological and behavioral trait differences between Drosophila species. A Ph.D. in a biological field as well as experience in Drosophila molecular genetics and quantitative genetics are required. Experience in Drosophila cytogenetics and developmental genetics are preferred. Duration: two years Salary: \$35,000-40,000/yr

Interested applicants please send c.v. and the names and contact information of two references to: Evolutionary Genetics post-doc c/o Donna DiGiovanni ddigiovanni@notes.cc.sunysb.edu Dept. of Ecology and Evolution Stony Brook University 650 Life Sciences Bldg. Stony Brook, NY 11794-5245

jrtrue@life.bio.sunysb.edu

TulaneU EvolutionHawaiianFish

A postdoctoral 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 of amphidromous fishes across the Hawaiian archipelago emphasizing comparison of genetic assays

of dispersal with estimates based on otolith microchemistry. The incumbent will be encouraged to develop and pursue additional research areas that complement these set objectives.

Preference will be given to candidates experienced with carrying out field based studies of freshwater fishes and laboratory studies involving modern molecular techniques. An initial appointment will be for one year, with continuation for up to two additional years dependent upon performance. A start date of June 2008 or a mutually agreeable date early in Summer 2008 is strongly preferred. Salary will be commensurate with experience and qualifications. REQUIREMENTS: Ph.D. in ecology, genetics, or closely related field. 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/ADA Employer. Women and minorities are encouraged to apply.

mjblum@tulane.edu mjblum@tulane.edu

UArizona EvolabilityTheory

A postdoc position is 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. Funding is not tied to a specific project, but applications and enquiries that do not demonstrate substantial familiarity with our work will not receive a reply. Ph.D. with strong quantitative background and computational and/or modeling experience is required. A background in evolutionary theory is strongly preferred. Funding is secured and the position is renewable over multiple years, with a start date in mid-2008. Contact Joanna Masel at masel@u.arizona.edu for more information and to apply.

masel@U.Arizona.EDU masel@U.Arizona.EDU

UArizona MulticellularityEvol

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Richard E. Michod (<http://www.eebweb.arizona.edu/Michod/>) in the Department of Ecology and Evolutionary Biology at the University of Arizona (Tucson, AZ; <http://www.eebweb.arizona.edu/>). We are looking for a motivated, enthusiastic and independent individual with a strong background in evolutionary biology and/or genomics and/or molecular biology to address questions concerned with the evolution of multicellularity, using the green algal group, Volvocales, as a model experimental system. Experience working with green algae is not critical. Current projects in the lab include studying the genetic basis for the evolution of germ-soma differentiation, measuring life history trade-offs as colony size increases, and artificial selection experiments on body size in volvoclean green algae.

To apply, please e-mail (shanley@email.arizona.edu) with the following information: a statement giving your research interests and qualifications, a CV, and the names and contact information of three references.

The initial appointment is for one year, with an additional two years' funding available conditional on satisfactory performance. The position is funded by an NSF grant, at 35K per year (plus benefits). The start date is flexible but the position is available immediately.

The University of Arizona is an EO/AA Employer.
michod@u.arizona.edu michod@u.arizona.edu

UBritishColumbia ComparativeGenomics

Postdoctoral Position in Comparative Genomics

University of British Columbia, Vancouver, Canada

A postdoctoral position is available in the area of comparative genomics of conifers. Specific activities may include sequence analysis across conifer taxa, association genetics of white spruce (combined QTL mapping and SNP associations), expression QTL mapping,

and inferences about conifer genome structure via targeted BAC sequencing. The person will be member of a large, interactive forestry genomics group, involved with many aspects of genomics including EST sequencing, databasing, microarrays, proteomics, and SNP discovery/assay. See www.treenomix.ca for further details.

This is a multi-investigator grant with PIs Joerg Bohlmann, and K. Ritland at UBC, and is funded by Genome Canada and the Province of B.C.

Please send your C.V. to: Email: Kermit.Ritland@ubc.ca. The position is available immediately.

Kermit Ritland <kermit.ritland@ubc.ca>

UCaliforniaSantaBarbara Phylogenetics

The Oakley Lab at the University of California-Santa Barbara seeks a highly motivated and productive postdoctoral researcher to work on NSF-funded research (<http://nsf.gov/awardsearch/showAward.do?AwardNumber=0643840>) on the phylogeny, divergence times, and rates of molecular and morphological (especially eyes) evolution in ostracod crustaceans.

The position requires an individual with a PhD and experience in molecular evolution, phylogenetic systematics, paleontology, or related fields. Outstanding molecular, computational and/or quantitative skills are particularly advantageous.

Funding is available for a minimum of 1 year, and may be extended upon mutual agreement. Preference will be given to candidates with a high probability of applying for (with the help of the PI) and obtaining independent funding; for example through the University of California Presidents Postdoctoral Fellowship, NIH-NRSA fellowship, NSF Postdoctoral fellowships, or other funding agencies.

The starting date is flexible, and the position will remain open until filled. For primary consideration, applicants should apply by April 15, 2008. Informal inquiries are welcomed, prior to formal application.

Lab Website: <http://www.lifesci.ucsb.edu/eemb/labs/oakley/> To apply, please send the following:

1. A curriculum vitae
2. Names of 3 referees willing

to provide a letter of recommendation upon request 3. A brief statement of how your research goals fit with research of Oakley's Lab 4. A brief statement of interest, ideas, and qualifications for independent fellowship and/or grant applications

E-mail applications are preferred: oakley@lifesci.ucsb.edu

Mailed applications are also acceptable to: Todd Oakley Ecology Evolution Marine Biology University of California- Santa Barbara Santa Barbara, CA 93106

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

UCollegeCork Arabidopsis Variation

UniCollegeCork Arabidopsis Reproduction & Natural Variation

Our lab is seeking applications from highly motivated postdocs to work on genetics of reproduction in *Arabidopsis thaliana* polyploids. The successful applicant will work within a small team of researchers investigating sexual and asexual reproduction (apomixis). We seek enthusiastic and highly motivated candidates with excellent and proven skills in plant genetics, genetic mapping, molecular biology and reproduction (as demonstrated by their publication record). We particularly seek candidates with experience of association/QTL mapping, DIC/fluorescence microscopy, in situ hybridisation, cytogenetics and chromatin analysis in *Arabidopsis thaliana*. The project is funded for three years and collaborators include Dr Magnus Nordborg (Uni of Southern California), Dr Tom Juenger (Uni of Texas) and Dr Tim Sharbel (IPK Gatersleben). The successful applicant will work closely with two PhD students working within the same funded project.

Prospective applicants should send an e-mail outlining your research interest and motivations, including; (a) your C.V. (please list publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to: Dr. Charles Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland. E-mail: c.spillane@ucc.ie

Lab website: www.ucc.ie/spillane Deadline: 20th March 2008 UCC is an equal opportunities employer

"Spillane, Charles" <C.Spillane@ucc.ie>

UGreifswald StemCellBioinformatics

Postdoctoral Researcher: Bioinformatics of Stem Cell data; Bioinformatics Research Group, University of Greifswald, Germany

A 3-year postdoctoral position is available in the bioinformatics group at the University of Greifswald in northeastern Germany. In a project funded by the German research foundation (DFG), methods of machine learning and evolutionary analysis will be applied to stem cell data (genome, transcriptome, interactome) to study the regulatory and interactory circuitry behind pluripotency (stemness), re-programming and cellular differentiation. As the project is part of a German-wide collaborative effort, interaction with a large number of leading scientists is anticipated, resulting in a deeper understanding of some of the processes that are fundamental to Life.

The position requires an enthusiastic researcher with an interest in applying in-silico analyses in a field with exciting prospects, towards a major goal of regenerative medicine, that is, generating cells that may be transplanted in case of disease and that are derived from somatic cells (e.g. muscle cells) of the patient.

Applicants should hold a doctorate and have previous experience in data analysis and programming. They may hold a degree in biology, computer science, physics, chemistry, mathematics or a related area. A keen interest in science is more important than previous experience in the field, although experience with (high-throughput) biological data in general and comparative / evolutionary analysis in particular is considered a plus. Exceptional candidates without a doctorate may be considered, too. The successful applicant will have access to a computer cluster that will be bought during the next months.

Please email applications to Georg Fuellen (fuellen@alum.mit.edu) (CV, statement of research interests and qualifications), quoting "07/B82 / FU583/2-1" in the subject line. Review of applications will begin March 30 and continue until the position is filled.

Greifswald is very close to a major German recreational area, the Baltic coast, including the islands of Ruegen and Usedom. It hosts one of the most modern University Hospitals in Germany.

Prof. Dr. Georg Fuellen Bioinformatics Research

Group Office: Institute for Mathematics and Computer Science Franz-Mehring-Str. 48 Ernst-Moritz-Arndt-University Greifswald 17489 Greifswald Jahnstr. 15a Phone +49 3834 86 4618 D-17489 Greifswald Fax +49 3834 86 80026 Germany

<http://alum.mit.edu/www/fuellen/>
ellen@alum.mit.edu

fuellen@uni-muenster.de

UIdaho PlasmidHostRangeEvolution

Postdoctoral Position in Plasmid Host Range Evolution:

A postdoctoral position is immediately available in the laboratory of Dr. Eva Top at the University of Idaho (UI) (lab website: <http://www.uidaho.edu/biology/labs/top/>). He/she will study the adaptive changes that expand, contract, or shift the host range of a plasmid during evolution in various bacterial hosts. In order to evaluate the role of plasmids in the emergence of highly resistant pathogens, a fundamental understanding of the evolution of plasmid host range is essential. Our overall hypothesis is that the host range of plasmids can evolve, much like that of parasites, to become wider or narrower over evolutionary time. To test this hypothesis, the postdoctoral scientist will address at least one of the following specific aims: 1) To elucidate evolutionary changes that permit a narrow-host-range plasmid to expand or shift its host range, and 2) To elucidate evolutionary changes that cause host range contraction of a broad-host-range plasmid as a result of long-term association with a single host.

