EvolDir

April 1, 2010

Month in Review

Foreword

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

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

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

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Conferences

Amsterdam EvolutionaryMedicine Apr1

Dear colleague,

On April 1st 2010, the Royal Netherlands Academy of Arts and Sciences (KNAW) hosts a full day symposium on Evolutionary Medicine. It gives a excellent overview of current research in evolutionary medicine and human evolutionary genetics in the Netherlands. For more information, location, and the program, please see: http://www.healthy-ageing.nl/UserFiles/file/KNAW_Evolutionary_Medicine_F inal_Invitation.pdf

Admission if free but please register by email at a.peters@aig.umcn.nl

"The role of evolution in health and disease is a relatively neglected area of research. In daily practice of clinical medicine virtual no attention is paid to the notion that modern human disease often has an important evolutionary component. This symposium is meant to explore the effects of evolution on human health and will attempt to bring together the available information from different disciplines."

Organisers: Jos W.M. van der Meer Jan P. Vandenbroucke Mihai G. Netea Rudy Westendorp

On behalf of the organisers,

Jeroen Pijpe, PhD

Leiden University Medical Center Department of Human Genetics Forensic Laboratory for DNA Research

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Beijing PlantSystematicsEvolution Jul7-9

New Frontiers in Plant Systematics and Evolution Beijing, China July 7-9, 2010

FIRST ANNOUNCEMENT

Objectives Systematic biology faces tremendous challenges and opportunities at the present time. This conference aims at providing an opportunity for plant systematists and evolutionary biologists to review the progress, evaluate the current status, and look into the future of the field. China hosts enormous plant diversity that has supported its long history and continuous advancement in studying plant systematics. With especially rapid progress made during the recent years, 2010 comes to be the time for China to invite colleagues from the world to discuss the new frontiers of systematic biology. This would provide an ideal forum for Chinese and international colleagues to present research results, exchange ideas, discuss common interests, develop collaborations, stimulate young students, and move the field of systematic biology forward. The conference will include talks, posters, and open discussions on recent progress and future directions of the following areas: 1) Taxonomy, collections, and databases; 2) Phylogenetics, phylogenomics, and the Tree of Life; 3) Biogeography and phylogeography; 4) Speciation, hybridization, and adaptation; 5) Molecular evolution, evolutionary genetics and genomics, and Evo-Devo.

Organizers Botanical Society of China (BSC) Chinese Academy of Sciences (CAS) International Association for Plant Taxonomy (IAPT)

Conference Venue The conference will be held at the Xiangshan Jinyuan Hotel. This five-star hotel is located in the southeast foot of the Fragrant Hill (Xiangshan), one of Beijing's most famous scenic and historical sites. It stands near the precious royal garden with 800 years of history, beautiful landscapes, and elegant environment. The hotel is within walking distance to the Beijing Botanical Garden and the Institute of Botany, the Chinese Academy of Sciences.

Confirmed International Speakers Richard Abbott (University of St. Andrews, UK) Bruce Baldwin (UC Berkeley, USA) Spencer CH Barrett (University of Toronto, Canada) David Baum (University of Wisconsin, USA) Daniel Crawford (University of Kansas, USA) Claude DePamphillis (The Pennsylvania State University, USA) Mitsuyasu Hasebe (National Institute for Basic Biology, Japan) Elizabeth A. Kellogg (University of Missouri, USA) David Mabberley (Royal Botanic Gardens, Kew, UK) Thomas Mitchell-Olds (Duke University, USA) Rémy J. Petit (National Institute for Agricultural Research, France) Yin-long Qiu (University of Michigan, USA) Richard Ree (The Field Museum, Chicago, USA) Tao Sang (Michigan State University, USA) Doug Soltis (University of Florida, USA) Pam Soltis (Florida Museum of Natural History, USA) Peter Stevens (Missouri Botanical Garden, USA) Tod Stuessy (University of Vienna, Austria) Warren L. Wagner (Smithsonian Institution, USA) Jun Wen (Smithsonian Institution, USA) Jenny Xiang (North Carolina State University, USA)

Contact Information Conference Secretariat Institute of Botany, Chinese Academy of Sciences 20 Nanxincun, Xiangshan, Beijing 100093, China Email: fengmin@ibcas.ac.cn, zouxh@ibcas.ac.cn Fax: +86-10-62590843

http://www.syst-evol.cn Qiu-Yun (Jenny) Xiang, Ph.D. Associate Professor Department of Plant Biology North Carolina State University Gardner Hall 2115 Raleigh, NC 27695-7612 USA Phone: 919-515-2728 Fax: 919-515-3436 Homepage: http://www4.ncsu.edu/~qyxiang > >

Jenny Xiang <jenny_xiang@ncsu.edu>

Berlin Biosystematics Feb21-27

Biosystematics: Berlin, 21 â 27 February 2011

www.biosyst-berlin-2011.de The Botanic Garden and Botanical Museum at the Freie Universität Berlin (BGBM) and the Museum für Naturkunde, Leibniz Institute for Research on Evolution and Biodiversity at the Humboldt- Universität Berlin (MfN), are pleased to be the host institutions for the 7th International Congress of Systematic and Evolutionary Biology (ICSEB VII), 12th Annual Meeting of the Society of Biological Systematics (Gesellschaft für Biologische Systematik, GfBS), and 20th International Symposium âBiodiversity and Evolutionary Biologyâ of the German Botanical Society (DBG).

The scope of this joint congress is to bring together evolutionary biologists and systematists working on plant, animal, and microscopical organisms to discuss and debate topics of common interest. The focus will be on innovative and forward-looking ideas, concepts, and methods in systematic and evolutionary biology. It will also provide a unique opportunity to highlight topics of biodiversity. We hope to attract many researchers from different fields to this congress and look forward to welcoming you in Berlin in February 2011.

Venue The congress will be held at the Seminaris Science & Conference Center conveniently located in Berlin-Dahlem, on the campus of the Freie Universität Berlin.

Topics The congress will open with a plenary lecture on Paradigm Shifts in Systematics and Evolution. Further plenary talks will be on the following five major conference topics: â Trends in Taxonomy â Evolution and Organisms in Time and Space â The Evolutionary Thought: History, Philosophy and Society â Evolution of Form and Function â Inventorying and Managing Biodiversity An evening lecture on Alexander von Humboldtâs scientific work on tropical biodiversity will be given.

Call for Symposia Proposals for symposia are currently being invited. For submitting a proposal, please contact the congress office at berlin2011@bgbm.org. Proposals corresponding to the five major conference topics are especially encouraged, but all relevant topics will be considered by the organizers. The deadline for submission of symposia proposals is 31 May 2010.

Contributed Papers and Call for Abstracts The contribution of papers for oral or poster presentations are encouraged. All participants interested in presenting a scientific contribution are kindly requested to submit a one-page abstract in English to the congress office together with their registration. Abstract submission and registration start 1 July 2010, deadline for abstracts and early registration is 30 September 2010.

Workshops and Satellite Meetings Pre- and post-congress workshops are planned on different topics and will be announced in the second circular. Organizers of additional workshops and satellite meetings are welcome. Please contact the congress office at berlin2011@bgbm.org. Deadline for workshop proposals is 31 May 2010.

Time Schedule and Deadlines 31 May 2010 Call for workshops & symposia closes 1 July 2010 Abstract submission and online registration opens 30 September 2010 Deadline for submission of abstracts and early registration 21 â 27 February 2011 Congress For individual pre-registration please contact the congress office. Your coordinates will be added to our mailing-list.

Organizing Committee Prof. Dr. Thomas Borsch (IOSEB President, BGBM) Dr. Regine Jahn (GfBS President, IOSEB Secretary General, BGBM) Prof. Dr. Dirk Albach (Section âBiodiversity and Evolutionary Biologyâ of DBG, Speaker) Dr. Peter Giere (GfBS Council, MfN) Prof. Dr. Werner Greuter (IOSEB Council, BGBM) Dr. Christoph Häuser (MfN) Jana Hoffmann (GfBS Council, MfN) Dr. Cornelia Löhne (BGBM) Dr. Diana Mutz (Dahlem Centre of Plant Sciences, DCPS) Dr. Michael Ohl (GfBS Secretary General, MfN) Congress Office and Contact Birgit Nordt, berlin2011@bgbm.org Mailing address: Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin Königin-Luise-Str. 6-8, 14195 Berlin, Germany Phone: ++49/30/838 50 383, Fax: ++ 49/30/841 729 52

Chris Cameron <ccameron@bms.bc.ca>

Braga Portugal DNABarcoding Jun2-4

Dear Colleagues

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

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

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

Sincerely,

Filipe Costa

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

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

Mónica Landi <mlandi@bio.uminho.pt>

Braga Portugal DNABarcoding Jun2-4 DeadlineExtended

Dear Colleagues

The Organizing Committee thanks all the abstract submissions to 2nd Conference of the European Consortium for the Barcode of Life (ECBOL2).

Due to some difficulties in the online registration and abstract submission website during the last week, the deadline for abstract submission has been postponed to the 15th of April.

We hope this extra time will encourage more of you to consider participating and to submit your abstracts as soon as possible on the conference website.

We are very pleased to announce our confirmed invited speakers:

Bob Ward (CSIRO, Australia)

Paul Hebert (University of Guelph, Canada)

Pete Hollingsworth (Royal Botanical Gardens, Edinburgh)

Peter Bonants (Wageningen University, The Netherlands)

Mehrdad Hajibabaei (University of Guelph, Canada)

Simon Creer (Bangor University, UK)

Stuart Pimm (Duke University, USA)

We are looking forward for your participation in this exciting scientific event,

Filipe Costa

ECBOL2 Chair

Mónica Landi <mlandi@bio.uminho.pt>

Copenhagen AncientDNA Sep7-11

Dear Friends and Colleagues,

This is the first official call for abstracts for the Fourth International Symposium on Biomolecular Archaeology (ISBA4), which will be held in Copenhagen, Denmark, between 7-11 September, 2010. The symposium aims to highlight recent advances in biomolecular archaeology and to provide an international forum to present and discuss research results. This year's symposium is being hosted by the Center for GeoGenetics of the University of Copenhagen and will be held at the Geocenter in central Copenhagen.

Judging by the three previous meetings in Amsterdam, Stockholm, and York, we anticipate a wide range of interesting podium and poster presentations on all aspects of research in biomolecular archaeology, including proteomics, ancient DNA and stable isotope analysis. In addition, we are pleased to announce several keynote speakers, including Anne Pedersen from the National Museum of Denmark, Eske Willerslev from the Centre for GeoGenetics, and T. Douglas Price from the University of Wisconsin, Madison.

To register for the symposium, please go to our website at www.isba4.net and follow the links to registration. Once you have registered online you will receive an email, containing the payment details. The registration fee is 130 Euros, if you register before 1 June 2010. Thereafter, the registration fee will increase to 150 Euros. This includes a symposium pack, lunch, wireless access, and a buffet reception at the Carlsberg Academy on Friday evening (but NOT accommodation). Registration closes 25 August.

To submit an abstract please use the abstract template provided on our website and submit it no later than 1 May 2010. We welcome submissions on all aspects of research on ancient biomolecules, including recent applications of biomolecular techniques to archaeological questions, as well as papers dealing with recent technological advances and the use of newly emerging technologies in biomolecular archaeology, such as high-throughput sequencing or laser ablation isotope analysis. A selection of papers will be published in a special issue of the Journal of Archaeological and Anthropological Sciences.

For more information on the symposium, including an outline program, as well as other useful information regarding travel to Copenhagen, the location of the symposium venue, and accommodation options please visit our website at www.isba4.net . We look forward to welcoming you to Copenhagen!

The ISBA4 committee

"info@isba4.net" <info@isba4.net>

Edmonton ButterflyEvolution Jun29-Jul2 2

Dear butterfly biologists everywhere!

The deadline for lower-cost registration is coming soon for the 6th International Conference on the Biology of Butterflies. Held this year during June 29 - July 2 at the University of Alberta, this meeting has taken place at irregular intervals since 1981 and recognizes the role that the study of butterflies has played in our understanding of both evolutionary biology and ecology.

Please view the Conference webpage at: http://www.biology.ualberta.ca/biobutterfly2010 Deadline for lower-cost Registration: March 31, 2010 Deadline for Abstract submission: May 17, 2010

Felix Sperling <felix.sperling@ualberta.ca>

ESEB travel award 2010

*ESEB travel award *These awards are for students and young scientists to attend an SSE meeting in the US or an ESEB meeting in Europe. For 2010, participants of the SSE meeting in Portland can apply. The award will cover: 1. Support toward travel and living expenses. 2. SSE/ESEB Registration fees (the award will not cover late registration fees).

Eligibility: Applications can be submitted by young scientists at various stages of their professional career that do not yet have a permanent position. Applicants should be ESEB members (for becoming a member of ESEB, see _http://www.eseb.org/). Proposals can be submitted several times, but if successful, winners are not eligible for a second award for a period of 5 years. They must present either an oral communication or a poster to be eligible for the award.