The postdoctoral scientist will be part of our IBEST group at the UI (<http://www.ibest.uidaho.edu/ibest/index.html>), a dynamic and interdisciplinary research group with excellent resources, funded by an NIH Center for Biomedical Research Excellence (COBRE).

The successful candidate should have 1. A Ph.D. degree in molecular biology, microbiology or related discipline. 2. At least one year of experience in working with bacterial cultures and in the use of contemporary molecular biology methods, such as DNA cloning and sequencing. 3. Demonstrated ability to write and publish scientific papers in English as first author in peer-reviewed journals. 4. Demonstrated ability to present data at scientific meetings. 5. A fundamental understanding of

the ecology and evolution of plasmids 6. Some knowledge of prokaryotic molecular biology or genetics and molecular evolution

Other requirements are listed in the Position description posted on the Human Resources website (see below). Salary will be commensurate with the qualifications and experience of the applicant. For more information candidates can write to Dr. Eva M. Top (evatop@uidaho.edu). Qualified candidates should apply as soon as possible via the following website: <https://www.sites.uidaho.edu/AppTrack/Agency/Applicant/CurrentOpenings.asp?category=1> (look for Postdoctoral Fellow in Dept. of Biol. Sci.). Applications should include an uploaded letter and curriculum vitae. Notice that the deadline is in less than one week: March 11, 5pm PST !! The University of Idaho is an equal opportunity/affirmative action employer

Dr. Eva Top Associate Professor Department of Biological Sciences University of Idaho 258 Life Sciences South Moscow ID 83844-3051 Phone: 1-208-885-5015 Fax: 1-208-885-7905 E-mail: evatop@uidaho.edu <http://people.ibest.uidaho.edu/~etop/> evatop@uidaho.edu

UKonstanz MolEvolGenomics

TWO POSTDOC POSITIONS - molecular evolution, genomics or bioinformatics

At the University of Konstanz we expect to have two postdoc positions available starting on April 1, 2008 in the lab of Prof. Axel Meyer at the Department of Evolutionary Biology and Zoology at the University of Konstanz in Germany.

Due to the funding of the University of Konstanz through the "excellence initiative" of the German government we are in the process of establishing a genomics/proteomics center at the university that will include microarray facilities and second generation sequencing technologies. Therefore, we are particularly interested in postdocs with expertise in molecular evolution, molecular phylogenetics and bioinformatics. We expect that a "junior professorship" in bioinformatics will be advertised shortly as well. These positions are affiliated with the new graduate school in chemical biology - for more information visit <http://www.chembiol.uni-konstanz.de/>. For this new program we invite applications of qualified Masters students as

well as Ph.D. candidates.

The postdoc projects we are interested in have to do with fish genomics and in particular comparative genomics of cichlid fish. Other projects deal with the evolution of gene families the evolution of the genome in early chordates and vertebrates. Candidates should have a strong interest in bioinformatics, developmental and evolutionary biology and should be experienced in molecular techniques and/or computational biology.

Appointments are for up to two years initially with a salary according to German TVL salary scale that includes extensive health and retirement benefits. The initial contract period would be for two years with the potential for additional years of funding.

Informal inquiries should be addressed to Prof. Axel Meyer (axel.meyer@uni-konstanz.de). Further information on our research can be obtained from our web page: www.evolutionsbiologie.uni-konstanz.de. For publications see <http://www.evolutionsbiologie.uni-konstanz.de/index.php?sectionQ> Applications should include a CV, statement of research interests and email addresses of two references. Review of applications will commence on March 15th 2008. Starting dates are flexible. Applications should be sent as one pdf file to axel.meyer@uni-konstanz.de - or by mail to Prof. Axel Meyer, Department of Biology, University of Konstanz, D-78457 Konstanz, Germany. This search will remain open until the positions are filled.

– Prof. Axel Meyer, Ph.D. Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 7531 88 4163 fax + 49 7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 7531 88 3069

www.evolutionsbiologie.uni-konstanz.de Axel Meyer
<axel.meyer@uni-konstanz.de>

ULausanne PlantReproductiveEvolution

Postdoctoral researcher: Plant reproductive evolution - Switzerland

A postdoctoral research position is available to collaborate with projects focussing on the reproductive evolution of the dioecious plant *Silene latifolia*

(Caryophyllaceae) and its specialist pollinator/seed predator *Hadena bicurris* (Noctuidae).

Specific research topics will be determined based on the interests of the successful candidate, but may potentially include: applying microsatellite DNA analysis to investigate the determinants of seed paternity in natural populations and after experimental pollinations, and the analysis of traits involved in plant/pollinator interactions.

Funding is available for one year, starting April 1st 2008 (or later) until March 31st 2009. Prolongation for up to three years is possible. We offer a competitive salary, excellent facilities and high quality of life in a historical town close to lakes and mountains. The position will be based at the Institute of Biology, University of Neuchâtel, Switzerland (http://www2.unine.ch/biol/-page4606_en.html), which harbours the National Competence Center of Research on Plant Survival (<http://www2.unine.ch/nccr/>).

Candidates should have strong interests in analyzing experimental and molecular data to investigate plant/pollinator interactions, and a background in one or more of the following areas: population genetics and microsatellite DNA analysis, experimental pollination ecology, quantitative genetics. The ideal candidate will be independent, highly motivated, and willing to contribute to a productive and friendly work atmosphere.

Please email your application to Giordina Bernasconi (giordina.bernasconi@unil.ch / subject line "Postdoctoral position") as one pdf file including a CV with publication list, statement of research interests and experience, and the names of three people who can be contacted for letters of reference. Evaluation of applicants will begin March 26th and will continue until the position is filled.

Giordina Bernasconi web: <http://www.unil.ch/dee/page7005.html> http://www.unil.ch/dee/-page10687_en.html Giordina Bernasconi SNF professor Department of ecology and evolution University of Lausanne Biophore CH-1015 LAUSANNE Switzerland +41 21 692 41 88 (phone) giordina.bernasconi@unil.ch
Giordina Bernasconi <Giordina.Bernasconi@unil.ch>

ULyon BacterialEndosymbionts

Title : Diversity and epidemiological consequences of

bacterial endosymbionts in arthropod vectors of vertebrate diseases : application to blood-sucking acarian

A post-doctoral position is available immediately at the University of Lyon (France), to work on symbiotic bacteria of hematophagous acaria particularly Ticks. The project is entitled: Diversity and epidemiological consequences of bacterial endosymbionts in arthropod vectors of vertebrate diseases : application to blood-sucking acarian. Aims are the identification of endosymbiotic bacteria of Ticks, the measurement of their prevalence in natural populations, the analysis of multiple infections looking for possible association or exclusion among symbionts and pathogens. The localization and colocalization of symbiotic bacteria inside the tick body will also be analyzed. The second part of the project has the objective to determine the consequence of symbiotic bacteria on phenotypic traits of their hosts and their ability to transmit pathogen agents. The problem of Rickettsia will be particularly studied. The objective is to tackle the question of the possible interactions (antagonistic or synergetic) between symbiotic bacteria and pathogen agents transmitted by ticks.

For this position, a Ph.D. in parasitology, symbiotic interactions, bacterial ecology, host-parasite genetics and ecology, or related field is required. The candidate should be familiar with molecular biology and have an interest in applying this knowledge to evolutionary & ecological questions about bacterial symbionts and arthropod vectors. Candidates should have experience in standard tools of molecular biology, including standard DNA extraction, PCR set up and sequencing. He/she should also be willing to interact with the other group members working on bacterial endosymbiont of arthropods and he/she would be encouraged to design and be responsible for independent research that involves the collection, analysis and publishing of data. Knowledge of the French language is not required.

This position is for one year, with a 40 800 TTC gross annual income.

Candidate must contact F Fleury (fleury@biomserv.univ-lyon1.fr) or Lionel Zenner (l.zenner@vet-lyon.fr) as soon as possible and send a CV with list of publications. We will then send in return a completed application form which must be received by the above mentioned resource persons by March 28 2008.

F. Fleury Equipe Génétique et Evolution des Interactions Hôte-Parasite Laboratoire de Biométrie et Biologie Evolutive UMR 5558 - Bat. G. Mendel Université Claude Bernard - LYON1 16, rue Raphaël DUBOIS 69622 VILLEURBANNE Cedex - FRANCE
Tel: 0472431921 Fax. 04 72 43 13 88 Mel:

fleury@biomserv.univ-lyon1.fr

Frédéric Fleury <fleury@biomserv.univ-lyon1.fr>

UManchester YeastBioinformatics

Three research positions are available at the University of Manchester.

The positions will be based in the Faculty of Life Sciences in the recently completed Michael Smith Building. The Faculty of Life Sciences is one of the largest and most successful unified research and teaching organisations of its kind in Europe. Research spans all fields of biology, with a strong emphasis on a collaborative integrative approach. Our unified structure and single site location promote collaboration and facilitates centralised provision of state of the art equipment. Further information relating to the Faculty of Life Sciences and the University of Manchester can be obtained at <<http://www.manchester.ac.uk/lifesciences>>.

See <<http://www.manchester.ac.uk/bioinformatics>> for further details of our research in the areas of evolutionary and computational biology. Note, the closing date for applications is Friday 28th March 2008.

INVESTIGATING SPECIFICITY OF YEAST PROTEIN COMPLEXES USING BIOINFORMATICS METHODS (Ref LS/80100)

Based in the bioinformatics laboratories of Drs Simon Lovell and David Robertson, we seek a capable and enthusiastic computational biologist to study protein-protein interactions, specifically to investigate determinants of binding specificity in protein complexes. This will involve the use of evolutionary and structural information to gain insight into the nature of protein interactions in the cellular interactome. The post forms part of an interdisciplinary project with Dr Daniela Delneri and a complementary molecular biology post is advertised (see LS/80101). You should have (or expect to hold shortly) a relevant PhD. Experience of computer-based research is required and experience in protein structure analysis and/or molecular evolution an advantage.

Informal enquiries may be addressed to: Dr. Simon Lovell, Tel.: +44 (0)161275 5748, <E-mail: simon.lovell@manchester.ac.uk>.

INVESTIGATING SPECIFICITY OF YEAST PROTEIN COMPLEXES USING EXPERIMENTAL

METHODS (Ref LS/80101)

Based in the laboratory of Dr Daniela Delneri, we seek a capable and enthusiastic molecular biologist to study protein-protein interactions, specifically to understand the efficiency with which homologous proteins from different species are able to interact to form complexes. The position will involve the use of substantial molecular biology and biochemistry including classical genetic tools, gene targeting, protein purification and analytical techniques. The post forms part of an interdisciplinary project with Drs Simon Lovell and David Robertson and a complementary computational biology/ bioinformatics post is also advertised.

Informal enquiries may be addressed to: Dr. Daniela Delneri, Tel.: +44 (0)161275 5686, <E-mail: d.delneri@manchester.ac.uk>.

A RATIONAL IN SILICO APPROACH TO MAPPING INTERACTOMES, APPLIED TO CANDIDA GLABRATA (Ref LS/80102)

Based in the bioinformatics laboratories of Drs Simon Lovell and David Robertson, we seek a capable and enthusiastic computational biologist to study protein-protein interactions networks, specifically to develop evolutionary and structure-based methods to infer interaction networks between species. The post forms part of an interdisciplinary project in collaboration with Imperial College London. Our combined aim is to develop a rational and integrated approach to reliably and comprehensively predict protein interactions using sophisticated bioinformatics, statistical and comparative approaches. You should have (or expect to hold shortly) a relevant PhD. Experience of computer-based research is required and experience in protein structure analysis, network analysis and/or molecular evolution an advantage.

Informal enquiries may be addressed to: Dr Simon Lovell, Tel.: +44 (0) 161275 5748, E-mail: <simon.lovell@manchester.ac.uk>.

FURTHER DETAILS:

All posts are funded by the BBSRC and are tenable immediately for up to 3 years. Salary range is £26,666 - £32,796 per annum. If appropriate, please apply for more than one post.

Application forms and further particulars can be obtained at <[http:// www.manchester.ac.uk/-lifesciences/jobs](http://www.manchester.ac.uk/-lifesciences/jobs)> or from: The Directorate of Human Resources, Tel: +44 (0)161 275 8836, E-mail: <lifesciences-hr@manchester.ac.uk>. Please quote appropriate reference.

***The closing date for applications is 28 March

2008.***

david.robertson@manchester.ac.uk

UMemphis Bioinformatics Computational Genomics

Applications are invited for a one-year postdoctoral position (may be renewed for one additional year) in bioinformatics/computational genomics in the laboratory of Dr. Victor Jin in the Bioinformatics Program, Department of Biology at the University of Memphis (Memphis, TN). The research focus will be in the cutting edge research area of computational genomics. The successful candidate will be expected to develop new algorithms and software tools for the identification and characterization of genomic regulatory elements and networks from the cancer epigenetic and gene regulatory data generated from high throughput technologies such as ChIP-chip, ChIP-Seq, and Micro-array, and to develop bioinformatics tools for sequence and structural analysis and build databases for cancer epigenetics and transcriptional regulation data. The position actively involves working cooperatively with other lab members and outside collaborators. The ideal candidate will be enthusiastic, highly motivated, and independent with good skills in mathematics and computer science, and a strong record of accomplishment in research.

Required qualifications: Ph.D. in bioinformatics, computer science, statistics, molecular biology, applied mathematics, or a related field.

Research experience (with first-author publications) in computational genomics

Proficiency in programming, ideally in C/C++ as well as in scripting languages such as perl/python, or R. -Should be comfortable in a linux environment, with large data sets, computer clusters, and database software.

To Apply: Submit a CV, a short (roughly one-page) description of research interests and experience, and contact information for at least two references by e-mail to hsmith@memphis.edu. Informal inquiries are welcome.

Deadline: Review of applications will begin May 1, 2008 and may continue until the position is filled.

Victor Jin <jxh123@hotmail.com>

UNebraska PopulationBiology

Postdoctoral Fellowship Program (CALL FOR APPLICATIONS NOW OPEN!)

The University of Nebraska Program Of Excellence in Population Biology announces two-year Postdoctoral Fellowships in Population Biology. The successful Population Biology postdocs will bring new skills, new ideas, and new excitement to UNL programs. Two Postdoctoral positions will be advertised internationally every two years; thus, new highly-qualified individuals will regularly join the Population Biology group. Candidates will develop a research project with a faculty member associated with the Program (see list of core faculty). These positions will provide recent graduates the opportunity for independent research in association with a growing, integrative, and cross-disciplinary program. Applicant selection will be based on a research proposal to work with an established Population Biologist at UNL, but once in residence post-docs will be expected to interact more broadly with the group and participate in graduate instruction through courses and seminars.

New opening for a postdoctoral Fellow: applications due May 1, 2008, starting date as soon as June 2008. Qualified candidates are encouraged to contact potential faculty advisor from the list of core faculty associated with the program (<http://popbio.unl.edu/corefaculty.htm>). A Ph.D. and expertise in any aspect of population biology is required. To apply, send a CV, a up to 1-page research proposal, 1 page previous research/teaching experience and an up to 1 page description of potential graduate seminars and arrange for three letters of reference, one of which must be from the proposed faculty sponsor, to the Population Biology Post-doctoral Fellowship Selection Committee, School of Biological Sciences, University of Nebraska- Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118.

Closing date is May 1, 2008. Fellowship position will remain open until suitable candidates are selected. UNL is committed to a pluralistic campus community through Affirmative Action and Equal Opportunity, and is responsive to the needs of dual career couples. We assure responsible accommodation under the Americans with Disabilities Act.

Diana Pilson <dpilson1@unl.edu>

UNebraska ViralEvolution

Post doctoral Research Opportunity in Viral Evolution

The Lab of Dr. Charles Wood from the Nebraska Center for Virology (<http://www.unl.edu/virologycenter/-faculty/wood.shtml>), at the University of Nebraska is looking for a highly motivated individual to study the molecular evolution of HIV. The laboratory investigates HIV and human herpesvirus, and the roles these viruses play in immunosuppression and cancer development. Three of the foci of interest in the lab, are the 1- mother to infant HIV transmission, 2- longitudinal evolution of patient with different rates of disease progression, and 3- the differences in the development of ART resistance among patients. The candidate will have ample opportunities for interaction with other post-docs in the lab, and there is also the possibility of working on the transmission and evolution Human Herpesvirus 8 (HHV-8), a virus linked to Kaposi's Sarcoma, a rare cancer often found in AIDS patients. Most of our data comes from collaborative projects being carried out in Africa.

The position requires a highly motivated, enthusiastic, and independent individual with a background in population genetics, phylogenetics, evolutionary biology, and statistics, or related fields. Molecular experience is advantageous but not essential.

For additional information, and applications contact

Charles Wood Nebraska Center for Virology School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone - 402.472.4550 Fax - 402.472.8722 cwood1@unl.edu

"Federico G. Hoffmann"
<federico.g.hoffmann@gmail.com>

UNewBrunswick PopulationGenetics

Postdoctoral Fellow Population and Conservation Genetics and Genomics

Faculty of Forestry and Environmental Management
University of New Brunswick

A postdoctoral fellow position is available immediately to assist with research projects on population and conservation genetics and genomics of forest trees. The projects aim to examine population genetic diversity, spatial genetic structure, pollen gene dispersal, minimum viable population size, and genetic and evolutionary impacts of forest fragmentation, forest fires and forest management practices. A combination of molecular, population, conservation and evolutionary genetics, and genomics approaches are applied. The PDF also will be expected to analyze the data and prepare the manuscripts from previously completed work and to help graduate students in solving problems.

The PDF will work in the Forest Genetics and Genomics lab, as a member of the research team consisting of Ph.D., masters and undergraduate students, technical and research assistants and postdoctoral fellows. The Forest Genetics and Genomics lab has state-of-the-art molecular, population genetics, genomics and bioinformatics facilities, including high throughput DNA extraction, genotyping and sequencing systems and a bioinformatics server. The PDF will also interact with collaborators from the Canadian Forest Service, Ontario Ministry of Natural Resources, UNB Biology Department and other national and international organizations. The position will provide with excellent opportunities for a large number of high impact publications.

The PDF position requires an independent, innovative, highly motivated and productive

researcher with excellent writing, data analysis and leadership skills, who has a keen interest in population and conservation genetics and genomics of forest trees. The applicant should have Ph.D. and experience in relevant population and conservation genetic aspects. Experience in population genetic modeling will be an asset.

The PDF position is for one year. It may be renewable for a second year subject to availability of funds and satisfactory performance. The fellowship amount will commensurate with the qualification and experience of the candidate.

Please send your application to Prof. Om Rajora via e-mail (Om.Rajora@unb.ca), consisting of a letter of application, statement of research interests and qualifications, complete CV, and names, addresses (e-mail and postal) and telephone numbers of three referees. Evaluation of the applications will commence on March 31, 2008 and will continue until the position is filled.

Om P. Rajora, Ph.D. Professor and Senior Canada Research Chair in Forest and Conservation Genomics and Biotechnology Faculty of Forestry and Environmental

Management P.O. Box 44555, 28 Dineen Drive, University of New Brunswick Fredericton, NB E3B 6C2 Canada

E-mail: Om.Rajora@unb.ca Phone: (506) 458-7477 or (506) 458-7475 Fax: (506) 453-3538

orajora@unb.ca

UOregon Metagenomic Informatics

Postdoctoral Positions in Metagenomic Informatics

Microbes play fundamental roles in all biology-associated processes on the planet. A powerful new tool in such studies is metagenomics wherein one uses high throughput DNA sequencing methods on DNA isolated directly from environmental samples. Metagenomics has the potential to revolutionize our understanding of the normally hidden yet incredibly important world of microorganisms. However this great potential comes with enormous challenges in the analysis of the sequence data, including (i) the fragmentary nature of sequence data, (ii) the sparse sampling of genomes, populations and communities, and (iii) the unknown phylogenetic diversity and ecological structure of the communities being sampled.