The application should be no more than 2 pages long and include: name of the applicant; meeting name and dates; budget, including sources of additional support; an explanation of how attendance to the meeting will further their professional goals (preferably as a single pdf-file). A CV and a support letter from the applicant advisor/mentor are also required. Support letters should be sent to the same email address (C.J.M.Egas@uva.nl) by the applicant mentor. The deadline for applications is 6 April 2010.

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Martijn Egas, assistant professor Institute for Biodiversity and Ecosystem Dynamics, http://www.science.uva.nl/ibed Department of Population Biology, http://www.science.uva.nl/ibed-pb/ University of Amsterdam

P.O. box 94248 tel: 00 31 20 525 7748 1090 GE Amsterdam fax: 00 31 20 525 7832 email: C.J.M.Egas@uva.nl

C.J.M.Egas@uva.nl C.J.M.Egas@uva.nl

Freiburg PhD student EvolBiol Apr16-18

ANNUAL MEETING, PhD Students Evolutionary Biology

The annual meeting of the study group evolutionary biology of the German zoological society (DZG) is a unique opportunity for graduate students (Diploma, Master, PhD) in evolutionary biology to present their projects and to get to know each other both on a scientific as well as on a personal level. This yearís meeting will be held in Freiburg im Breisgau from the 16th to the 18th of April 2010 and is organised by the groups of PD Dr. Martin Schaefer and Dr. Thomas Schmitt.*

*We encourage all Diploma, Master and PhD students, who are interested in any aspect of evolutionary biology to join the meeting. Traditionally, the meeting is organized by the DZG (German Zoological Society), but botanists, mycologists, microbiologists and theoretical biologists are equally welcome. The meeting will provide an optimal opportunity to give a talk about your Diploma, Master or PhD thesis. In addition to that, it is a great way to find out what other fellow evolutionary biologists are working on, and perhaps to find out where you would like to do your PhD or Postdoc.

Invited speakers:

- Prof. Dr. Ole Seehausen; Univ. of Bern & EAWAG - Prof. Dr. Peter Kappeler; Univ. of Göttingen - Dr. Stefan Jarau; Univ. of Ulm

!! Registration & Abstracts welcome until MARCH 15TH !!

Find out more:

http://www.biologie.uni-freiburg.de/data/bio1/evo/-index.htm Dr. Gregor Rolshausen Dept. of Animal Ecology and Evolutionary Biology Faculty of Biology University of Freiburg 79104 Freiburg Germany Tel: ++49-761 203 2559 Fax ++49 761 203 2544

gregor rolshausen <gregor.rolshausen@biologie.uni-freiburg.de>

Ghent AlgalGenomics Apr7-9

ESIL2010: A decade of algal genomics (April 7-9, Ghent)

Dear colleagues and friends,

If you haven't already registered for the ESIL2010 "A decade of algal genomics" meeting, do so by March 7. in order to receive the early registration discount. After March 7, the registration fees increase from 140 to 220 for full delegates and from 90 to 150 for students. http://www.phycology.ugent.be/ectocarpus/-index.html If you have not yet booked your accommodation, it may be interesting to know that the IBIS hotels (Kathedraal and Opera both in the centre of Ghent) offer a discount to the delegates of the ESIL meeting. Do state explicitly that you are part of the Ectocarpus meeting when you make a reservation.

The complete preliminary program, with platform sessions and posters included, will be available online shortly after the closure of early registration.

See you in Ghent!

Olivier De Clerck

Olivier De Clerck Onderzoeksgroep Algologie, UGent. Krijgslaan 281, S8, 9000 Gent; Belgium NEW TEL. -32-9-2648500 // Fax. -32-9-2648599 http://www.phycology.ugent.be/ Olivier De Clerck <odclerck@gmail.com>

Gordon MetabolicEvolution Jul18-23

Hi,

This summer's Gordon Conference on the Metabolic Basis of Ecology and Evolution should interest some viewers. The URL is http://www.grc.org/-programs.aspx?year=2010&program=metbasis Evolution isn't officially in the title despite its being a significant part of the program. An aim is to advance integration of evolution and ecology by means of a focus on energy and adaptation.

Leigh Van Valen

leigh van valen <leigh@uchicago.edu>

Gordon QuantitativeGenomics Feb20-25

Gordon Research Conference in Quantitative Genetics & Genomics

February 20-25, 2011 Hotel Galvez Galveston, TX

Chair: Peter M. Visscher <mailto:PETER.VISSCHER@QIMR.EDU.AU> Vice Chair: Jack Dekkers <mailto:JDEKKERS@IASTATE.EDU>

>From genome to phenotype. Quantitative genetics aims to link phenotypic variation for complex traits to its underlying genetic basis in order to better understand and predict genetic architecture and long term change within natural, agricultural, and human populations. Traditionally built upon statistical abstractions of genetic effects, the field is now rapidly advancing by making use of recent exciting developments in genetic and genomic technologies to reveal explicit links between genes and complex phenotypes, and therefore serves as a focal point for bringing together many emerging areas of genetics, genomics, physiology, statistics, bioinformatics, and computational biology. This synthesis is already having a large impact on the areas of evolutionary biology, plant and animal breeding, and the genetic analysis of human disease.

The strength of the Gordon Conference on "Quantitative Genetics & Genomics" has historically been the bringing together of leaders in each of these fields to explore and exchange areas of shared interest and cutting edge developments, with the potential to impact all researchers within the broad field of quantitative genetics. Building upon the tremendous success of our conferences in recent years, we will again focus on many cutting-edge developments in the field, including whole genome approaches to understanding and exploiting genetic variation, the use of next generation sequence data to identify causal genes and pathways, genome architecture and regulation, systems genetics, non-traditional forms of inheritance, and statistical genetics.

Check http://www.grc.org/programs.aspx?year=2011&program=quantgen for updates on the Preliminary Program.

Peter Visscher <Peter.Visscher@qimr.edu.au>

KansasCity ArthropodGenomics Jun10-13 EarlyRegistration

Arthropod Genomics: New Approaches and Outcomes

4th ANNUAL ARTHROPOD GENOMICS SYMPOSIUM

June 10 - 13, 2010, in Kansas City, USA

www.k-state.edu/agc/symp2010

Deadline to Register at Early-Bird Rates: Friday, March 26, 2010 ***Please share this announcement with colleagues and students!***

Other important deadlines:

*Poster Abstract Submissions: Wednesday, May 19

*Hotel Reservations: Wednesday, May 19, or until room block is filled

REGISTRATION: The early registration fee is $295 ($150 for graduate and undergraduate students) on or before Friday, March 26, and will include a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and breakfast on Sunday.

VENUE: The symposium will take place at the Kansas City Marriott on the beautiful Country Club Plaza. Participants are invited to dine Saturday night at an optional banquet at the BRIO Tuscan Grille.

PRE-SYMPOSIUM WORKSHOP: Thursday afternoon, June 10, 4:00-6:00 pm

Navigating NCBIs resources for insect genomics. Terence Murphy, NCBI/NIH, will provide training on utilizing NCBIs resources for insect genomics. Topics will include accessing data in the RefSeq and Entrez Gene databases, BLink, BLAST, NCBIs Map Viewer, and other resources. Issues regarding the submission of data to NCBI and options for linking outside resources to NCBIs databases will also be discussed. There is no cost to attend this optional workshop, but registration is requested.

WORKSHOP/SEMINAR: Saturday morning, June 12, 10:00-11:30 am

MAKER: Genome annotation made easy. Carson Holt, University of Utah, will provide a basic overview of MAKER and demonstrate both the command line version and the new online MAKER Web Annotation Service (MWAS). MAKER is a portable and easily configurable genome annotation pipeline. Its purpose is to allow smaller eukaryotic and prokaryotic genome projects to independently annotate their genomes and create genome databases. MAKER identifies repeats, aligns ESTs and proteins to a genome, produces ab initio gene predictions and automatically synthesizes these data into gene annotations having evidence-based quality values. Several use-case scenarios with example data and results will also be presented.

FUNDING AGENCY PRESENTATIONS: Representatives from national funding agencies will make short presentations about funding philosophies and opportunities within their programs. Following each presentation, the floor will be open for questions and discussion. Speakers include:

Alan Christensen, NSF

Adriana Costero, NIAID, NIH

Mary F. Purcell-Miramontes, USDA, NIFA

ORGANISM MEETINGS: Friday afternoon/evening, June 11, 5:15-? p.m.

Meet with scientists who are also working with your organism of interest during small group gatherings. Group leaders will be identified to coordinate topics and lead discussions. Additional information will be posted to the conference website as details are finalized.

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

POSTER SESSIONS: There will be two poster sessions. Six platform presentations will be chosen from submitted poster abstracts.

Abstract Submission Deadline: Wednesday, May 19, 2010.

SYMPOSIUM PROGRAM: The symposium sessions will begin Thursday evening, June 10, and continue on Friday and Saturday, with additional events Saturday evening and Sunday morning. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Workshops will be held Thursday prior to the Symposium and Saturday morning. Activities will conclude by noon on Sunday, June 13.

Keynote Speaker:

Nora J. Besansky

University of Notre Dame

Population genomics of adaptation and speciation in malarias vector

Featured Speakers:

Michael Akam

University of Cambridge, United Kingdom

The genome of the Geophilomorph centipede, Strigamia maritima

Scott J. Emrich

University of Notre Dame

Opportunities and challenges of non-model transcriptome sequencing: From corn to wild butterflies and moths

Matthew Hudson

University of Illinois at Urbana-Champaign

Exploring the evolution of social behavior using genome sequencing and analysis

Anthony A. James

University of California

Message in a battle, using whole genome expression analyses to fight vector-borne diseases

Michael R. Kanost

Kansas State University

Functional genomics of cuticle sclerotization in Tribolium castaneum

Fabrice Legeai

INRA, Rennes, France

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

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London MEE Launch Symposium Apr22 reminder

Dear colleague,

Just one month before "Methods in Ecology and Evolution Launch Symposium", a one-day symposium to mark the launch of MEE, the new journal of the British Ecological Society. The symposium will take place on April 22 2010 at Charles Darwin House, the new BES office. We have an excellent line-up of speakers, please see the website below.

Registration and further particulars are available online at http://www.methodsinecologyandevolution.org/view/0/launchsymposium.html There are spaces left but register soon as we are restricted to 120 delegates.

We look forward to meeting you there, Graziella Iossa and Rob Freckleton

Dr Graziella Iossa

Journal Coordinator Methods in Ecology and Evolution

Tel. +44(0)207 685 2518 Fax +44(0)207 685 2501 Email coordinator@methodsinecologyandevolution.org Web http://www.methodsinecologyandevolution.org/ Submit to MEE http://mc.manuscriptcentral.com/mee-besjournals MEE Launch Symposium - 22 April 2010, book online: http://www.britishecologicalsociety.org/journals_publications/methodsinecologyandevolution/booking.php Think before you print...

Graziella Iossa

coordinator@methodsinecologyandevolution.org

Lyon SMBE 2010 Jul4-8 Registration

Dear all,

We are happy to announce that the online registration, abstract submission, and application to the Fitch prize and travel awards for the 2010 SMBE meeting in Lyon are now open.

Please visit our website to register now and benefit from the early registration rates:

http://smbe2010.univ-lyon1.fr/en With best regards, Gabriel Marais & Manolo Gouy, On behalf of the SMBE 2010 Organizing Committee

Gabriel Marais <gabmarais@gmail.com>

Marseilles 14thr EvolBiol Sep21-24

Dear All,

We are pleased to inform you that the 14th Evolutionary Biology Meeting at Marseilles will take place on 21-24 September 2010 and that titles of first accepted abstract (early registration) are now available on: http://sites.univ-provence.fr/evol-cgr For more information, do not hesitate to contact us.

Yours sincerely,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

Montpellier DispersalEvolution Jun13-18 2

Dear all,

The deadline for the submission of oral contributions and posters to the FSD2010 conference and for the registration at normal fee is coming soon (March 14, 2010).

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

Please visit our website (www.fsd2010.org) for the updated program and any other additional information. We hope to see you soon in Montpellier, The organizers

Helene.FREVILLE@cefe.cnrs.fr

Moscow MolecularPhylogenetics May18-21

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

This is the final call for submissions. The submission and registration deadline is extended until 12 April 2010.

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

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

Confirmed invited speakers:

Sudhir Kumar - Center for Evolutionary Functional Genomics, Arizona State University, Tempe AZ, USA Lecture title Â≪Statistics and truth in phylogenomicsÂ≫.

Dietmar Quandt - Nees-Institute fur Biodiversitat der Pflanzen, Bonn Universitat, Germany Lecture title Â≪Mutational dynamics, phylogenetic structure and utility of fast evolving DNAÂ≫.

Natalia Ivanova - Canadian Centre for DNA Barcoding, Biodiversity Institute of Ontario, University of Guelph, Canada Lecture title Â≪iBOL â the International Barcode of Life ProjectÂ≫.

Yuri I. Wolf - Evolutionary Genomics Research Group, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda MD, USA Lecture title Â≪Search for a Tree of Life in the phylogenetic forestÂ≫.

Igor B. Jouline - Joint Institute for Computational Sciences, University of Tennessee, Oak Ridge National Laboratory, TN, USA Lecture title Â≪Origins and diversification of a complex signal transduction system in prokaryotesÂ≫.

Martin Embley - Institute for Cell and Molecular Biosciences, Newcastle University, UK Lecture title Â≪The archaebacterial origins of eukaryotesÂ≫.

Francois-Joseph Lapointe - Laboratoire d'Ãcologie MolÃ©culaire et Ãvolution, UniversitÃ© de MontrÃ©al, MontrÃ©al, QuÃ©bec, Canada Lecture title Â≪Measuring and representing incongruence in phylogenetic forestsÂ≫.

Jane Rogers - The Genome Analysis Centre, Norwich Research Park, Colney Norwich, UK Lecture title Â≪Recent advances in plant genomicsÂ≫.

Wolfgang Wägele - Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany Lecture title Â≪The instability of the animal tree of life: causes of error in molecular systematicsÂ≫.

Andrei Kozlov - Biomedical Center, St Petersburg State University, Russia Lecture title Â≪Expression of evolutionarily new genes in tumors and the possible role of tumors in evolutionÂ≫.

Harald Schneider - Natural History Museum, London, UK Lecture title Â≪Employing molecular phylogenetic hypotheses to reconstruct temporal-spatial events shaping the Tree of LifeÂ≫.

Hugues Roest Crollius - Laboratoire DYOGEN, Centre National de la Recherche Scientifique (CNRS), Paris, France Lecture title Â≪Paleogenomics in silico: reconstruction of ancestral genomes in vertebrates using gene phylogeniesÂ≫.

The conference is organized and supported by the Faculty of Biology and Research & Training Center âEvolutionary Genomics and Bioinformaticsâ (Moscow State University), Belozersky Institute for Physicochemical Biology (Moscow State University), Institute for Information Transmission Problems (Russian Academy of Sciences), Central Botanical Garden (Russian Academy of Sciences), Russian Academy of Natural Sciences, Moscow Society of Naturalists, Russian Foundation for Basic Research, HealthGene Corp., and Applied Biosystems (Life Technologies).

The working conference language is English.

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

roussine@yandex.ru

Odense Denmark EvolutionaryDynamics Aug19-23

There will be a session on "Evolutionary Dynamics" at this year's Artificial Life Conference ("ALife 12") 12), which will take place in Odense (Denmark) August 19-23, 2010.

The theme of the conference is "Critical properties of living systems", but for this session, we are soliciting contributions that study evolutionary dynamics from a computational, theoretical, or experimental point of view. The deadline for submission is soon: this March 31st. Authors will be notified about their contributions May 7th. Please see the conference web site http://www.alife12.org for more details.

Chris Adami, for the Scientific Advisory Committee of the Alife 12 conference:

Chris Adami John McCaskill Mark Bedau Takashi Ikegami Norman Packard

chrisadami@gmail.com

OregonStateU PhylogeneticInformatics Jun29-30

The Call for Abstracts for full talks is now open for the inaugural conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), at http://ievobio.org/ocs/index.php/ievobio/ 2010. See below for instructions.

Accepted talks will be about 15-20 minutes in length and will be presented during the full talk sessions in the morning of each of the two conference days, following the day's keynote presentation.

Submitted talks should be in the area of informatics aimed at advancing research in phylogenetics, evolution, and biodiversity, including new tools, cyberinfrastructure development, large-scale data analysis, and visualization.

Submissions consist of a title and an abstract at most

1 page long. The abstract should provide an overview of the talk's subject. As the number of program slots for full talks is limited, the abstract should give enough detail so reviewers can decide whether the submission merits a full talk or whether it should be moved to one of the lightning talk sessions. If the subject of the talk is a specific software for use by the research community, the abstract must state the license and give the URL where the source code is available so reviewers can verify that the open-source requirement(*) is met.

The deadline for submission is April 8, 2010. We intend to notify authors of accepted talks before early registration for iEvoBio (and Evolution) ends. Further instructions for submission are at the following URL: http://ievobio.org/ocs/index.php/ievobio/2010/information/presenters Full talks are 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Lightning talks (5 mins long), 2) Challenge entries, 3) Software bazaar demonstrations, and 4) Birds-of- a-Feather gatherings. The Call for Challenge entries is already open (see http://ievobio.org/challenge.html), and information on how to contribute to the other 3 sessions is forthcoming.

More details about the program and guidelines for contributing content are available at http://ievobio.org. You can also find continuous updates on the conference's Twitter feed at http://twitter.com/iEvoBio . iEvoBio is sponsored by the US National Evolutionary Synthesis Center (NESCent) in partnership with the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2010 Organizing Committee: Rod Page (University of Glasgow) Cecile Ane (University of Wisconsin at Madison) Rob Guralnick (University of Colorado at Boulder) Hilmar Lapp (NESCent) Cynthia Parr (Encyclopedia of Life) Michael Sanderson (University of Arizona)

(*) iEvoBio and its sponsors are dedicated to promoting the practice and philosophy of Open Source software development (see http://www.opensource.org/docs/definition.php) and reuse within the research community. For this reason, if a submitted talk concerns a specific software system for use by the research community, that software must be licensed with a recognized Open Source License (see http://www.opensource.org/licenses/), and be available for download, including source code, by a tar/zip file accessed through ftp/http or through a widely used version control system like cvs, Subversion, git, Bazaar, or Mercurial. Authors of full talks who cannot meet this requirement at the time of submission should state their intentions, and are advised that the requirement must be met by June 27 at the latest.

hlapp@nescent.org

Paris Archaeozoology Aug23-28

The 11th International Council for Archaeozoology will take place in Paris from 23 to 28 August 2010. 725 oral/poster presentations have already been accepted and spread over the 30 thematic sessions. Therefore we now require final registration and the last proposals for the general sessio

You will find the online third circular at: http://www.alexandriaarchive.org/icaz/index.htm: - a registration form (either online or through pdf files which can be printed and send by post) for the conference, the different optional events, for the excursions and for hotel bookings, with indications for payment (which will be increased after the 30^th April; - call for presentations in the general session, the only one for which it is still possible to propose a poster/oral presentation (deadline 31^st March) - complete program of the seven parallel sessions, - list of oral and poster presentations accepted in each of the 30 thematic sessions, - information about the venue, the hotels and other accommodation - information about the dates, duration, programme and cost of the excursions - information regarding the final version of your abstract (deadline 30^th April) - a guide for the preparation of oral and poster presentations - information regarding the management of the sessions (for session organisers only).

Please note that the accepted poster presentations in the thematic sessions, cannot now be transferred to the general session.

A fourth circular will be sent at the beginning of summer with final information.

For any further information: icaz2010@mnhn.fr

Regards

For the Organizing Committee

Jean-Denis Vigne

Jean-Denis Vigne <vigne@mnhn.fr>

Perth Impact of Symbiosis Oct2 ExtendedDeadline

Extended Deadline March 31, 2010 for the ISBE Satellite Symposium on the Impact of Symbiosis on Behaviour - in combination with the ISBE 2010 (Perth, Western Australia).

CALL FOR ABSTRACTS

CLOSES 31 March, 2010

In association with the 13th International Behavioural Ecology Congress 2010 we invite submission of abstracts for your chance to be a part of the ISBE Satellite - Symposium “Impact of Symbiosis on Behaviour” which will be held 8:30am-12:30pm of October 2, just following the 13th ISBE Conference in Perth, Western Australia from 26 September - 1 October 2010.

Please submit abstracts for oral presentations to wolfgang.miller@meduniwien.ac.at.

The abstract submission closing date is 31 March 2010.

Speakers will be notified via email before the end of April 2010. Registration for ISBE includes this satellite symposium and will be open following the Abstracts submission closing date.

For more information about the ISBE conference visit the website at http://www.isbeperth2010.com/ Please distribute this information widely to interested colleagues so that they can submit an abstract or register their interest online and join our database to receive future notifications.

Kind Regards

Wolfgang J. Miller, Medical University of Vienna

Elisabeth Mc Graw, University of Queensland

Markus Riegler, University of Western Sydney

Miller Wolfgang <wolfgang.miller@meduniwien.ac.at>

Perth ISBE 2010 Sep26-Oct1 Extended

CALL FOR ABSTRACTS

EXTENDED UNTIL 5 MARCH 2010

The Organising Committee for the 13th International Behavioural Ecology Congress 2010 (see http://www.isbeperth2010.com/index.html) has extended the deadline for abstract submission until Midnight Australian Western Standard Time Friday 5 March 2010.

The guidelines for online submission are available via the ISBE website at http://www.isbeperth2010.com/abstracts.html Travel grants are available and can be applied for here: http://www.isbeperth2010.com/grants.php In the tradition of the Society, all abstracts proposed for posters that represent legitimate behavioral ecological research will be accepted. Since we anticipate receiving more requests for oral presentations than slots available for talks, two behavioral ecology experts in the relevant topic area will review each abstract proposed for oral presentation. Review outcomes will be communicated via E-mail before the end of April 2010. Unsuccessful oral submissions will be offered a poster slot. As with submissions to the journal, the review of abstracts will be blind.

Please pass this information onto your colleagues so that they can submit an abstract.

We are very much looking forward to welcome you in Perth

The ISBE organizing committee

A/ Prof. Boris Baer CIBER: The Collaborative Initiative for Bee Research Website: www.ciber.science.uwa.edu.au MCS Building M 310 The University of Western Australia Crawley WA 6009 Australia phone: +61 8 6488 4495 fax: +61 8 6488 4401 E-mail: bcbaer@cyllene.uwa.edu.au

Boris Baer <bcbaer@bi.ku.dk>

Stockholm FloweringPlantPhylogenetics Sep6-10

The 5th international Rubiaceae and Gentianales Conference Stockholm, Sweden, September 6-10, 2010. (http://www.bergianska.se/b3/)

Phylogenetic analyses and the use of historical data have greatly enhanced our ability to understand biodiversity in space and time. This international conference will focus on recent progress in the use of biodiversity data for improved estimation of phylogeny and its various applications. This will hold promise for the future use of Rubiaceae and the Gentianales as model systems for understanding flowering plant evolution. The meeting will be an exciting opportunity to exchange new ideas, to share results, as well as to strengthen international collaboration.

Conference Themes: Biodiversity, taxonomy and species richness, Progress in phylogeny, Turning phylogenies into classifications, Dating lineages, Biogeography and paleoclimates, Character evolution.

Detailed information on the conference sessions, invited speakers, and the programme will appear at the conference web site as soon as they are available. Please visit http://www.bergianska.se/b3/ for much more information.

With best wishes, Lena Struwe

Lena Struwe <struwe@AESOP.Rutgers.edu>

Tours BehaviourEvolution Apr12-16

Dear All,

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

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

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

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

Each session will be introduced by two invited professors specialized in this field of research, followed by 8-10 postgraduate student research presentations and discussions. In addition, poster sessions and three "theme evenings" designed for a broad public are planned. Participants are expected to give a 15-minute talk. In order to register please submit the abstract of your talk (or poster) (250 words maximum) on the website: http://serl2010.univ-tours.fr (see the website for supplementary information). Registration are opened until 5nd March 2010.

Hope to see you in April,

SERL Association 2010.

serl.univtours@gmail.com

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

serl.univtours@gmail.com

UEdinburgh Evolution and Infection Apr28

Immunopathology & Immunosenescence: an evolutionary perspective

A one day symposium,

April 28, 2010

University of Edinburgh

Ashworth Laboratories, Lecture Theatre III

Kings Buildings, West Mains Road, Edinburgh

Organisers: Dan Nussey (dan.nussey@ed.ac.uk) & Tom Little (tom.little@ed.ac.uk)

Hosted by The Centre for Immunity, Infection and Evolution (CIIE; http://ciie.bio.ed.ac.uk/), a Wellcome Trust-funded initiative to connect evolutionary biology to infection research and gain an interdisciplinary perspective on challenges to global health.

Symposium remit: the study of disease has often been separated from the study of 'normal' or 'healthy' ageing, but it is now clear that immunopathology and immunosenescence play an integral role in the process of aging. Evolutionary theory provides a unifying framework from which to understand variation in the ageing process, but this has not been as widely applied as it might be. This symposium brings together researchers from a range of disciplines with the aim of integrating evolutionary, immunological and epidemiological thinking on the causes of variation in immunopathology and immunosenescence amongst individuals, populations and species.