We are seeking five post-doctoral scientists and a bioinformatics engineer to work on methodology for analysis of metagenomic data as part of a new collaborative project: Integrating Statistical, Evolutionary and Ecological Approaches to Metagenomics (iSEEM). The iSEEM Project, funded by the Gordon and Betty Moore Foundation, takes an integrated, interdisciplinary approach to metagenomic analysis. We will be working with the Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis (CAMERA) to make any methods we develop available to the broader community. The project spans three labs, each with different areas of focus and two institutions (UC Davis and U Oregon). Each position will be associated with one of the PIs at their home institution.

More information available at: <http://iseem.org> Qualifications We are looking for people with a demonstrated interest in working at the interface between the quantitative and biological sciences. We will offer a generous salary and benefits commensurate with experience. Postdocs: Applicants should have a PhD in a biological, computational, mathematical, or statistical field. Pro-

programming skills are highly desirable. Bioinformatics Engineer: Applicants should have substantial experience with database programming (e.g. SQL), scripting (e.g. Perl or Python), and bioinformatics tools.

Term Appointments will last 2 years beginning in Summer 2008.

To apply Please complete the appropriate online form at the iSEEM job application website. Postdocs: http://jobs.genomecenter.ucdavis.edu/-start_app.php?job_idw Bioinformatics Engineer: http://jobs.genomecenter.ucdavis.edu/-start_app.php?job.idx

You will be requested to upload the following materials: (1) a brief cover letter explaining your background, career interests, and preferred geographical location for work (if any), (2) CV (including publications), (3) names and contact information for three references.

All applications will be evaluated by all PIs. The locations of hires will be determined mutually by the applicants and the PIs. We will evaluate applications as they arrive, until the positions are filled.

The Labs Jonathan A. Eisen (UC Davis) U. C. Davis Genome Center Center for Population Biology Section of Evolution and Ecology Department of Medical Microbiology and Immunology http://128.120.136.15/mediawiki/index.php/Main_Page Jessica L. Green (U Oregon) Center for Ecology and Evolutionary Biology Department of Biology <http://biology.uoregon.edu/people/green/index.html> Katherine S. Pollard (UC Davis) U. C. Davis Genome Center Center for Population Biology Department of Statistics <http://docpollard.com/> jlgreen@uoregon.edu

UOslo FungalSpeciation

POST-DOCTORAL RESEARCH FELLOW

Post-doctoral research fellowship in evolutionary biology

Available at Microbial Evolution Research Group (MERG), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo

The position is available from 1. June 2008 for a period of three years.

In this project, processes and mechanisms involved during fungal speciation will be analyzed, employing em-

pirical and experimental inferences and using various fungi (basidiomycetes) as model organisms. The candidate will work together with a group of researchers at the Department of Biology and outside. Periods abroad (US, Sweden) are to be expected. The fellowship is funded by the Norwegian Research Council. The research program MERG has status as a "Strategic Research Initiative" at the University of Oslo. The vision of MERG is to develop an internationally leading and dynamic multidisciplinary research environment focusing on ecological, evolutionary and systems biology research on prokaryotic and eukaryotic microbes, their communities and interactions.

The candidate will be expected to participate in both field work, generating data, perform data analyses, to work cooperatively with other lab members and outside collaborators and to actively publish and present results. The ideal candidate will be enthusiastic, highly motivated, independent and will have a strong background in one or more of the areas of focus.

Please contact Assoc. Prof. Håvard Kausrud at the address below for more details.

Candidates must have a PhD in evolutionary biology or a related discipline, strong experience in molecular techniques (cloning, DNA-sequencing, fingerprinting-techniques, etc.) and in handling and analysing DNA data. Experience in mycology (including culturing of fungi), speciation, phylogenetics, phylogeography and molecular evolution will be considered advantageous.

Applicants must hold a degree equivalent to a Norwegian doctoral degree. The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines. The position is available from 1. June for a period of three years. No one can be appointed for more than one specified period at the same institution.

Applicants should submit a letter of application, a CV, a list of published and unpublished works, and a document summarizing the applicant's scientific work and interests and giving some thoughts on how the applicant would fit into the project, four set of copies of certificates, and copies of at most five publications. Applicants may be called in for an interview.

Applications should be sent to the Faculty of Mathematics and Natural Sciences, (marked with the REF:NR. 2008/1988), Attn.: Senior Executive Officer Bente Schjoldager, P.O.Box 1032, 0315 OSLO, NORWAY.

Please also refer to the regulations pertaining to the conditions of employment for post-doctoral fellowship positions: <http://www.uio.no/>

admhb/reglhb/personal/tilsettingvitenskapelig/-guidelinespostdoctor.xml The University of Oslo is an equal opportunity employer and seeks in particular to increase its number of female scientists. Women are therefore particularly encouraged to apply. The University of Oslo also wants more people with an immigrant background in permanent academic posts. Such people are encouraged to apply.

The University of Oslo has an agreement for all employees aiming to secure rights to research results a.o.

Contact Persons: Associate professor Håvard Kauserud, tlf. +47 22854832, e-mail: haavarka@bio.uio.no.

Pay grade: 54-60 (from NOK 394 700,- to NOK 439 300,- (equals ca 49 300- 54 900) depending on qualifications and seniority)

Application deadline: 31. March 2008

Ref. No.: 2008/1988

Application, CV (marked Ref. No. 2008/1988), confirmed certificates etc., up to 5 scientific papers (4 copies), should be sent to: Faculty of Mathematics and Natural Sciences, attn. Senior Executive Officer Bente Schjoldager, P. O. Box 1032 Blindern, N-0315 Oslo, Norway

Applications which are incomplete and applications per e-mail will not be considered.

Application papers will not be returned.

– Håvard Kauserud Department of Biology University of Oslo P.O.Box 1066 Blindern N-0316 Oslo, Norway

Phone: +47 22854832 (office) +47 99697116 (mob)

Web: <http://biologi.uio.no/meb/db03-staff/-Haavard.html> havard.kauserud@bio.uio.no
haavarka@bio.uio.no

UOslo TheoreticalBiol

Post-doctoral position in theoretical biology

Available at the Center for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo

I want to draw your attention to a three-year postdoctoral position available to work on topics in evolutionary theory and/or biostatistics/bioinformatics. The position is to be associated with the project “Selec-

tion and Evolvability: Concepts, measurements, and statistical modeling” headed by Thomas F. Hansen and Tore Schweder, and involves the collaboration of David Houle (Florida State University), Hirohisa Kishino (Tokyo University), and Günter Wagner (Yale University). The idea behind the project is to explore how fundamental parameters in evolutionary theory are defined, measured, and analyzed, and in particular to explore the relationship between theoretical models that define the parameters, and the experimental and statistical methods that are used to study them. We will explore conflicts between the demands of statistical models and the need to preserve the theoretical meaningfulness of the estimates. We will critically evaluate how concepts such as evolvability, fitness, selection, evolution rates, epistasis, pleiotropy, integration, etc. are defined and given meaning in a theoretical context, and how they are measured and manipulated during experiment and data analysis. The successful candidate is expected to participate in the general discussions and development of the project, which includes organizing a workshop, and to conduct original research on topics within the broad outline of the project. The position offers ample opportunity to work at the interface between theory and data analysis within a broader group of researchers and students with strong expertise in theoretical and statistical modeling. The ideal candidate has broad interests in theoretical and conceptual issues of evolutionary biology, and in statistical modeling and analysis. Expertise in one or more of the following areas is particularly relevant: Biostatistics, bioinformatics, population genetics, and evolutionary biology. Applicants must hold a degree equivalent to a Norwegian doctoral degree. Please contact Thomas Hansen or Tore Schweder at the below address for more detail on the project and possible research topics, and refer to <http://www.cees.uio.no/-about/vacancies/sff2008.html> for information on how to apply. The CEES is a semi-autonomous interdisciplinary research group within the Department of Biology that combines the skills of population ecologists, evolutionary biologists, geneticists, and statisticians. It has a strong international flavor, and currently employs 13 faculty, 33 postdocs/researchers, 49 graduate students, and 16 associate scientists. The CEES has been awarded status as centre of excellence by the Norwegian Research Council, and is well funded. See <http://cees.no/> Contact Person: Professor Thomas F. Hansen, e-mail: thomas.hansen@bio.uio.no. Tore Schweder, email: tore.schweder@econ.uio.no. Pay Grade: 54-62 (NOK394700,-NOK456600, approx. 50000 - 58000, \$71000-\$82000 depending on qualifications and seniority). Application Deadline: March 15. Starting date: As soon as possible.

Thomas Hansen <t.f.hansen@bio.uio.no>

UPenn Microbe Evolution

A postdoctoral position is available in the group of Dustin Brisson at the University of Pennsylvania to study evolution of infectious microbes. The position requires a highly motivated, enthusiastic, and enquiring individual. Competitive individuals will have a strong background in evolutionary biology (population genetics / population biology), statistics, and quantitative skills. Molecular and field experience would be advantageous.

The University of Pennsylvania has a strong group of evolutionary biologists and ecologists in the biology department that frequently interact with each other and with an accomplished group of microbiologists in the Medical and Veterinary schools.

The position is available as early as June 2008; the starting date is flexible and I am willing to wait for an outstanding candidate.

For informal enquiries and formal applications including curriculum vitae, list of publications, a one page statement of research interests (in a single file applying by email), and two letters of recommendation, can be submitted to:

Dustin Brisson Department of Biology University of Pennsylvania Leidy Laboratories, 326 433 South University Avenue Philadelphia PA 19104-6018
<http://www.bio.upenn.edu/faculty/brisson/> <http://-/brisson.bio.upenn.edu/> dbrisson@sas.upenn.edu
 V:(215) 746-1731

UPierreMarieCurie AntEvol

A post-doctoral position is opened at the University of Paris (see below). It should (I hope!) be of interested to evolutionary biologists.

Many thanks

Thibaud Monnin

REPRODUCTION BY COLONY FISSION IN ANTS

A post-doctoral position is opened at the Laboratory of

Ecology, University Pierre and Marie Curie (UPMC), Paris. The position is funded for 18 months by ANR (Agence Nationale de la Recherche).

The applicant will work with a team studying the reproduction of social insects by colony fission, at both proximate and ultimate levels. The subject of the post-doc is flexible within this general research theme. We aim at increasing the general knowledge on the production of new colonies by fission, using the Mediterranean ants *Cataglyphis cursor* and *Aphaenogaster senilis*. More specifically, we seek (i) to analyse the factors that trigger colony fission, such as colony size, nest densities and resources availability, (ii) to investigate the trade off between number and size of daughter colonies produced, and (iii) to study the social conflicts associated with colony fission. For instance, in the highly polyandrous *C. cursor* new queens can be produced either sexually or by parthenogenesis, so that during colony fission workers may join parthenogenetic queens, sister queens or half-sister queens.

The applicant will be based at the laboratory of ecology in Paris, and will participate to experimental works at a field station in Banyuls-sur-mer, southern France. The applicant should have a formation in Behavioural Ecology and in Evolution, and preferentially some knowledge of social insects.

The salary is ca 2,300 per month, depending on the experience of the post-doc. The post-doc will preferentially start between April and June 2008. The position will remain opened until it is filled. Applicants should submit their CV, a short summary of research interests and contact information of two references to Thibaud Monnin (tmonnin@snv.jussieu.fr).

Dr Thibaud MONNIN Laboratoire Écologie & Évolution CNRS UMR 7625, Université Pierre et Marie Curie 7 quai St Bernard, Bâtiment A 7ème étage, Case 237 75 252 Paris Cedex 05, France

Tél: (+33) (0)1 44 27 36 10; Fax: (+33) (0)1 44 27 35 16 e-mail: tmonnin@snv.jussieu.fr
<http://ecologie.snv.jussieu.fr/monnin> Thibaud Monnin <Thibaud.Monnin@snv.jussieu.fr>

UWisconsinMadison PlantEvolution TrophicInteractions

Postdoctoral Position

Trophic Interactions, Evolution, Chemical Ecology, and

Community/Ecosystem Genetics
University of Wisconsin - Madison

A postdoctoral Research Associate position will be available spring/summer 2008 to work at the interface of plant evolution, genetics/chemistry, trophic interactions, and community/ecosystem and ecology. Our research program explores the genetic basis of community dynamics and ecosystem processes, using poplar (aspen and cottonwood) as a model system. Specific research projects can be designed consistent with the interests of the individual. Research could be integrated with a large, multi-investigator, multi-institutional project funded under NSF's Frontiers in Integrative Biological Research (FIBR) program. (See the feature article on "genes to ecosystems" by Whitham et al. [2006. *Nature Reviews Genetics* 7:510-523].)

Primary responsibilities of the Research Associate are to develop, coordinate and execute pioneering studies relevant to the general theme of research in the Lindroth group. Specific areas of research are open, and candidates will be encouraged to develop new research avenues.

For more information about our current research, see: <http://entomology.wisc.edu/~lindroth/>

Qualifications include expertise in any of the following: plant evolution, chemical analyses, trophic interactions, community genetics, and/or forest ecosystem dynamics. Strong interpersonal, laboratory, statistical and writing skills are essential.

Salary and benefits: \$33,000 - 36,000, commensurate with experience. Excellent family medical/dental health plans available at minimal cost.

Duration of position: two years.

Application: Applications will be accepted through April 15, 2008, or until a suitable applicant is found. Send c.v., names/addresses of three references, representative reprints, and a letter detailing your fit to the position to:

Dr. Rick Lindroth lindroth@entomology.wisc.edu

Dept. of Entomology 1630 Linden Dr. University of Wisconsin-Madison Madison, WI 53706 (608)263-6277

UW - Madison is an equal opportunity employer

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Richard L. Lindroth, Ph.D. Dept. of Entomology 1630 Linden Dr. University of Wisconsin Madison, WI 53706 U.S.A.

Phone: 608-263-6277 Fax: 608-262-3322 E-mail: lindroth@entomology.wisc.edu <http://->

entomology.wisc.edu/~lindroth/
lindroth@entomology.wisc.edu

UWyoming EvolutionaryStructural-Bioinformatics

Postdoctoral Researcher in Evolutionary Structural Bioinformatics

A position is currently available for a postdoctoral researcher in evolutionary structural bioinformatics in the Liberles Research Group at University of Wyoming. The position has guaranteed funding for one year, with extension possible depending upon performance and available funding. Applicants should have skills in programming, knowledge of statistics, knowledge of protein structure and physical chemistry, as well as interest in evolutionary biology and population genetics. Research will involve work at the interface of structural and evolutionary bioinformatics to understand how structure constrains sequence evolution as well as how and why the genome-specific distribution of structures changes between species.

For more details on research in the Liberles Research Group, please see <http://www.wyomingbioinformatics.org/LiberlesGroup>.

To apply, please send a CV, contact information for three references, and 2 .pdf copies of your favorite (significant) papers you have published together with a cover letter to liberles@uwyo.edu.

David Liberles <liberles@uwyo.edu>

UWyoming SalmonComparativeGenomics

Postdoctoral Researcher in Experimental Salmon Comparative Genomics

A position is currently available for a postdoctoral researcher in experimental salmon comparative genomics in the Liberles Research Group at University of Wyoming. The position has guaranteed funding for one year, with extension possible depending upon performance and available funding. Applicants should have

good skills in molecular biology, including DNA extraction, primer design, sequencing, PCR, and Northern and Southern blotting. The applicant will have a chance to work closely with computational researchers and will learn about evolutionary theory and potentially about techniques of growing popularity like ancestral sequence reconstruction/resurrection.

For more details on research in the Liberles Research Group, please see <http://www.wyomingbioinformatics.org/LiberlesGroup>.

To apply, please send a CV, contact information for three references, and 2 .pdf copies of your favorite (significant) papers you have published together with a cover letter to liberles@uwyo.edu.

David Liberles <liberles@uwyo.edu>

Valencia ComparativeGenomics

We are seeking a highly motivated postdoctoral researcher to work in our group at the Instituto de Biomedicina de Valencia (Spain). Lab Website: <http://www.uv.es/~genomica/eng/index.htm> Topic: Comparative genomics and bioinformatics of genes involved in neurodegenerative diseases

The position requires an individual with a PhD and experience in molecular evolution, comparative genomics and/or bioinformatics.

The candidate will apply for his/her own funds to the Juan de la Cierva (<http://www.mec.es/planidi/juandelacierva-eng/>) and/or Ramon y Cajal (<http://www.mec.es/planidi/ramonycajal-eng/>) programmes.

Conditions:

For the Juan de la Cierva Programme: PhD obtained within the last three years or to be obtained within the next months. Funds can be obtained for three years.

For the Ramon y Cajal Programme: PhD obtained within the last ten years. Positions funded for 5 years.

To apply, please send the following:

1. Curriculum vitae
2. Names of 2 referees willing to provide a letter of recommendation upon request
3. A brief statement of your research goals and interests for future grant applications

E-mail applications can be sent to Ignacio Marin: imarin@ibv.csic.es

imarin@ibv.csic.es

Vienna Zebrafish Evolutionary Biol

POST-DOCTORAL POSITION: Behavioral Ecology/Evolutionary Biology Konrad Lorenz Institute for Ethology, Vienna - Austria

We seek a highly motivated and interactive scientist to collaborate with Drs. Sarah Zala and Dustin Penn on research on zebrafish. Specific research topics will be determined based on the interests of the successful candidate. Applicants must have a strong background with fish, behavioral ecology or evolutionary biology and preferably with some experience with molecular genetics or population genetics. Good English skills are necessary (our institute operates bilingually, and English is widely spoken in Vienna). The position is for two years (with the possibility of extension) and the salary depends upon experience. Review of applications begins immediately and the dead line is May 15, 2008.

The Konrad Lorenz Institute for Ethology is located in the Vienna Woods, on the outskirts of Vienna. We work with a variety of fish, bird, mammals and other vertebrates and have excellent fish facilities (see www.oeaw.ac.at/klivv).

To apply, please send (1) a CV, (2) 2-3 publications, (3) a brief statement of research interests and (4) names of three people who can be contacted for letters of reference to the address below:

Alexandra Katzer, Secretary Konrad Lorenz Institute for Ethology - Austrian Academy of Sciences Savoyenstrasse 1a, A-1160 Vienna, Austria Tel: +43 51581 2700, Fax: +43 51581 2800, office@klivv.oeaw.ac.at www.oeaw.ac.at/klivv

WilliamMaryCollege Biomath

This position announcement may be of interest to early career academics who are interested in combing behavioral and evolutionary research with training in undergraduate mentoring and teaching. Please circulate to anyone you think may be interested. Thanks - John Swaddle.

The Department of Biology at the College of William and Mary seeks applications for a one year (which could be extended to two years) Visiting Assistant Professor postdoctoral position in biomathematics. The candidate should be trained in modeling approaches to population ecology and evolution and exhibit a sincere commitment to undergraduate education and research. Specifically, the biomath postdoc will mentor undergraduates in quantitative and modeling projects, related to population ecology and evolution, and collaborate with faculty in the biology, mathematics, and applied science departments on new and existing research projects. The postdoc will also help develop lab activities associated with an introductory biomathematical modeling class. Therefore, some experience of empirical systems is strongly desired. More information about ongoing projects can be found on the faculty research pages of the Biology (www.wm.edu/biology), Mathematics (<http://www.wm.edu/mathematics/index.php>), and Applied Science departments (www.as.wm.edu).