Speakers:

Tom Kirkwood (Newcastle University, UK)

David Gems (University College London, UK)

Dan Promislow (University of Georgia, USA)

Graham Pawelec (Tübingen University, Germany)

Daryl Shanley (Newcastle University, UK)

Matt Tinsley (University of Stirling, UK)

Andrew MacColl (University of Nottingham, UK)

Arne Akbar (University College London, UK)

David Constantini (University of Zurich, Switzerland)

Schedule 10:00-18:00 (approx, detailed schedule to follow)

The symposium is free, including lunch and refreshments, but please register at:

http://ciie.bio.ed.ac.uk/node/276

Tom Little Wellcome Trust Senior Research Fellow in Basic Biomedical Sciences Institute of Evolutionary Biology Kings Buildings University of Edinburgh EH9 3JT UK

+44 131 650 7781

tom.little@ed.ac.uk

http://www.biology.ed.ac.uk/research/groups/tlittle/

Tom Little <Tom.Little@ed.ac.uk>

UExeter InterdiscEvolution Sep21-24

Dear Brian,

The below announcement is to a second instalment of a small but scientifically diverse meeting. It has a strong evolutionary flavour to it, in fact, it uses evolution as a wide-arching umbrella to bring together very diverse topics/approaches used in biology these days.

best regards,

Orkun S. Soyer, PhD Lecturer in Systems Biology Engineering, Mathematics and Physical Sciences University of Exeter Tel: +44 (0)1392 723615 URL: http://people.exeter.ac.uk/oss203/ ANNOUNCEMENT:

Dear Colleague,

I would like to draw your attention to a unique meeting: "Frontiers of Multidisciplinary Research: Mathematics, Engineering and Biology" to be held at the University of Exeter, 21-24 September 2010.

"Frontiers of Multidisciplinary Research" is designed to foster interdisciplinary thinking without defining any a priori scientific boundaries. The meeting will bring together scientists who would normally not attend the same conferences and facilitate their interaction. This will be achieved by a list of carefully selected invited speakers:

Ralf Sommer, MPI Tubingen | Sebastian Bonhoeffer, ETH | Andreas Wagner, Uni Zurich | Uwe Sauer, ETH | Mark Isalan, CRG-Barcelona Luca Cardelli, Microsoft Research | Michael Stumpf, Imperial | *Judy Armitage, Oxford University | Andrew Millar, Edinburgh Laurence Hurst, Bath | Susan Rosser, Glasgow | David Rand, Warwick | Peter Swain, Edinburgh | Martin Howard, John Innes Centre Mark Goulian, University of Pennsylvania | *Kevin Foster, Harvard University | Michael Savagaeu, UC Davis

and by several structural features:

- limited attendance to 70, allowing almost every attendee to present - well-embedded poster sessions - an "un-crowded" presentation schedule - long lunch breaks with plenty of time (and dedicated space) for interaction

In addition to the invited speakers, up to 15 speakers will be selected from submitted abstracts. Each of the speakers will have 25+5mins of presentation time.

We're now accepting abstract submission for the meeting. Please visit:

www.exeter.ac.uk/frontiers Best Regards,

Orkun Soyer, on behalf of the organising committee: Orkun Soyer (Exeter), Ruth Baker (Oxford), Ozgur Akman (Exeter), Nick Buchler (Duke), Steve Porter (Exeter)

Orkun S. Soyer, PhD Lecturer in Systems Biology Engineering, Mathematics and Physical Sciences University of Exeter Tel: +44 (0)1392 723615 URL: http://people.exeter.ac.uk/oss203/ "Soyer, Orkun" <O.S.Soyer@exeter.ac.uk>

Uruguay VertMorphology Jul26-31 SupportForParticipants

Dear Evolutionary Biologists,

The 9^th International Congress of Vertebrate Morphology offers limited support for participants that plan to attend the Congress at Punta del Este, Uruguay, from 26^th to 31^st July 2010. The final deadline for support applications is extended until 31^th March. Please, visit our website at: http://icvm-9.edu.uy/ and see the conditions and requirements to apply

Sincerely,

Alejandro D'Anatro.

On behalf of the Local Committee of the 9^th ICVM .

passer@fcien.edu.uy

UStAndrews PoeciliidFishBiodiversity Jun13-16

The Fish Behaviour and Biodiversity Research Group is delighted to be hosting the 4th European Conference of Poeciliid Biologists at the University of St Andrews, Scotland (www.st-andrews.ac.uk). The conference, which will take place from the 13th to 16th June 2010 will have a strong evolutionary theme reflecting the importance of these fish in evolutionary research. The deadline for the submission of abstracts is 31 March, and registration closes on April 30th. Please visit our website biology.st-andrews.ac.uk/poeciliid/ where you can register and submit your abstract, and where you will find more information about the meeting and about St Andrews.

– Anne Magurran Professor of Ecology & Evolution Scottish Oceans Institute School of Biology University of St Andrews St Andrews, Fife, KY16 8LB Scotland, UK aem1@st-and.ac.uk

Anne Magurran <aem1@st-andrews.ac.uk>

WashingtonState EvolutionaryBiol Apr23-25 3

Just a reminder that the registration deadline (March 15) for the EVO-WIBO (Pacific Northwest Evolutionary Biology) meeting is rapidly approaching!

This year's meeting will be held April 23-25 at Fort Worden State Park on Washington's Olympic Peninsula. Complete meeting information and registration is available at www.zoology.ubc.ca/evo-wibo/.

Scott Nuismer Associate Professor Department of Biological Sciences University of Idaho Moscow, Idaho 83844 Phone: 208 885 4096 http://www.webpages.uidaho.edu/˜snuismer/Nuismer_Lab/ Scott Nuismer <snuismer@uidaho.edu>

WashingtonState EVO-WIBO Apr23-25 RegistrationExtended

The registration deadline for this year's EVO-WIBO (Pacific Northwest Evolutionary Biology) meeting has been extended until March 21.

EVO-WIBO is a biennial meeting of Pacific Northwest Evolutionary Biologists and will be held this April 23-25 at Fort Worden State Park on Washington's Olympic Peninsula. Our plenary speaker this year will be Stevan J. Arnold.

More information and online registration online is available at http://www.zoology.ubc.ca/evo-wibo/ . snuismer@uidaho.edu snuismer@uidaho.edu

GradStudentPositions

AgroParisTech HostParasiteNetwork

PhD Student Position in Theoretical Ecology

A PhD student position in theoretical ecology is available in the Department of Mathematics Informatics & Physics at the AgroParisTech, Paris, France (http://www.agroparistech.fr/-English-version-.html).

The aim of the project is to model the topology of ecological networks with the last developments of statistical models for heterogeneous random graphs. During the first year of the project, the candidate will review the clustering algorithms and mixtures models aimed at identifying modules in graphs. He will define the most appropriate methods for studying ecological networks. During the second year of the project, he will use the selected methods to elucidate the topology of a host-parasite interaction network (tree-parasitic fungus network). The impacts of (1) the nature of data (binary versus quantitative) (2) the spatial and temporal scales of sampling and (3) the integration of other interaction types (tree-phytophageous insects) on the modularity of the network will be studied. During the third year of the project, the candidate will get an insight into the impact of climate change on the topology of the network through the statistical analysis of the data arising from a metagenomic experiment.

The position is funded for three years by the French National Institute for Agricultural Research (INRA, http://www.international.inra.fr/). The ideal starting date would be in September 2010. The successful candidate may follow the international interdisciplinary PhD program of the FdV graduate school (http://www.fdv-paris.org/en/ecole-doctorale-fdv/; Application deadline: April 30). Applicants should have a Master degree in Mathematics or Statistics and a strong interest for ecological applications, or a Master degree in Ecology or Evolution and a strong interest for theoretical approaches. Applications should include a description of research interests, a complete CV and the names and email addresses of 2 professional references. Applications should be sent by email before the 5th of April 2010 to the supervisors: 1) Pr Jean-Jacques Daudin (AgroParisTech, daudin@agroparistech.fr, http://www.agroparistech.fr/-Jean-Jacques-Daudin-.html) 2) Dr Corinne Vacher (INRA-Bordeaux, corinne.vacher@pierroton.inra.fr, http://w3.pierroton.inra.fr/biogeco/pathologie/vacher/-vacher.html)

cvacher@bordeaux.inra.fr cvacher@bordeaux.inra.fr

CornellU BearPopulations

Graduate Research Assistantships (2)

New York Cooperative Fish and Wildlife Research Unit

Cornell University, Department of Natural Resources

Two graduate research assistantships are available with the New York Cooperative Fish and Wildlife Research

Unit and the Department of Natural Resources at Cornell University to research black bear ecology in New York: 1) M.S. or Ph.D. student to model bear-habitat relationships and develop metrics of landscape permeability that represents the utilization likelihood of black bears across their range in New York. Student will be advised by Dr. Angela Fuller. 2) M.S. or Ph.D. student to design a large-scale DNA mark-recapture study using hair snares to be used for population abundance estimation, and to evaluate northeast regional population structure of black bears. Student will be co-advised by Dr. Angela Fuller and Dr. Matthew Hare.

Qualifications: The successful applicants will have an outstanding academic background including a B.S. or M.S. degree in Ecology, Natural Resources, Wildlife Science, Conservation Biology, or a closely related field. Both projects will require an exceptional work ethic, strong interpersonal skills, strong English writing and oral communication skills, and field-based research experiences. For project #1) I seek a highly motivated individual who desires to combine extensive fieldwork with GIS analysis and modeling. Preference will be given to applicants with prior experiences in one or more of the following: capturing, handling, and immobilizing large mammals, practical experiences using GIS, excellent quantitative skills, and/or previous experience leading field crews. For project #2) preference will be given to applicants with strong molecular genetic laboratory skills (e.g., PCR, sequencing, genotyping), prior experience leading field crews, and/or excellent quantitative analytical skills.

Potential candidates who meet the stated qualifications should send a cover letter detailing your research interests, a CV, photocopy of transcripts and GRE scores, and contact information for 3 references to angela.fuller@cornell.edu (or mail to the address below). Please submit application materials by 9 April, 2010. Questions regarding these positions should be directed via e-mail to Dr. Angela Fuller, angela.fuller@cornell.edu or Dr. Matthew Hare, mph75@cornell.edu.

Dr. Angela K. Fuller

New York Cooperative Fish and Wildlife Research Unit

Department of Natural Resources

209 Fernow Hall

Cornell University

Ithaca, New York 14853

Matt Hare <mph75@cornell.edu>

ETH Zurich PopulationGenetics

Dr Chris Kettle

Ecosystem Management < http://www.ecology.ethz.ch/people/pstdocs/people/pstdocs/ckettle >

ETH Zurich

Switzerland

PhD Studentship on Population Genetics and Tropical Forest Ecology

Fully funded PhD studentship offered in the Professorship of Ecosystem Management, Institute of Terrestrial Ecosystems, ETH Zurich, Switzerland

Title Genetic processes underlying species coexistence in tropical rain forests: is competition intensity shaped by genetic relatedness?

Start Date probably July 2010

Project This project seeks to explore differences among tree species in gene flow (by pollen and seed dispersal) in relation to patterns of tree distribution, and the further implications of differential gene flow and seed dispersal for seedling competition in the lowland rainforests of Malaysian Borneo. Ultimately, the research aims to contribute to an understanding of the mechanisms that maintain tree species diversity in tropical forests.

The project combines population biology, experimental ecology and molecular ecology.

Collaborators This research will be conducted in collaboration with the Sepilok Forest Research Centre in Sabah, Malaysia, and the University of Aberdeen, UK.

Relevance Aside from the scientific interest, the outputs of this project will be relevant for tropical forest conservation, management and restoration across Southeast Asia.

Supervisors: Prof. Dr. Jaboury Ghazoul (ETH Zurich); Dr. Chris Kettle (ETH Zurich); and Dr David Burslem (University of Aberdeen)

Requirements We are seeking highly motivated applicants with a desire to work on tropical forest ecology as part of a dynamic team. You will ideally have a B.Sc and M.Sc degree, in ecology, evolutionary biology, population genetics or other related field. Very good spoken and written English are essential; knowledge of German or Bahasa Malaysia would be advantageous but not required. Applicants should enjoy working in challenging tropical field conditions, and also be prepared to spend substantial time in the lab. An ability to work independently is highly desired, although we place strong emphasis on cooperation and team work.

Group The Professorship of Ecosystem Management comprises around 25 researchers and staff and has a diverse international composition. Research within the group tackles a range of topics relating to plant ecology, conservation and ecosystem management in both temperate and tropical systems. See our web site for more details (www. ecology.ethz.ch). Facilities We offer a dynamic and stimulating scientific environment with world-class facilities, including well equipped genetic and ecological labs, and access to the newly established ETH Zurich Genetic Diversity Center. Facilities at the Sepilok Forest Research Centre will support the ecological work. Technical support will be available for molecular work at ETH Zurich. Conditions Three year appointment at ETH Zurich with a starting salary of CHF 44,000 (gross). The position will be based in Zurich, but will require extended periods of fieldwork in Sepilok Forest Reserve, Sabah, Malaysia.

Application Applications should consist of (1) a letter describing research interests and reasons for doing a PhD; (2) a full CV, including any relevant experience; and (3) names, addresses and emails of two referees. Applications shoule be sent to Ankara Chen by e-mail: chen@env.ethz.ch. Please quote reference ETHIIRA 2010 in the subject line. Closing date for applications is 21 April 2010. The position is open to candidates of all nationalities.

For a more detailed PhD description email Ankara Chen. For other informal enquiries contact Jaboury Ghazoul (jaboury.ghazoul@env.ethz.ch).