Informal enquiries and requests for more information

should be directed to Dan Cristol (dacris@wm.edu) or John Swaddle (jpswad@wm.edu) in the Biology department. Review begins April 10, 2008 and will continue until an appointment is made. Submit a letter of application, curriculum vitae, statements of research plans and teaching philosophy, and contact information for three references to Dan Cristol, Biomathematics Search, Department of Biology, The College of William and Mary, P.O. Box 8795, Williamsburg, VA 23187-8795, or by email to dacris@wm.edu. Electronic applications are encouraged. The College is an EEO/AA employer.

Dr. John Swaddle

Before June 2008: Sabbatical Fellow National Center for Ecological Analysis and Synthesis 735 State Street, Suite 300 Santa Barbara, CA 93101 Office: 805-892-5035 Cell: 757-272-2124 Fax: 805-892-2510

After June 2008: Director of Environmental Science and Policy Program Biology Department College of William & Mary Williamsburg, VA 23187-8795 Office (Biology): 757-221-2231 Office (Env Sci): 757-221-2096 <http://jpswad.people.wm.edu/> jpswad@wm.edu

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Budapest BayesianPhylogeny Jun25-29

Dear Colleagues,

we would like to cordially invite you, your colleagues and students to participate in the Bayesian Phylogeny Workshop, which will be held at the Renyi Institute, Budapest, Hungary, from the 25th of June till the 29th of June, 2008.

The goal of the conference is to give a comprehensive overview of Bayesian phylogeny and its widely used

techniques like Markov chain Monte Carlo. Each day will be dedicated to a specific topic. The topics will be introduced by top-qualified researchers during the morning sessions, the afternoon sessions are devoted to discussions, software demos, tutorials and short presentations. We encourage MSc and PhD students to participate in this workshop, where they can significantly improve their knowledge and skills in the topic.

There is no registration fee for this workshop; however, registration is necessary due to the limited space. Therefore if you would like to participate in the workshop, please register as early as possible. Proposals for short talks are welcome. The homepage of the conference is

<http://www.renyi.hu/conferences/bp2008/> Istvan Miklos <miklos@stats.ox.ac.uk>

CornellU MarinePhylogenomics

Cornell University, Shoals Marine Laboratory, Appledore Island, Maine, USA. <http://www.sml.cornell.edu/> MARINE PHYLOGENOMICS: BIOSM 472, is an intensive four-credit laboratory- and field-oriented summer course aimed at helping motivated undergraduate students and working professionals integrate advances in molecular biology and genomics with field-based research in ecology and evolution. Appledore Island is situated in the Isles of Shoals archipelago ten miles off the New England coast in the heart of the Gulf of Maine. The archipelago is rich in biological diversity, seabird and marine mammal breeding areas and has a long and colorful maritime history. The Shoals Lab hosts a vibrant and diverse international community of students and investigators throughout the summer field season in an intimate island setting immersed in natural history and regional culture. The course enjoys full tech support from Cornell University, Harvard University, and the nearby Hubbard Center for Genomics Research at the University of New Hampshire.

Dates: JULY 21 - AUGUST 4, 2008 Credit Hours: 4 semester credits Total Cost: \$3,769 (includes room, board and tuition)

Prerequisites: One year of college-level biology. Recommended: Genetics and/or cell biology with laboratory components. Helpful: Evolutionary biology, ecology, invertebrate or vertebrate zoology.

An introduction to basic concepts in systematic biology, comparative genomics, evolutionary genetics, molecular ecology, and conservation biology emphasizing the natural history of marine organisms. Students integrate field sampling techniques, taxonomy, and curation of specimens from Appledore Island and surrounding waters with molecular diagnostics and bioinformatics completed in the laboratory. Standard methods for DNA purification, amplification, sequencing and genotyping are used to address questions about population structure, kinship, and species phylogeny.

Faculty: Dr. Andrew M. Shedlock Harvard University, Museum of Comparative Zoology, Depts. Organismic & Evol. Biol. and Molec. & Cell Biol. Email: shedlock@oeb.harvard.edu

Objectives: * Explore the genetic basis of biological diversity in the Gulf of Maine * Learn basic theory and applications in the emerging field of phylogenomics * Design and execute field sampling of specimens for molecular research * Extract, purify and curate DNA samples for comparative analysis * Complete amplification, genotyping and sequencing of DNA samples * Use informatics, model genome databases, and software to analyze DNA results * Test hypotheses of relationship and demographics using genetic markers * Summarize findings with a research proposal and brief scientific communication.

Tentative Guest Lectures: Steve Bogdanowicz (Cornell) - Molecular Markers in Population Analysis Chris Botka (Harvard Med School) - Bioinformatics and Genome Databases Jim Coyer (U. Groningen) - Benthic Community Ecol. & Genetics Scott Edwards (Harvard) - Seabird Molecular Ecol. & Evol. Akiko Okutsu (Simmons) - Marine Invertebrate Phylogeography Hal Weeks (Cornell) - Marine Fisheries Ecol. & Evol.

shedlock@oeb.harvard.edu shedlock@oeb.harvard.edu

Guarda EvolBiol Jun21-28

“Evolutionary Biology in Guarda 2008” is open for registration.

It is my pleasure to announce this years Guarda workshop in Evolutionary Biology. The main aim of this 1 week course is to develop the skills to produce an independent research project in evolutionary biology. The course is for master students and first or second year PhD students with a keen interest in evolutionary biology.

Course dates: 21. - 28. June 2008 (Saturday to Saturday). Location: The village Guarda in the Swiss Alps.

Course faculty * Dr. David Haig (Harvard University, USA) * Dr. Bruce Levin (Emory University, Atlanta, USA) * Dr. Sebastian Bonhoeffer (ETH Zürich) * Dr. Dieter Ebert (Basel University) (course organizer)

For more information: <http://www.evolution.unibas.ch/teaching/guarda/> Please communicate this information to interested students.

If you receive this email twice, please excuse me.

With best wishes

dieter ebert

—

Dieter Ebert [[Mailto:dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch)] <http://evolution.unibas.ch/> Universität Basel, Zoologisches Institut, Evolutionary Biology Vesalgasse 1 4051 Basel, Switzerland Tel. +41-(0)61-267 03 60 FAX +41-(0)61-267 03 62

dieter.ebert@unibas.ch dieter.ebert@unibas.ch

Kristineberg Sweden MarineGenomics Jul15-24

A Marine Genomics Europe summer course Analysing Biodiversity & Life History Strategies 15th - 24th of July, 2008 Sven Lovén Centre for Marine Science - Kristineberg (Former Kristineberg Marine Research Station) Fiskebäckskil, Sweden

Info doc & application form at www.marine-genomics-europe.org

Deadline for application is May 19, 2008

Aims to present the diversity of animal life in the ocean and introduce the latest methods in analyzing this variation. To foster cross-over between ecological/whole-organism and molecular approaches.

Topics

Diversity of meiofauna, phylogenomics, phylogeography of marine species, DNA barcoding and modern taxonomy, marine life cycles and larval diversity, reproductive systems in marine invertebrates, biodiversity indices and marine communities

General outline

The goal of the course is to introduce the participants

to the diverse marine fauna of the Swedish west coast and debate current topics in biodiversity research and developmental biology. The course has a rather broad focus and will concentrate on methods and applications in these fields, while less emphasis will be placed on theoretical backgrounds. Principally we will use the mornings for lectures given by experts in the field and the afternoons for practical work such as software exercises and wet labs. The course focuses almost exclusively on marine invertebrate animals.

Target group

PhD students (at least in their second year) and post docs with basic knowledge in phylo- and population genetics. This course is open to MGE members as well as non-members.

Costs; course, accommodation and meals

The course fee is paid by the MGE Network for all academics (pre and post doc). Lunches and coffees are included in the course fee as well as the excursion (Sunday the 20th) and the farewell dinner (Thursday the 24th). All participants pay their own travel and accommodation. Participants are offered (and encouraged as there are no real options around) to be accommodated at the station. The costs for this is approx 70 ??? in single room and 60 ??? in double room per night including breakfast and supper.

Application

To apply, please fill in the application form and e-mail to Ulrika Hjelm (ulrika.hjelm@kmf.gu.se), together with a 2-page CV before May 19, 2008. This information + application form can also be found on the MGE website: www.marine-genomics-europe.org < <http://www.marine-genomics-europe.org/> > under Training & Education.

Matthias Obst, PhD Göteborg University Sven Lovén Centre for Marine Sciences Kristineberg 566 450 34 Fiskebäckskil Sweden Tel: +46 (0) 523 18553 Fax: +46 (0) 523 18502 Email: Matthias.Obst@biology.au.dk or matthias.obst@zool.gu.se

Matthias Obst <matthias.obst@kmf.gu.se>

NESCent Computational Phyloinformatics Jul24-Aug4

Computational Phyloinformatics: A Course at NESCent. 24 July - 4 August 2008

<http://www.nescent.org/courses/2008/comphy/>

Course Director: William Piel (piel@treebase.org)
 Course Administrator: Jory Weintraub (jory@nescent.org)
 Organizing Committee: Hilmar Lapp, William Piel, Todd Vision, Jory Weintraub

Computational Phyloinformatics is a 10-day summer course sponsored by and held at the National Evolutionary Synthesis Center (NESCent) in Durham, North Carolina (USA) that 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 more elaborate analytical methods. Seldom is it sufficient to run a dataset through 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, Java, or R for phyloinformatics applications.

The course is divided into three parts:

- Part I: A tutorial review of either Perl, Java, or R (while optional, this part is strongly recommended).
- Part II: Students have the choice of pursuing (1) a Perl track, with focus on BioPerl and Bio::Phylo; (2) a Java track, with focus on how to write a Mesquite module and program workflows that utilize Mesquite modules; or (3) an R track, with a focus on comparative phylogenetic analysis using the libraries Ape, Ouch, and Phylobase.
- Part III: Students choose between (1) a database track (with focus on SQL, BioSQL and database queries of phylogenetic trees); (2) a HyPhy track (with focus on scripting molecular evolution hypothesis tests in a phylogenetic framework); or (3) an advanced R track (with focus on automating analyses using vectorized calculations, advanced plotting and animations, and the R-LaTeX document system using Sweave).

Students in all tracks 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 (depending on the track) such as alignment of large numbers of sequences, ancestral state reconstruction, testing for positive selection, etc.

INSTRUCTORS James Balhoff, Marguerite Butler, R. Todd Jobe, Hilmar Lapp, Darin London, David Maddi-

son, Spencer Muse, Jeff Oliver, Brian O'Meara, William Piel, Sergei L. Kosakovsky Pond, Ryan Scherle, Todd Vision, Rutger Vos

PREREQUISITES Biology: A solid understanding of phylogenetics - for example, having already taken the Workshop on Molecular Evolution (<http://www.molecularevolution.org/>) or equivalent coursework or experience. Computing: Prior experience with Perl, Java, or R; 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 their own Mac OSX computer (a limited number of loaners are available upon request).

FEES Tuition is \$600.00. Accommodation is \$50/night for a single occupancy apartment, \$26/night for double occupancy apartment in housing provided at Duke University (students are also free to make their own housing arrangements). Travel awards of up to \$450 each are available to subsidize travel expenses for applicants from underrepresented groups.

HOW TO APPLY Apply through the course website (<http://www.nescent.org/courses/2008/comphy/>). You will be asked to provide a resume, two references, a brief description of your computational and phylogenetic background, and your reasons for taking the course. Applications are due by April 15, 2008. International students may wish to apply for Travel Awards from the Society of Systematic Biologists (due date: March 31, 2008, see website for details).

william.piel@yale.edu william.piel@yale.edu

NESCent GMOD Jul11-13

GMOD Summer School July 11-13, 2008 National Evolutionary Synthesis Center (NESCent) Durham, North Carolina, USA

The first GMOD Summer School (http://gmod.org/-GMOD_Summer_School) will be held July 11-13, 2008 at the National Evolutionary Synthesis Center (NESCent), in Durham, North Carolina, USA. GMOD is a collection of interoperable open source software components for managing genomic data. GMOD components are used in diverse contexts, with both emerging and established model organisms.

The course will provide an overview of GMOD and cover these popular components in detail: * Chado - a modular and extensible database schema * Apollo -

genome annotation editor * GBrowse - genome viewer
 * CMap - comparative map viewer * Community Annotation System - GMOD's most popular components in a single system

This is a 2 1/2 day hands-on workshop aimed at teaching new GMOD users how to get up and running with popular GMOD components. There will also be a concurrent 1 day session aimed at principal investigators that will give decision makers an overview of what GMOD can do, how the project operates, and what level of resources are needed to use GMOD.

The National Evolutionary Synthesis Center (NESCent, <http://nescent.org>) has joined the GMOD project with the goal of lowering the barrier to entry for research communities focused on emerging model organisms. The GMOD Summer School is a part of this effort. NESCent is also extending GMOD components, particularly Chado, to better support comparative and evolutionary data.

If you are interested in attending the GMOD Summer School please submit a Statement of Interest before April 15, 2008. The course is free but enrollment is limited. For application information and a tentative program see:

http://gmod.org/GMOD_Summer_School Please let me know if you have any questions, comments, or requests.

Thanks,

Dave Clements GMOD Help Desk help@gmod.org
clementsnescent@gmail.com

Portugal EvolutionaryCellBiol May9-10

Announcing: Workshop in Evolutionary Cell Biology - May 9 & 10 (2008), Portugal.

Date: May 9th- 10th, 2008 Location: Instituto Gulbenkian de Ciencia, Oeiras Portugal (a small seaside village close to Lisbon and its international Airport) Cost: free

An exploratory workshop on the intersection of evolution and cell biology, organised in the context of the PhD Program in Computational Biology.

Confirmed Participants include: -Andrew Murray - Eugene Koonin -Martijn Huynen -Mark Field, Joel

Dacks -Patricia Beldade.

The target audience are cell and evolutionary biologists interested in crossing the boundaries of each other's disciplines.

Registration is free but necessary.

Details and registration on www.evocell.org/-evocell2008 Jose Pereira Leal, PhD Computational Genomics Laboratory & Bioinformatics and Computational Biology Unit Instituto Gulbenkian de Ciéncia Apartado 14 P-2781-901 Oeiras Portugal

phone: +351 21 446 4528 fax: +351 21 440 7973

<http://www.evocell.org>

bioinformatics.igc.gulbenkian.pt

jleal@igc.gulbenkian.pt

<http://->

Roscoff MarineEvolutionaryGenomics Jun16-27

MGE Summer Course Marine Evolutionary & Ecological Genomics June 16th-27th, 2008 Station Biologique de Roscoff, France

Aims: to give an introduction on genomic approaches to analyze genetic variation 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 - molecular evolution through sequences, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies * Population genetics - molecular evolution through allele frequencies, population genetic techniques (structure, selection, gene flow, bottlenecks, assignment), 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. What is environmental 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) 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). Lunches and coffees are included in the course fee as well as the excursion (incl dinner) and farewell dinner. * All participants pay their own accommodation and travel. * 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 supper for a cost of ???5.50 per person and meal.

Application: To apply, please fill in the application form and e-mail to Ulrika Hjelm (<mailto:ulrika.hjelm@kmf.gu.se> ulrika.hjelm@kmf.gu.se), together with a 2-paged CV before April 14, 2008. 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. Relation to network
2. Relevance of project for the course
3. Background and experience of applicant

We aim at mixing people from different research areas and therefore, in the cases of MGE applicants, probably no more than one person per partner will be considered. We will also aim at an equal distribution of women and men.

The selected persons will get 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.

Confirmed teachers Sandie Baldauf, Univ of York, UK Galice Hoarau, Univ of Groningen, NL Michael M. Hansen, Danish Institute for Fisheries Research, DK Wiebe Kooistra, SZN, IT Jeanine Olsen, Univ of Groningen, NL Frederique Partensky, SB-Roscoff, FR Klaus Valentin, AWI-Bremerhaven, DE Anti Vasemägi, Univ of Turku, FI Frédérique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

Organizing committee Ulrika Hjelm, KMRS, SE Hélène Huelvan, SB-Roscoff, FR Jeanine Olsen, Univ of Groningen, NL Arnaud Tanguy, SB-Roscoff, FR Frédérique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

Contact person Ulrika Hjelm Training & Education Programme Manager Kristineberg Marine Research Station S-450 34 Fiskebäckskil Sweden Phone: ++46 (0) 523 18548 Fax: ++46 (0) 523 18502 Mobil: ++46 (0) 70 344 2371 E-mail: ulrika.hjelm@kmf.gu.se

Disclaimer: http://www.kuleuven.be/-cwis/email_disclaimer.htm Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

SanDiego DrosophilaGenomics Apr5

Dear colleagues,

Chuck Langley, Chip Aquadro, and I are organizing a workshop at the annual Drosophila Research Conference in San Diego on “Drosophila Population Genomics” (Saturday night Apr 5), with emphasis on:

1. complete genome resequencing and targeted regional sequencing of multiple lines —trade-off of depth vs. sample size —efficacy of recovery of frequency spectrum
2. shared recombinant populations, collaborative cross designs, and RI lines —value of shared genotyping and phenotyping of such lines
3. genome-wide SNP arrays - how many SNPs, how to pick them, market size?

A particular emphasis is to identify mechanisms whereby junior faculty perceive easy and inviting paths to be part of these projects.

Anyone is invited to speak, very informally, about any of these topics, with priority for folks with direct experience and data to show. In order to help organize things, please email the three of us giving a clue regarding the topics you would like to cover. We will also be fingering a few people to round things out. We want to encourage open discussion as well.

Please share this note with other lab members and anyone else you think might have an interest.

Andy Clark Chip Aquadro Chuck Langley
ac347@cornell.edu ac347@cornell.edu

Singapore ComputationalBiol
Aug10-16

UMassAmherst ComparativeBiol
May31-Jun7

Dear Colleagues,

We are pleased to inform you about the upcoming workshop:

“Computational biology: From genomes to cells & systems”

in Singapore sponsored by the EMBO World Practical Course program.

The 7-day workshop (August 10-16th 2008) introduces advanced methods and applications in computational biology ranging from molecules to cellular systems.

Participation is restricted to 20 graduate students and postdocs, who will work on biological problems that could even lead to scientific discoveries made during the course. For all participants, fellowships will be made available covering housing, subsistence and registration. No funding are available for travel costs.

Further information and registration: at <http://cwp.embo.org/wpc08-08> Email: genomes2ecosystems@googlegroups.com

Yours

francesca ciccarelli, for the organizers*

* Organizing Committee of the EMBO Workshop on Computational biology: “From genomes to cells & systems” Singapore, Temasek LifeSciences Laboratory, August 10-16, 2008:

Dr. Peer Bork, EMBL Heidelberg, Germany
Dr. Frank Eisenhaber, Temasek Life Sciences Laboratory, Singapore (Local Organizer)
Dr. Francesca D. Ciccarelli, EIO Milan, Italy
Dr. Jan Korbel, Yale University, New Haven, CT USA
Dr. Roland Krause, Max-Planck-Institute Berlin, Germany

– Francesca D. Ciccarelli, PhD Biocomputing IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303-053 fax +39-02 94375990 web: <http://ciccarelli.group.ifom-ieo-campus.it/fcwiki/>

3-Dimensional Model Building for Finite Element Analysis: A Workshop for Comparative Biologists

Date: May 31st - June 7th, 2008 Location: University of Massachusetts, Amherst Cost: \$800 USD (students), \$1,050 (non-students)

Finite element analysis (FEA) is a technique that uses 3-dimensional computer models to analyze and predict how structures will behave under physical stresses and loads. For biologists the method holds great promise for the analysis of systems such as skeletal bone, arthropod exoskeleton, or any other system in which behavior under load is of interest. One factor that has limited the use of FEA for biological research is the overwhelming shape complexity of most biological structures; the capabilities of computers and software have often proven unequal to the task of performing these analyses. Recently, new software and advances in computing power have greatly improved our ability to perform FEA on biological systems. This workshop will introduce attendees to the methods and software that have allowed us to do this, and ideally will allow them to build and analyze their own model from a stack of CT slice images. You can see the results of last year’s workshop at this link: FEA workshop 2007 < http://www.biomesh.org/-workshop07_report.phtml >.