Kettle Chris <chris.kettle@env.ethz.ch>

GeorgAugustU EvolutionAgeing

Graduate position: sex-specific ageing in a wild primate population

The Anthropology/Sociobiology department at the Georg-August University Göttingen, Germany (http://www.soziobio.uni-goettingen.de) is offering a PhD position for 3 years in a DFG-funded project starting on 1 July 2010 or as soon as possible thereafter (payment: 65% TVL, West).

We seek a highly motivated Ph.D. student who will work on the topic of ageing in wild primates within an evolutionary framework. The project focuses on sex differences in demographic and physiological ageing in the gray mouse lemur Microcebus murinus. Field work will be conducted at the DPZ field station in Kirindy Forest, Western Madagascar (http://www.soziobio.uni-goettingen.de/Mada/madagaskar-menu-en.htm). The methods to be employed include capture-mark-recapture, functioning experiments and parasitological analyses.

We offer a stimulating scientific environment in an international research group whose members work on a variety of topics in behavioral and evolutionary biology. The graduate student will be enrolled in the GAUSS program (Georg-August University School of Science, http://www.gauss.uni-goettingen.de/general.html). Göttingen is a pleasant medium-sized university town located in the middle of Germany with a lively cultural scene.

Applicants should have a Master degree (or equivalent) in evolutionary biology, population biology or a closely related field. Further job requirements include field experience (preferably in the tropics), the ability to work independently as well as basic French skills. Good quantitative, analytical, and English skills are also essential. Familiarity with animal handling techniques, capture-mark-recapture modeling, parasitological methods and field experiments are highly desirable.

Candidates should submit their application by e-mail as a pdf containing a cover letter, CV and the contact information of two referees.

Application received until 20 April, 2010 will be fully considered, but the position remains open until a suitable candidate has been identified. Please send applications to

Dr. Cornelia Kraus Department of Sociobiology/Anthropology Johann-Friedrich-Blumenbach-Institute for Zoology and Anthropology Georg-August University of Göttingen Kellnerweg 6 D-37077 Göttingen Germany

ckraus1@gwdg.de

"Kraus, Cornelia" <Cornelia.Kraus@biologie.uni-goettingen.de>

INRA FrenchGuiana TreePopulationGenetics

A grant for a Ph.D. thesis, followed by a two-years postdoc, is available at INRA at Kourou, French Guiana, and Nancy, France. The topic combines ecology, quantitative genetics, genomics and ecophysiology to study the evolutionary bases of adaptation of Neotropical rainforest trees to their environment. More information (in French) can be obtained at the following webpages:

http://www.rp2e.inpl-nancy.fr/fileadmin/rp2e/-propositions_theses/autres/CJS2010Presentation.doc http://www.rp2e.inpl-nancy.fr/index.php?id=5 Interviews will be held in Nancy in June 2010. Please contact the Lab leaders for more details on the research topic:

Forest tree species are dominant components (in terms of biomass and as ecological drivers) of one of the most diverse ecosystems, the tropical rainforest. Their environmental adaptations, and their potential to face climatic changes, determine both the structure of these ecological communities and their fate under global change.

The diversity of the response of tropical trees to their environment is being elucidated, and in particular, it has been found that several genera harbor species that differentiate along the water availability axis (drought/flooding) (Baraloto et al., 2007). It has also been shown that closely related species, with slightly different ecological properties, can be differentiated by genetic markers (Duminil et al., 2006). Recently, sequences of genes involved in plant water balance (aquaporins) have been isolated in a set of tropical tree genera (Audigeos et al., submitted; Brousseau 2009; Scotti 2009a) at UMR EcoFoG and a large-scale greenhouse experiment, with 2000 seedlings from eighteen half-sib families of Eperua falcata, is under way in the same research centre, with the goal of evaluating genetic and environmental components of responses to water stresses (Scotti 2009b). The existence of a relevant genetic component of quantitative trait diversity in rainforest tree populations has been recently proven (Scotti et al. 2010). These preliminary data set the conditions for addressing the question of the understanding of ecophysiological and genetic mechanisms of the adaptation of trees to their environment in natural conditions. The hypothesis to test is that trees growing in different conditions show differential adaptation to their respective environments, and that both physiological adjustments and genetic adaptation contribute to this behaviour. In particular, the Ph.D. student will be proposed to:

- build a genetic linkage map and identify the genetic basis of quantitative traits based on the greenhouse experiment and data by using AFLP and gene-based (Audigeos et al. submitted; Brousseau 2009) markers

- setup a reciprocal transplant experiment in natural conditions, with half-sib families of species of the genus Eperua, with the aim of evaluating genetic and environmental components of environmental adaptations, as well as phenotypic plasticity and genotype × environment interactions; analyse the ecophysiological and growth traits of the transplanted seedlings and identify the genetic components of differences among sites and among environments, and compare the results obtained across genera.

- validate the genetic bases, identified in (a), based on quantitative data obtained in (b), by genotyping seedlings grown in reciprocal transplants with markers that have shown correlation with the traits, and by validating the correlation in the natural setting of reciprocal transplants.

Supervising scientists. Ivan SCOTTI (CR1 INRA - UMR EcoFoG, 97387 Kourou - Guyane française) (supervisor) ; ivan.scotti@ecofog.gf

Erwin DREYER (DR1 INRA - UMR EEF, 54280 Champenoux) (co-supervisor)

Life in French Guiana

Scientific life is very active at the EcoFoG research centre in Kourou, French Guiana, with weekly seminars, journal clubs and training courses. Lab equipments are standard international level in genetics and plant physiology. The climate is hot and humid, but largely mitigated by trade winds on the coast (where Kourou is located), with alternating rainy and dry seasons. The main asset for leisure time in French Guiana is its outstanding natural setting (the tropical rainforest); the Carnival in French Guiana is also unique. Everyday life can be expensive, in particular for housing and import goods. A vehicle is generally necessary for travel between towns. Life is generally laid back, although with occasional insecurity problems.

VISITORS TO FRENCH GUIANA MUST HOLD A VALID YELLOW FEVER VACCINE CERTIFICATE

Ivan Scotti INRA - UMR 0745 ECOFOG “Ecologie des Forêts de Guyane” / “Ecology of Guiana Forests” Laboratoire de Génétique écologique / Ecological Genetics

Laboratory Campus agronomique, Avenue de France
BP 709 - 97387 Kourou CEDEX FRANCE

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JagiellonianU EcologyEvolutionaryBiology

Institute of Environmental Sciences at the Jagiellonian University, Kraków, Poland (www.eko.uj.edu.pl)

Is opening applications for:

4-year interdisciplinary doctoral studies programme in ecology in English, with net-scholarships 2200 PLN per month, offering research in Poland and half-year placements in academic centres outside Poland and a choice of 4 out of 8 courses from different scientific disciplines conducted by eminent Polish and foreign specialists

Application deadline: 10 June 2010

Detailed information, containing the list of research topics proposed for PhD students, profile of the applicant and the application instructions are available at:

www.eko.uj.edu.pl/ecology < http://www.eko.uj.edu.pl/ecology >

Project co-financed by the European Union under the European Social Fund

"ecology@uj.edu.pl" <ecology@uj.edu.pl>

KULeuven Belgium Cichlid parasites

Dear Evoldir members,

4 YEAR PhD POSITION IN EVOLUTIONARY BIOLOGY Katholieke Universiteit Leuven, Belgium

A 4 year PhD position for an evolutionary biologist is immediately vacant at the Laboratory of Animal Diversity and Systematics (Katholieke Universiteit Leuven and the Royal Museum for Central Africa in Tervuren, Belgium) in the research group of Prof. Filip Volckaert to study micro-evolutionary responses in Lake Tanganyika cichlids.

Description: The project investigates the role of parasitism and immunogenetic adaptation in the diversification of Lake Tanganyika cichlids. Parasites may play an important role in cichlid adaptive radiation as they may influence both naturally and sexually selected traits, speeding up the evolution of reproductive isolation. Field studies, mate-choice experiments and molecular work will be carried out to investigate parasite community structure, mating isolation, the potential role of parasites in mate choice, and local immunogenetic adaptation (MHC). The comparison between cichlid species showing extreme versus no chromatic differentiation will clarify whether parasites, immunogenetic adaptation and colour polymorphism have a synergistic effect in cichlid mate choice. Evolution of cichlids and their parasites has been studied in our team over the past 3 years, while the Royal Museum for Central Africa is a world expert in cichlid systematics (see http://bio.kuleuven.be/de/dev/pubs.php for publications). The project starts on 01/04/2010 and is supervised by prof. Filip Volckaert and dr. Joost Raeymaekers.

The team: The Laboratory of Animal Diversity and Systematics has a strong expertise in neutral and adaptive evolution of fishes and their parasites, including field monitoring, experimental design, medium-throughput genotyping, the analysis of genetic, genomic, and phenotypic data with up-to-date statistical approaches. Topics addressed include phylogeny, barcoding, phylogeography, population genetics, local adaptation and rapid evolution (natural and fisheries induced), enhanced selection in aquaculture (aquaculture genomics), co-evolution between host and parasite, spatio-temporal dynamics of nursery grounds and the management of aquatic habitats. Our team comprises 6 PhD students, 4 postdocs, 2 technicians and a team leader. The historic KULeuven, founded in 1425, has a very stimulating research environment. The modern city of Leuven with its medieval roots offers a high quality of life.

Profile: High motivation, background in evolutionary biology, interest or experience in field based experimental research is strongly recommended. Research will be carried out in collaboration with a multidisciplinary team specialised in evolutionary biology, molecular parasitology and population genomics. Mate choice experiments will be carried out at the University of Graz (Prof. C. Sturmbauer).

Financing: The successful candidate is funded by a national project (Research Fund - Flanders; salary of approximately 1700 /month net). The candidate is expected to apply for a national Research Fund - Flanders or IWT fellowship.

Application deadline: Please apply at http://phd.kuleuven.be/set/-voorstellen_departement?departement=-50000454#detail, send a letter of motivation, and two letters of reference to Filip Volckaert by 15 April 2010.

Contact: Prof. Filip Volckaert Katholieke Universiteit Leuven Laboratory of Animal Diversity and Systematics Ch. Deberiotstraat 32 Postbox 2439 B-3000 Leuven, BELGIUM Phone: +32 16 32 39 72 (office) or +32 16 32 39 66 (secretariat) Fax: +32 16 32 45 75 Mailto:filip.volckaert [at] bio.kuleuven.be URL: http://bio.kuleuven.be/de/dev/index.php Tine Huyse <Tine.Huyse@bio.kuleuven.be>

KULeuven InsectEvolutionaryGenetics

Genetics/Genomics of edge populations in a northward moving damselfly

GENERAL THEME: The PhD project is embedded in a larger research program where we compare the evolutionary ecology of edge and central populations in damselfly species that are expanding their range northwards and thereby shed light on the consequences for local ecological interactions and the potential for further range expansion. We are documenting how edge populations differ in a number of ecologically-relevant traits. To understand phenotypic differentiation in these traits we are quantifying associated selection pressures and patterns of divergence at neutral and quantitative genetic traits, as well as functional genetic/genomic variation. The latter genetic/genomic aspect will be the focus of this PhD project.

PRACTICAL WORK will be a combination of (1) sampling campaigns in natural field populations in collaboration with other team members, and (2) genetic/genomic analyses. We have excellent research facilities with a well-equipped laboratory for studying genetic variation. Focus will be on population genetics (microsatellite analyses) and the study of differentiation between edge and central populations in candidate genes related to dispersal and activity. Population genetic analyses will de done in close collaboration with the Genetic Diversity group of the Research Institute for Nature and Forest (INBO, Dr. Joachim Mergeay). Genomic analyses will be done in close collaboration with Dr. Phill Watts (University of Liverpool, UK).

PROFILE: master degree in Biology, Biotechnology, Bio-engineering or related field and with a strong interest in genetic/genomic work. Preference will go to candidates with experience in genetics/ genomics, or at least proven experience with laboratory work and a very strong motivation to learn relevant techniques. The candidate should be willing to do study visits abroad (e.g. Univ. Liverpool, UK).

OFFER: A full time job (salary according to the University of Leuven salary system, ca. 1900/ month) guaranteed until the end of 2013. If necessary, more funding will be applied after this. Leuven (http://www.leuven.be) is a pretty, historical university city with a very high and pleasant standard of living. The historic university, founded in 1425 (http://www.kuleuven.be/english), has a top research and teaching standard. Within our research group we have ample expertise working with damselflies (http://bio.kuleuven.be/de/dea/-people_detail.php?pass_id=u0034380).

INTERESTED? Please send your CV, a letter of motivation including relevant experience, and contact details of two referents to Prof dr. Robby Stoks (robby.stoks@bio.kuleuven.be), University of Leuven, Laboratory of Aquatic Ecology and Evolutionary Biology, Deberiotstraat 32, B-3000 Leuven, Belgium. Applications will be reviewed until the position is filled. The preferred starting date would be in May 2010.

robby.stoks@bio.kuleuven.be

LaurentianU BenthicInvert CrypticDiversity

M.Sc. Position at Laurentian University, Ontario

Cryptic Genetic Diversity in Hyalella azteca.