Attendees will learn to use VGStudioMax 1.2, Geomagic Studio 10.0, and the Strand7 FEA package to build, simplify, and analyze a 3-D model of their data, all in the space of a week! Workshop cost includes dorm-room lodging and most meals. Space is limited.

Contacts: Betsy Dumont - bdumont@bio.umass.edu
Ian Grosse - grosse@ecs.umass.edu

Learn more about FEA in Biology at: www.biomesh.org – Dr. Elizabeth (Betsy) Dumont Associate Professor Department of Biology - UMass Amherst 221 Morrill Science Center Amherst, MA 01003

Phone: 413 545-3565 Fax: 413 545-3243 Website: www.biomesh.org

UMuenster EvoluitonaryBiol Summer

Dear EvolDir members

please feel free to distribute this information among Master students and early PhD students that you might think maybe interested. Thanks a lot!

Ignacio G. Bravo ---

The school The Bernhard-Rensch Summer School on Evolutionary Biology is organised by the Institute of Evolution and Biodiversity (<http://www.uni-muenster.de/Evolution/>) of the University Muenster (<http://www.uni-muenster.de/de/index.html>), and sponsored by the Volkswagen Foundation (<http://www.volkswagen-stiftung.de/>).

The aim The interest of the Bernhard-Rensch Summer School is Evolutionary Biology, in an open and broad sense. Interaction between students from different fields/orientations is explicitly wanted and encouraged.

The topic The specific topic this year will be phylogenetic reconstruction and deep phylogenetic relationships. Students working in a related topic will be invited to present their research in a short talk.

Evolution and the philosophy of biology The Summer School also wants to be a meeting point for students interested in the philosophy of science. Since evolution is the integrative framework for biology as a science, we could say that evolution is the philosophy of biology. We will discuss and share views on the structure of science and scientific theories, the paradigms of evolution and the position of evolutionary theory in present times.

The work during the summer school Each student should bring the own laptop. Tasks will include training in interdisciplinary components, improving transferable skills (writing, presenting, planning projects), team-work, working with scientific literature, developing a concept of philosophy of science.

The place The Summer School will take place at the marine biological station in Carolinensiel (<http://www.uni-muenster.de/Biologie.Zoophysiology/> Station/), located in the Wadden Sea National Park in Lower Saxony (<http://www.nationalpark-wattenmeer.niedersachsen.de/>

[master/C5912120_L20_D0.html](#)). Carolinensiel is not too easy to reach by public transportation. We will try to arrange a bus or to pick you up at Wittmund (details to be specified later on with the participants).

The timing From June 30th (Monday) to July 11th (Friday). Arriving date June 29th (Sunday) and leaving date July 12th (Saturday).

The faculty Herve Philippe (Montreal) Olaf Bininda-Emonds (Oldenburg) Walter Salzburger (Basel) Thorsten Reusch (Muenster) Erich Bornberg-Bauer (Muenster) Joachim Kurtz (Muenster) Ignacio G. Bravo (Muenster, Summer School coordinator)

The costs There will be a fee of approximately 200 euros per person, including accommodation and food. Travel expenses are not covered. Exact price will depend on the final number of participants, but will not differ much. Price will be paid in advance. Details will be later on specified with the participants.

The students The summer school is open for students from the MSc in Biologie at the University Muenster as a Masters Module. Master students and early PhD students from anywhere else are welcome to apply (final number of students around 22).

The application Deadline is April 30th. Please send an email including a short description of your scientific career and interests to igbravo@uni-muenster.de. Please include all the relevant information in the body of the email. Do not include attachments. Shortlisted students will be contacted by May 15th. Definitive participation will be subject to payment of course fees.

Ignacio González Bravo

Experimental Molecular Evolution Institute for Evolution and Biodiversity Westfaelische Wilhelms University Muenster Hüfferstrasse 1 48149 Münster Germany

phone +49 251 83 21637 +49 251 83 21027 (Secretary Ms Hitziger) fax +49 251 83 24668

email address: igbravo@uni-muenster.de

<http://www.uni-muenster.de/evolution/expmolevol/>
igbravo@uni-muenster.de

UVirginia EvolBiology Summer2008

ANNOUNCING: MLBS Summer 2008 Field Course

Opportunities Mountain Lake Biological Station
MLBS.org

Dear Colleagues, Students, and Friends,

Mountain Lake Biological Station (University of Virginia) is pleased to announce its 13-week summer program of field-based undergraduate and graduate-level credit courses and workshops offered by nationally recruited faculty. Learn more about the programs, complete an on-line applications, or download a flier to post: Course web page - <http://mlbs.org/courses.html>

Flier to Post -

<http://mlbs.org/download/MLBS.Poster.pdf> Please forward this information to colleagues or students you think might be interested. Thanks for your help! Best wishes, Butch Brodie, Director Eric Nagy, Associate Director **** Learn all about Mountain Lake opportunities at MLBS.org ****

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake Biological Station Research Assistant Professor, Department of Biology University of Virginia / P.O. Box 400327 Charlottesville, VA 22904-4327 USA street address: 485 McCormick Road / 219 Gilmer Hall tel: +1-434-243-4989 (+1-540-626-5227 summer) fax: +1-434-982-5626 (+1-540-626-5229 summer) cel: +1-434-906-3122 eml: enagy@virginia.edu

skype: flightofthesandor web: faculty.virginia.edu/nagy

MLBS web page: mlbs.org

enagy@virginia.edu

Venezuela AntEvolution Aug9-19

ANT COURSE 2008

ANT COURSE 2008, August 9- 19, Estacion Biologica Alberto Fernandez Yepez, Rancho Grande, Parque Nacional Henri Pittier, Aragua, Venezuela

In 2008 the courses focuses on the Ants of South America. English and Spanish are the official languages.

DEADLINE FOR APPLICATION: April 1, 2008

<http://www.antweb.org> COURSE OBJECTIVES. ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy. Emphasis is on the

classification and identification of more than 115 ant genera of South America. Lectures will include background information on the ecology, life histories and evolution of ants. The course also addresses the conservation of ants and their role as bioindicators and their importance in agroecosystems such as coffee and cocoa. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the major ant genera of South America; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the diversity of ants and their role in ecosystems, and 4) experience keying to the species level.

SPONSORS. California Academy of Sciences, Museum of Comparative Zoology, with funding in part from National Science Foundation.

BACKGROUND INFORMATION. ANT COURSE will be taught from August 9 19, 2008 at the Estacion Biologica Alberto Fernandez Yepez, Rancho Grande, Parque Nacional Henri Pittier, Aragua, Venezuela. The Station is centered amid one of the richest ant faunas in South America. This course is offered annually, and in 2008 the focus is on South American ants.

PARTICIPANT ACCEPTANCE CRITERIA. ANT COURSE is open to all interested individuals. Priority will be given to those students for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE 2008 will be presented in English as well as Spanish and is limited to 30 participants.

COSTS. Tuition for the 10-day COURSE is \$325 for current students and \$675 for non-students. In addition Rancho Grande Station fees for this period, covering dormitory room and board, are estimated at \$240. Transportation costs between home and Maracay or the nearby airports of Valencia or Maiquetia are to be borne by all participants.

FELLOWSHIPS. Four fellowships are available for 2008. Two fellowships cover tuition fees and two fellowships cover station fees. Students may apply for additional fellowships to assist in travel. Those inter-

ested in attending the course should seek all possible avenues to secure funding for the course. You should only apply for the Ant Course fellowship if you can not find other support and it is essential for your participation in the course. Beware that if you apply for an ant course fellowship it implies that fellowship funding is essential to your participation in the course. Thus, if you are not selected for a fellowship, you might not be accepted into the course. Please notify the course if your funding request status changes before the application due date.

COURSE APPLICATION. Find an application form in pdf or doc format posted on <http://www.antweb.org>. Send the COMPLETE application with subject line Ant Course application to bfisher@calacademy.org.

IMPORTANT DATES: Aug. 8 For those arriving to Maiquetia airport. Aug. 9 Travel to Rancho Grande field station Aug. 19 Graduation and farewell party Aug. 20 Departure at 8 am to airports (Maiquetia and Valencia)

2008 INSTRUCTORS (tentative): Brian Fisher (Coordinator), Dept. of Entomology, California Academy of Sciences, San Francisco, CA, USA, bfisher@calacademy.org John Lattke (Coordinator), Museo Inst.Zoología Agrícola, Universidad Central de Venezuela, Apartado 4579, Maracay 2101-A, VENEZUELA, piquihuye@fastmail.fm

Inge Ambrecht, Departamento de Biología, Universidad del Valle, Apartado Aereo 25360, Cali, Colombia Leeanne Alonso, Rapid Assessment Program, Conservation International, Washington, DC, USA Beto Brandao, Museu de Zoologia da Universidade de Sao Paulo, Av. Nazare 481, Sao Paulo SP, BRASIL 04263-000 Fabiana Cuezco, Instituto Superior de Entomología (INSUE), Facultad de

— / —

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>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.