A graduate student position is available at Laurentian University to examine genetic diversity and possible cryptic speciation in benthic invertebrates.

Freshwater benthic invertebrates generally have a relatively short reproduction time that, combined with a spectrum of selective pressures across varying habitats, make them strong candidates for diversification. Previous research using DNA barcoding suggests that a common species± of amiphipod may actually be 30 or more provisional species. The Greater Sudbury area watershed presents varying levels of heavy metal contamination possibly resulting in local adaptation or species differentiation. Previous work suggested that there are possibly two or more co-occurring species within this region possibly resulting from both isolation and habitat specialization. This isolation may predate the local contamination, but the contamination may be exaggerating the effects of longer term separation.

We are looking for an M.Sc. candidate to explore the possibility of cryptic amphipod species and the potential environmental causes of this speciation process. The student will work in the context of evolutionary ecology combining field work and possibly experimental studies depending on his/her interests. Good aptitude for fieldwork, molecular ecology skills and especially population genetics basics are expected as well as good communication skills.

Starting date: Candidates are expected to commence their studies in June 2010.

Full funding of approximately $15,000/year is guaranteed for 2 years. Additional scholarships will be available by competition.

How to apply: Interested students should contact Dr. David Lesbarrres (dlesbarreres@laurentian.ca) or Dr. Thomas Merritt (TMerritt@laurentian.ca), including a cover letter describing background and interests (including specific interests in this research project), cv, transcripts (unofficial is accepted).

– "It takes all the running you can do to keep in the same place."

Dr. David Lesbarrres Associate Professor & Graduate Coordinator

Genetic & Ecology of Amphibians Research Group (GEARG) Department of Biology - Laurentian University

http://biology.laurentian.ca/Laurentian/Home/-Departments/Biology/Faculty_and_Staff/Professors/-lesbarreres/lesbarreres.htm 935 Ramsey Lake Road, Sudbury, Ontario P3E 2C6, Canada phone: 705-675-1151 ext. 2275 Fax: 705-675-4859

David Lesbarreres <dlesbarreres@laurentian.ca>

Marseille CoralAdaptations

Dear all, here is a PhD proposal in the DIMAR laboratory in Marseille (France; http://www.com.univ-mrs.fr/DIMAR/)

PhD proposal: The DIMAR laboratory in Marseille offers a phD opportunity funded by the CNRS. This is a 3 years contract, which will start on october 2010. The PhD student will study the genetic consequences of past and present environmental changes on Mediterranean gorgonians (red coral, Corallium rubrum, and the red gorgonian Paramuricea clavata). The impact of past environmental fluctuations will be analysed by a compared study of the sequence diversity of several nuclear markers. The putative consequences of on going climate change will be studied by estimating the levels of expression of some candidate genes in experimental and natural conditions. This will be used in order to analyse the adaptation (sensu lato) of these organisms to some environment variable in space and time. This project will take advantage of several previous advances: - the development of some nuclear markers (introns) - the isolation of some candidate genes and the development of real-time PCR protocols - a 454 sequencing of the transcriptome for one of the model species - a microsatellite analysis of the genetic structure of these organisms.

Some skills in gene expression studies or sequence analysis are required. A good level in diving may be an advantage.

Please send your CV and a motivation letter before april 30, at the following adresses: didier.aurelle@univmed.fr, anne.chenuil-maurel@univmed.fr, jean-pierre.feral@univmed.fr More details and the application file can be found here: https://www2.cnrs.fr/DRH/doctorants-10/ Best regards Didier

– Didier AURELLE

Courriel: didier.aurelle@univmed.fr / aurelle.didier@gmail.com

Maître de Conferences UMR 6540 DIMAR Universite de la Mediterranee / Centre d'Oceanologie de Marseille Station Marine d'Endoume Rue de la batterie des Lions 13007 Marseille FRANCE Tel: + 33 4 91 04 16 18 Fax: + 33 4 91 04 16 35

http://sites.google.com/site/aurelledidier/ "Afin de contribuer au respect de l'environnement, merci de n'imprimer ce mail qu'en cas de necessite"

Didier Aurelle <didier.aurelle@univmed.fr>

MasseyU AltruismEvolution

EVOLUTION OF REPRODUCTIVE ALTRUISM

A doctoral fellowship is available to study the evolution of reproductive altruism at the New Zealand Institute for Advanced Study, Massey University, Auckland, New Zealand. The scholarship will cover tuition fees and provide a monthly stipend (for 3 years). The fellowship is open to all nationalities.

Working as part of a multidisciplinary team the successful applicant will drive an independent research project on the evolution of individuality within the context of the major (fraternal) evolutionary transitions. The project is primarily experimental and makes use of model bacterial populations.

Applications are welcomed from individuals passionate about evolutionary biology and the emergence of complexity. Hands-on research experience (e.g., at MSc level) would be a distinct advantage.

Applicants should send a covering letter describing their research interests, motivation, a CV, and contact information for three referees to Vesna Davidovic-Alexander (v.davidovic-alexander@massey.ac.nz).

Closing date for applications is Friday 9th April. The start date is negotiable, but ideally by the latter part of 2010.

Interested students should contact Paul Rainey for further information (p.b.rainey@massey.ac.nz)

Paul B Rainey New Zealand Institute for Advanced Study and Allan Wilson Centre for Molecular Ecology & Evolution Massey University at Albany New Zealand

http://evolution.massey.ac.nz/rainey
paulbrainey@gmail.com

MaxPlanck Leipzig ComputationalEvolutionaryBio

- PhD position in computational/evolutionary biology -

There is an opening (fall 2010) for a student with a strong academic background to pursue a PhD in our research group at the Max Planck Institute for Evolutionary Anthropology (Department of Evolutionary Genetics). One main aim in the laboratory is the characterization of genes whose protein functions require the trace element selenium. These genes incorporate selenium in the form of selenocysteine, the 21st amino acid in the genetic code, and are known as selenoprotein genes. Building on our expertise in the computational identification and annotation of selenoprotein genes in eukaryotic genomes, the student will apply population genetics/molecular approaches to study their evolution. We will focus on understanding the genetic basis of adaptations in selenoprotein gene regulation to levels of dietary selenium in primates. Re-sequencing and comparative expression experiments will be used. Ample opportunities for the analysis of primate genomes in collaboration with other groups in the Department will exist.

We are seeking a motivated, well-organized and creative person. Previous research experience is an advantage. The student will receive a payment according to Max Planck Institute rates. The working environment of the institute is English-speaking, and the members constitute a highly international group. The institute is in Leipzig, a pleasant city of 500,000 inhabitants situated two hours from Berlin and three hours from Prague. Applicants should send their CV, transcripts and name and address of two references (in PDF format) to Dr. Sergi Castellano (castellanos@janelia.hhmi.org).

Some articles of interest to candidates are:

S Castellano, AM Andrés, E Bosch, M Bayes, R Guigó and AG Clark Low exchangeability of selenocysteine, the 21st amino acid, in vertebrate proteins Molecular Biology and Evolution, 26, 2031-2040 (2009)

S Castellano, VN Gladyshev, R Guigó and MJ Berry SelenoDB 1.0: a database of selenoprotein genes, proteins and SECIS elements Nucleic Acids Research, 36, D339-D343 (2008)

S Castellano, AV Lobanov, C Chapple, S Novoselov, M Albrecht, D Hua, A Lescure, T Lengauer, A Krol, VN Gladyshev and R Guigó Diversity and functional plasticity of eukaryotic selenoproteins: identification and characterization of the SelJ family Proceedings of the National Academy of Sciences USA, 102, 16188-16193 (2005)

GV Kryukov, S Castellano, SV Novoselov, AV Lobanov, O Zehtab, R Guigó and VN Gladyshev Characterization of mammalian selenoproteomes Science, 300, 1439-1443 (2003)

S Castellano, N Morozova, M Morey, MJ Berry, F Serras, M Corominas and R Guigó in silico identification of novel selenoproteins in the Drosophila melanogaster genome EMBO reports, 2, 697-702 (2001)

– Sergi Castellano

East Lab, 2E.290 Janelia Farm Research Campus Howard Hughes Medical Institute 19700 Helix Drive Ashburn, VA 20147 (USA)

http://selab.janelia.org/people/castellanos Ph: 571 209 4000 ext. 7160 Fax: 571 209 4095

castellanos@janelia.hhmi.org

MNHN Paris HumanPopulationGenetics

PhD position in human population genetics

A PhD position is available in the genetic anthropology and human ecology team (UMR 7206) in Paris, France. This lab is part of the Centre National de la Recherche Scientifique (CNRS) and the National Museum of Natural History (MNHN).

In humans, evolution is not only biological but also cultural. Social organization is a key factor influencing gene transmission to the next generation and gene dispersion within and among populations. Ethnologists have described the impressive complexity of social organizations in human populations, and in particular the complex rules of alliance (which determine mate choice), rules of descent (which affiliate individuals to kin groups), and rules of residence (which indicate where married couples settle down). In this context, this PhD project aims at better understanding the impact of kinship systems on the genetic evolution of human populations. It is part of a four years ANR funded research program (2009-2013).

In this PhD project, multidisciplinary models of gene pool evolution under different types of social organizations will be developed. Special attention will be given to matrilineal, patrilineal and cognatic social organizations with different level of exogamy and different residence rules. Individual-based simulations will be performed in order to implement complex models of alliance, descent and residence rules. This will allow investigating the patterns of genetic diversity (neutral and counter-selected) expected under different kinds of social organizations.

Then, the outcome of these simulations will be compared to genome-wide genetic patterns observed in South-East Asian populations presenting a wide range of social organizations. When appropriate, social organization parameters (such as kin group extinction rate or migration rates of men and women between kin groups) will be estimated. The complexity of the envisioned model in terms of social, demographic and genetic parameters will be circumvented by the use of ABC (Approximate Bayesian Computation). This approach may also help detecting populations having experienced a recent transition in their social organization.

This position is funded for three years by the Ecole doctorale Diversité du Vivant (http://eddv.snv.jussieu.fr/) and starts in September 2010. Applicants should have a Master degree in population genetics, ecology or evolution and a strong interest for theoretical approaches. Applications should include a description of research interests, a complete CV and the names and email addresses of 2 professional references. Applications should be sent by email before the 18th of April 2010 to the supervisors, Pr Evelyne Heyer (heyer@mnhn.fr), Dr Raphaëlle Chaix (chaix@mnhn.fr) and Dr Bruno Toupance (toupance@mnhn.fr).

toupance@mnhn.fr toupance@mnhn.fr

NIOZ Netherlands BenthicMarineBiodiversity

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

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

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

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

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

REQUIREMENTS

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

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

Further information on the project and the position can be obtained from Dr Jan van Gils (Jan.van.Gils@nioz.nl or otherwise from Jolanda Evers, Human Resources (Email: Jolanda.evers@nioz.nl, phone +31-222-369371). General information about NIOZ can be found at: http://www.nioz.nl Application:

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

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

Jan.van.Gils@nioz.nl Jan.van.Gils@nioz.nl

Oxford BacterialGenomeEvolution

We are recruiting a PhD student to join the group of Dr. Daniel Wilson. The group is principally engaged in the activities of the UKCRC Consortium Modernising Medical Microbiology (www.modmedmicro.ac.uk), an ambitious project with the goal of revolutionising approaches to tracing and tracking clinically important micro-organisms in near-to-real time using whole genome sequencing technologies. The aim is to elucidate the evolution and epidemiology of four medically important pathogens, namely Mycobacterium tuberculosis, Staphylococcus aureus, Clostridium difficile and norovirus through the application and development of statistical analyses.

PhD Student £15,000 p.a. stipend A DPhil (PhD) studentship in conjunction with Prof. Peter Donnelly, fully funded to the Home/EU rate, is available for a candidate with good quantitative skills, an interest in evolution and evidence of excellent performance in a science or maths degree, particularly Biology or Statistics. Acquiring skills from the fields of population genetics, epidemiology, statistics and computing, you will apply and develop tools that deepen our knowledge and understanding of pathogens. Please direct informal enquiries by email to daniel.wilson@ndm.ox.ac.uk . Please quote reference HB-10-009-DW.

The closing date for applications is Friday, 2 April 2010.

Daniel Wilson <daniel.wilson@ndm.ox.ac.uk>

RoyalHolloway AdaptiveValueOfLearning

The adaptive value of learning in different ecological contexts

Despite a large amount of research into the mechanisms of learning we still know almost nothing about how cognitive traits might be adapted to different ecological conditions. This project provides a series of novel experimental approaches to address this issue. Anticipated environmental change is almost certain to affect the structure and dynamics of pollination systems. A more complete understanding of pollinator behaviour means we will be better able to predict how the pollination of crops and wild flowers will be affected by environmental change.

Learning, or the adaptive modification of behaviour based on experience, is an important way in which animals can respond to changes in their environment. Many pollinators are actually faced with a complex environment in which to collect food - this 'pollination market' may contain dozens of flower types which not only vary in colour, shape and scent, but also in the quantity and quality of rewards (principally pollen and nectar) they present. The rewards on offer may change very rapidly over the course of the day depending on the timing of reward provision by flowers, climatic conditions and the activity patterns of other flower visitors. Hence, learning to modify flower choices rapidly could be advantageous to a pollinator in circumstances where the floral market is highly dynamic. This view is supported by current data showing that colonies containing faster learning individuals are more efficient at collecting nectar in the field (Raine & Chittka 2008). However, there is actually a large range in learning performance among bee colonies with individuals in some colonies learning much faster than others. Therefore, a key question is what maintains this variability in cognitive abilities if faster learning performance appears to be at a selective advantage?

This project will investigate these questions using the bumblebee (Bombus terrestris) as a model system in both laboratory and field experiments. Previous work has shown that B. terrestris colonies are amenable to laboratory learning experiments and that the same colonies can subsequently be moved into the field to assess their foraging abilities (an established robust proxy measure of colony fitness) under ecologically relevant conditions (Raine & Chittka 2007; 2008). This approach enables us to examine potential links between cognitive abilities (tested in the laboratory) with foraging performance (assessed under field conditions). B. terrestris is an important pollinator species which is bred commercially for large-scale crop pollination. In the laboratory several generations of bees can be raised each year and this will form the basis of selection experiment to examine the heritability of learning performance. 'Fast' and 'slow' learning lines of bumblebee colonies will be selectively bred from the most extreme behavioural phenotypes observed in each generation. The foraging performance of these colonies will then be tested in a range of habitats to assess the ecological conditions to which particular cognitive behavioural phenotypes might be best adapted.

This project will also examine how variation in learning performance between isolated B. terrestris populations could be adapted to particular local floras. B. terrestris occurs throughout Europe including many isolated island populations. Preliminary data indicate a number of striking differences in learning ability between colonies tested from several isolated populations. This project will investigate whether these differences are predictably linked to differences in local flora in which they each forage, particularly with respect to the degree to which the most profitable flower species changes over time (a trait which could favour faster learning).

For further details about the project please contact Dr. Nigel Raine (nigel.raine@rhul.ac.uk).

Applications should be made by submitting a completed application form (available from http://www.rhul.ac.uk/BioSci/Vacancies/SBSPhD2010.doc) and a full CV by email to BioSciencesTemp@rhul.ac.uk by 20th March. Candidates should arrange for two academic references to be sent to the same email address (BioSciencesTemp@rhul.ac.uk) by the same date. It is anticipated that interviews will take place in April.

References

Raine NE, L Chittka (2007). The adaptive significance of sensory bias in a foraging context: floral colour preferences in the bumblebee Bombus terrestris. PLoS One 2: e556.

Raine NE, L Chittka (2008). The correlation of learning speed and natural foraging success in bumble-bees. Proceedings of the Royal Society of London Series B 275: 803-808.

NB: pdf versions of these papers can be downloaded from:

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UAntwerp BirdParasite

Call for applicants on bird-parasite research

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

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

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

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

If you are interested or need further information, contact Prof. Erik Matthysen at erik.matthysen@ua.ac.be

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

Groenenborgerlaan 171, 2020 Antwerpen +32 3 265 3464

erik.matthysen@ua.ac.be erik.matthysen@ua.ac.be

UBasel BacterialEvolutionaryGenomics

PhD position in Bacterial Evolutionary Genomics at the Biozentrum, University of Basel, Switzerland

Quantifying phenotypic evolution in microbes

A PhD position in combined experimental and computational microbial genomics is available at the Biozentrum of the University of Basel. We are looking for a highly motivated, skillful, and hard working individual who has a strong interest in microbial evolution. The project concerns a combined experimental and computational analysis of genome evolution in bacteria. Using high-throughput quantification of growth-phenotypes for a large collection of natural isolates of bacteria, in combination with genome sequencing of a large number of strains, we aim to infer the selective pressures that are driving adaptive phenotypic changes in bacteria on short evolutionary time scales.

An integral part of the project will be computational analysis of the data, including analysis of the relation between genotypic and phenotypic changes, and evolutionary modeling. Ultimately we aim to relate the results to patterns of genomic evolution that we have previously observed (e.g. van Nimwegen, Trends in Genet 19:9:479-484 (2003), Molina and van Nimwegen, Biol Direct 3:51 (2008)).

A master's diploma is required. Experience in one (or more) of the following would be highly preferred: evolutionary theory, microbiology, bioinformatics and computational biology, or molecular biology, as the project will involve both wet-lab and computational work. The candidates should have good knowledge of English. German knowledge is helpful but not necessary.

The position is in the group of Prof. Erik van Nimwegen at the Biozentrum, University of Basel. The group is highly interdisciplinary with members whose backgrounds range from molecular biology to theoretical physics. Although the main focus of the group has been on theoretical and computational analysis, we have recently added a wet lab component. The position will be co-supervised by Dr. Olin Silander, who heads the wet-lab. The Biozentrum in Basel offers a stimulating, international work environment with researchers working in related, relevant topics (microbiology, bioinformatics, etc). The working language at the Institute is English. The salary is generous and is set according to the guidelines of the Swiss National Science Foundation. The start date will by mutual arrangement.

To apply, please send a motivation letter, CV, and names and emails of two to three references by email to: erik.vannimwegen@unibas.ch

We will start reviewing applications from 31st March 2010 onward. Do not hesitate to contact me if you have further questions regarding the project.

Prof. Erik van Nimwegen erik.vannimwegen@unibas.ch Department of Bioinformatics Biozentrum, University of Basel Klingelbergstrasse 50/70 CH-4056 Basel / Switzerland http://www.biozentrum.unibas.ch/˜nimwegen olin.silander@unibas.ch olin.silander@unibas.ch

UBristol 2 Evolution

Two CASE NERC-funded studentships are available in the School of Biological Sciences at the University of Bristol, UK.

1) Predicting ecological and evolutionary responses of pollination networks to climate change: the impact of variation within species, with Dr Jon Bridle, Prof Jane Memmott, and Dr Lucy Rogers (Avon Wildlife Trust).

2) Ecological constaints on evolution: a case study with Lake Malawi's cichild fish, with Drs Martin Genner, Jon Bridle and Lukas Ruber (Natural History Museum, London).

For more details on these studentships, and descriptions of how to apply, please see:

http://www.bristol.ac.uk/biology/prospective-phd/studentships.html Or contact Dr Jon Bridle (jon.bridle@bristol.ac.uk), or Dr Martin Genner (m.genner@bristol.ac.uk) for enquiries for 1) or 2) respectively.

Eligibility for full-funding is restricted to UK citizens or residents of more than three years, with degrees of 2.1 standard of equivalent (See http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp)

Jon Bridle <Jon.Bridle@bristol.ac.uk>

UBritishColumbia Okanagan PopulationGenomics

A PhD graduate assistantship is available in the laboratory of Dr. Michael Russello at the University of British Columbia Okanagan (UBC O) in the area of population and conservation genomics starting September 2010. I am looking for a highly motivated graduate student to join our group studying fine-scale adaptive population divergence in a number of systems centering on vertebrate species of conservation concern. There are opportunities for both laboratory and field-based research, although all projects involve the use of high-throughout DNA-based methodologies. Individuals with experience and/or interest in SNP discovery using next-generation sequencing are especially encouraged to apply. Please visit my website for further details: http://people.ok.ubc.ca/mirussel/ Candidates should have a strong undergraduate background in biology, and prior research experience with molecular laboratory techniques and bioinformatics is desirable. For more information contact Michael Russello at michael.russello@ubc.ca. Additional information about our Biology graduate program at UBC O can be found at the following website: http://web.ubc.ca/okanagan/biophgeo/graduate.html Michael Russello Assistant Professor Department of Biology Centre for Species at Risk and Habitat Studies University of British Columbia Okanagan Kelowna, British Columbia Canada

michael.russello@ubc.ca

UCD Dublin EvolutionaryBiology

We are pleased to announce the birth of the new "Masters in Evolutionary Biology" at UCDDublin, Ireland. This is a full-time, 12-month course on the nature, relevance and far-reaching implications of evolutionary theory. The course features an outstanding diversity of topics and approaches in current evolutionary research (both organism-based and theoretical); and innovative educational approaches, including field-work, museum and laboratory training, data analysis and modelling.

To learn more, go to:

http://www.ucd.ie/lifesciences/-graduateschool/prospectivegraduatestudents/-taughtgraduateprogrammes/ Application deadlines are in two rounds: First: 25 March Second: 31 May

Masters in Evolutionary Biology UCDSchool of Biology & Environmental Science evolution@ucd.ie

evolution@ucd.ie

UEdinburgh PlantTaxonomy

MSc Degree/Postgraduate Diploma in the Biodiversity and Taxonomy of Plants

Royal Botanic Gardens Edinburgh/ University of Edinburgh

Programme Philosophy The MSc in Biodiversity and Taxonomy of Plants was established by the University of Edinburgh and the Royal Botanic Garden Edinburgh (RBGE) to address the growing worldwide demand for trained plant taxonomists and whole-plant scientists. A detailed knowledge of plants and habitats is fundamental to their effective conservation. To communicate such knowledge accurately and effectively, training is required in plant taxonomy ' the discipline devoted to plant diversity and evolution, relationships, and nomenclature. The MSc is perfect for those wishing to develop a career in many areas of plant science: Survey and conservation work in threatened ecosystems Assessment of plant resources and genetic diversity Taxonomic research Management of institutes and curation of collections A stepping stone to PhD research and academic careers

Edinburgh is a unique place to study plant taxonomy and diversity. The programme and students benefit widely from a close partnership between RBGE and the University of Edinburgh (UoE). RBGE has one of the world^{1}s best living collections (15,000 species across our four specialist gardens ' 5% of world species), an herbarium of three million specimens and one of the UK^{1}s most comprehensive botanical libraries. The School of Biological Sciences at UoE is a centre of excellence for research in Plant Sciences and Evolutionary Biology. Recognised experts from RBGE, UoE, and from different institutions in the UK deliver lectures across the whole spectrum of plant diversity. Most course work is based at RBGE, close to major collections of plants, but students have full access to the extensive learning facilities of the university.

Aims and Scope The MSc provides biologists, conservationists, horticulturists and ecologists with a wide knowledge of plant biodiversity, as well as a thorough understanding of traditional and modern approaches to pure and applied taxonomy. Apart from learning about the latest research techniques for classification, students should acquire a broad knowledge of plant structure, ecology, and identification.

Programme Structure This is an intensive twelve-month programme and involves lectures, practicals, workshops and essay writing, with examinations at the end of the first and second semesters. The course starts in September of each year and the application deadline is normally 31 March. Topics covered include: Functions and philosophy of taxonomy Evolution and biodiversity of the major plant groups, fungi and lichens Plant geography Ecology of plants and ecosystems Conservation and sustainability Production and use of floras and monographs Biodiversity databases Phylogenetic analysis Population and conservation genetics Tropical field course, plant collecting and ecology Curation of living collections, herbaria and libraries Plant morphology, anatomy and development Molecular systematics

Fieldwork and visits to other institutes are an integral part of the course. There is a two-week field course to Belize in which students are taught field collection and identification of tropical plants ecological survey techniques. The summer is devoted to four months of a major scientific research project of the student^{1}s choice or a topic proposed by a supervisor. These research projects link in directly with active research programmes at RBGE.

Entry Requirements Applicants should ideally hold a university degree, or its equivalent, in a biological, horticultural, or environmental science, and above all have a genuine interest in plants. Relevant work experience is desirable but not required. Evidence of proficiency in English must be provided if this is not an applicant^{1}s first language.

Funding The course is currently supported by eight Natural Environment Research Council studentships that are open to EU students only. Other international funding bodies have supported overseas students in the past.

Further Information For further details on the programme, including a course handbook please visit the RBGE website: http://www.rbge.org.uk/-education/professional-courses/msc-in-biodiversity-and-taxonomy-of-plants < http://www.rbge.org.uk/-education/professional-courses > You can also contact the Course director or Education Department at RBGE, or the Postgraduate Secretary of the University of Edinburgh:

MSc course Director, Dr Louis Ronse De Craene Royal Botanic Garden Edinburgh

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UGothenburg PlantMolecularSystematics

PhD Student Position â Plant Molecular Systematics

University of Gothenburg, Sweden

Short Description: The systematics and biodiversity research group is seeking to fill a doctoral student position within the subject area of plant molecular systematics. The research group is undertaking a project, funded in part by a grant from the Swedish Research Council, that seeks to develop new methods of analysis based upon the multispecies coalescent to distinguish between incongruence among gene trees caused by lineage sorting, hybridization or paralogy. This new approach requires novel data that will be drawn from the Mediterranean legume genus Medicago, making use of the nearly complete genome sequence available in M. truncatula. We also are seeking to optimize high throughput sequencing techniques to improve the efficiency for the kind of sampling used in systematic projects (i.e., many individuals for 5 â 20 unlinked genes). The successful applicant would be involved in some or all of these areas depending upon their inclination and skills.

Tasks The major task for the successful applicant will be to conduct their PhD research under the supervision and direction of Dr Bernard Pfeil. Secondary tasks will be to improve the applicantâs bench and analytical skills and theoretical breadth during their education. Specific tasks associated with the research project include: DNA extraction, PCR, molecular cloning, Southern probing, probe design, preparation of material for 454 sequencing, restriction enzyme digestion, PCR primer design, sequence contig assembly, phylogenetic analysis, assessment of incongruence, effective population size estimation, molecular dating, coalescent simulation.

Qualifications The applicant must have: –A Masterâs degree or a Fil. Mag. in Biology or similar (such as a four year undergraduate degree with a research thesis). This degree should emphasize biology, botany, and especially molecular systematics. –Good communication skills (written and verbal) in English, including the potential to teach in English. –Documented ability to perform basic research projects under supervision. –Good knowledge of molecular systematic theory, concepts, challenges and new developments. –Routine molecular systematics laboratory skills (e.g., PCR, DNA extraction, gel electrophoresis).

A complete description of the position and further information about **how to apply** may be obtained by emailing Dr Bernard Pfeil (email: bernard.pfeilATdpes.gu.se Âwith âPhD positionâ placed in the subject line.

ÂThe PhD position will begin during mid 2010, or by negotiation.

Bernard Pfeil

Associate Senior Lecturer Department of Plant and Environmental Sciences University of Gothenburg, Sweden

website in English: http://www.dpes.gu.se/english/Personnel/scientists_teachers/Bernard_Pfeil/ Bernard Pfeil <bernard.pfeil@gmail.com>

ULouisianaMonroe SnailGeneticDiversity

I am looking to recruit one M.S. student for Fall 2010 to work on population-level genetic diversity in freshwater snails. The student will screen ISSR primers for use with the pleurocerid snail Elimia potosiensis as part of a larger project examining the genetic and environmental components of shell shape.

Pending available funds, the student will receive an $8,000 teaching assistantship plus full tuition waiver for at least two years. Assistantships are available on a competitive basis.

More information on my lab can be found at http://www.ulm.edu/~minton. Applicants must have a minimum 3.0 undergraduate GPA and 1000 Q+V GRE score. Since assistantships are awarded on a competitive basis, the higher the GPA and GRE the better. Note that these values are higher than ULM's minimum graduate admissions standards.

Applicants must also have experience with standard DNA methods including extraction, PCR amplification, and agarose gel electrophoresis. At least one reference/recommendation must speak to the student's ability in the lab.

Interested students can contact me directly at minton@ulm.edu and browse to our departmental website http://www.ulm.edu/biology . Dr. Russ Minton Associate Professor of Biology University of Louisiana at Monroe Monroe, LA 71209-0520 318-342-1795 minton@ulm.edu

Russell Minton <minton@ulm.edu>

UMemphis InsectPhylogenetics

A teaching/research assistantship is available for a M.S. or Ph.D. student in the Department of Biology at the University of Memphis (TN) under the supervision of Dr. Duane McKenna, beginning Fall 2010. Students interested in insect (especially beetle) molecular phylogenetics/phylogenomics and the evolutionary ecology of insect-plant interactions are encouraged to apply. Candidates must have a strong interest in systematics and evolutionary biology, and prior laboratory and field experience.

Interested students may inquire by contacting dmckenna@memphis.edu. Further information about the Department of Biology and Graduate Program can be found at http://www.memphis.edu/biology/graduate.htm . Duane D. McKenna, Ph.D. Assistant Professor, Department of Biology Associate, Program in Bioinformatics University of Memphis 3774 Walker Avenue Memphis, TN 38152

phone: (901) 678-1386 email: dmckenna@memphis.edu website: https://umdrive.memphis.edu/dmckenna/public/index.html dmckenna@memphis.edu

UNorthCarolina Wilmington MarineMolecularEvol

Ph.D. assistantship in marine molecular evolution

A Ph.D. assistantship in marine molecular evolution is available at the University of North Carolina, Wilmington, to begin Fall 2010. The position is part of a funded collaborative project with colleagues at the University of New England, which examines the role of larval dispersal and physiological tolerance in establishing range limits of the northern blue mussel, Mytilus trossulus, in the Gulf of Maine. The selected candidate will work closely with a molecular ecologist, a benthic ecologist, and a physical oceanographer. The position is interdisciplinary and will involve intensive field and laboratory studies of patterns of dispersal, recruitment, and postsettlement mortality in relation to the Eastern Maine Coastal Current. The successful candidate should be highly motivated, work well in a team, and have solid molecular laboratory skills. Desired qualifications include an excellent academic record in marine biology and oceanography and a strong background in molecular ecology and evolution; an interest in the genetics of hybrid zones is also a plus. Candidates should email Dr. Michael McCartney a letter of interest and a C.V. (mccartneym@uncw.edu; http://www.uncw.edu/bio/faculty_mccartney.htm) and are encouraged to visit http://24.97.224.81/research/msc/faculty.cfm for information on PIs Dr. Phil Yund and Dr. Charles Tilburg. For details on applying to the Ph.D. in Marine Biology, visit http://www.uncw.edu/bio/grad-phd.html (deadline is April 15, 2010).

Michael A. McCartney Associate Professor Center for Marine Science UNC Wilmington 5600 Marvin Moss Lane Wilmington NC 28409 (910)962-2391 voice (910)962-2410 fax

"McCartney, Michael" <mccartneym@uncw.edu>

UppsalaU EvolutionaryGenetics

PhD-student position in Biology with specialization in Evolutionary Genetics, at the Department of Evolution, Genomics and Systematics, Uppsala University.

Starting date: preferably in August 2010 or as agreed upon.

The Department of Evolutionary Biology (http://www.egs.uu.se/evbiol/index.html) is situated in the Evolutionary Biology Centre in Uppsala. The working atmosphere is international with English as the working language. The Evolutionary Biology Centre (http:/-

/www.ebc.uu.se/index_eng.php) constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology. The successful candidate will join a research group led by Tanja Slotte (see http://www.anst.uu.se/taslo254) and will receive training within the EBC graduate school on Genomes and Phenotypes (http://www.ebc.uu.se/gradschool/). The position is financed for four full years.

We seek a highly motivated PhD-student to study the evolution of reproductive traits and genes in plants, with a focus on Arabidopsis relatives. The project will entail experimental work in the greenhouse and the lab, as well as a substantial amount of computational work, including analysis of next-gen sequencing data.

The ideal candidate should have a Master's degree or equivalent in biology, genetics or a related field, and a strong interest in population genetics and/or quantitative genetics. Documented interest in bioinformatics and programming, experimental work with plants and molecular genetic work is beneficial but not required. The person should work well as part of a team but also independently, and be proficient in both written and spoken English. In filling this position the university aims to recruit the person who, in the combined evaluation of competence, skills and documented qualifications, is judged most suitable to carry out and develop the work-in-hand and to contribute to a positive development of the department.

The PhD-student position is a 4-year appointment and the candidate shall primarily devote her/his time to own research studies. Other departmental work, such as educational or administrative can be part of the position (max 20 %). The applicant must be eligible for PhD studies at Uppsala University. Local guidelines at Uppsala University determine the salary levels.

How to apply: The application should be written in English and should include personal information/background, a description of research interests (max 1-2 pages), a complete CV, a description of undergraduate training and the names and email addresses of 2-3 professional references.

More information about the position can be obtained from Dr. Tanja Slotte, tel. 018-471 6466, e-mail Tanja.Slotte@ebc.uu.se. Union representatives are Anders Grundström, Saco-rådet, tel. 018-471 5380, Carin Söderhäll, TCO/ST, tel. 018-471 19 96, Stefan Djurström, Seko, tel. 018-471 3315. Note that this is a reposting of a position that was posted on evoldir on March 6, 2010.

All applications should be sent, preferably by e-mail to: registrator@uu.se , or by fax +46-18471 2000, or by mail to: Registrars Office, Uppsala University, Box 256, SE-751 05 UPPSALA, Sweden. In any corresponcence please use the reference number UFV-PA 2010/806. Application deadline on 12 April, 2010.

Tanja.Slotte@ebc.uu.se Tanja.Slotte@ebc.uu.se

UppsalaU PlantEvolutionaryGenetics

PhD Student position in Plant Evolutionary Genetics

A PhD student position in evolutionary genetics is available in the lab of Tanja Slotte at the Department of Evolutionary Biology, Evolutionary Biology Centre (EBC), Uppsala University.

I study the evolution of reproductive traits and genes in plants, with a focus on Arabidopsis relatives. There are currently two main projects in the lab: 1) Evolution of floral and reproductive traits in Capsella and 2) Genetics of adaptation to past and current climate change in Arabis alpina. There is an opportunity for a PhD student to work on either of these projects, which are outlined below.

In Capsella, marked changes in floral and reproductive traits have occurred in association with the shift to selfing, which is well- characterized and appears to have occurred relatively recently. It is therefore of considerable interest to understand the genetic basis and evolutionary forces underlying these rapid changes. To study these questions, we use a combination of approaches including QTL mapping and population genomics. Here, we are looking for a student who is interested in elucidating the role of regulatory changes for the evolution of reproductive traits in Capsella. The project will involve assessing genetic correlations between phenotypic traits and gene expression, as well as expression QTL mapping, and population genomic tests for selection.

Arabis alpina is an alpine plant species that occurs across a wide geographic area, and which offers an excellent opportunity to test hypotheses on local adaptation and sensitivity to climate change. Within this project, the student will test whether populations from different parts of the species' range differ in their responses to temperature treatments, map genomic regions responsible for such differences and test whether those genomic regions show a signature of divergent selection. Depending on the student's interests, there is also possibility for field work in collaboration with the group of Jon Ågren at the Dept of Plant Ecology at Uppsala University.

Both projects will entail experimental work in the greenhouse and the lab, as well as a substantial amount of computational work, including analysis of next-gen sequencing data. We therefore seek a highly motivated student with a Master's degree or equivalent in biology, genetics or a related field and with a strong interest in population genetics and/or quantitative genetics. Experience of experimental work with plants, molecular genetic work, and documented interest in statistics and programming is beneficial but not required. The person should work well as part of a team but also independently, and be proficient in both written and spoken English. The successful candidate will join a research group led by Tanja Slotte (see http://www.anst.uu.se/taslo254) and will receive training within the EBC graduate school on Genomes and Phenotypes (http://www.ebc.uu.se/gradschool/). The position is financed for four full years. Applications should be written in English and include i) personal information/background, ii) a description of research interests (max 1-2 pages), iii) a complete CV, iv) a description of undergraduate training, v) the names and email addresses of 2-3 professional references. Applications should be sent by email to Tanja Slotte (Tanja.Slotte@ebc.uu.se). Informal inquiries by email or phone (+46-18-4716466) are also welcome.

The position is open until a suitable candidate is found, but for full consideration please apply by the 5th of April 2010. The ideal starting date would be in August 2010.

The Dept of Evolutionary Biology (http://-www.egs.uu.se/evbiol/ index.html) is situated in the Evolutionary Biology Centre in Uppsala. The working atmosphere is international with English as the working language. The Evolutionary Biology Centre (http://www.ebc.uu.se/index_eng.php) constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm.

Tanja.Slotte@ebc.uu.se Tanja.Slotte@ebc.uu.se

USouthernMississippi ConservationGenetics

Graduate Assistantship - Conservation genetics of spotted seatrout.

The Department of Coastal Sciences at the University of Southern Mississippi is requesting applications from highly qualified students for its graduate program in coastal sciences. The Department of Coastal Sciences is located at the Gulf Coast Research Laboratory (http:/-/www.usm.edu/gcrl) in Ocean Springs, Mississippi.

The successful candidate will be involved in the development and application of molecular markers to assess genetic diversity and population structure of spotted seatrout (Cynoscion nebulosus) in the northcentral Gulf of Mexico and in the genetic monitoring of stock enhancement programs.

Successful candidate(s) should possess a B.S. or M.S. in biology or a related science and a minimum GPA of 3.0. The GRE (verbal and quantitative) and TOEFL (for non-native English speakers) are required. Salary starts at $1,600/mo and includes a tuition waiver. The position is available starting fall 2010.

Interested individuals should contact:

Dr. Eric Saillant Assistant Professor The University of Southern Mississippi Gulf Coast Research Laboratory 703 East Beach Drive Ocean Springs, MS 39564 E-mail: eric.saillant@usm.edu

Eric Saillant <Eric.Saillant@usm.edu>

UStirling ForestConservation

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

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

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

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

Closing date for application: 15 February 2010.

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

Cecile FE Bacles Ph.D. Lecturer in Ecological Genetics School of Biological and Environmental Sciences University of Stirling Cottrell Building 4B148 Stirling FK9 4LA Tel: +44 (0) 1786 46 ext 6897 Email:c.f.bacles@stir.ac.uk http://-www.sbes.stir.ac.uk/people/bacles Registration Now Open! Ecological Genetics Group 54th Meeting 6-8 April 2010 http://www.sbes.stir.ac.uk/egg Cecile Bacles <c.f.bacles@stir.ac.uk>

USussex SocialBeesWasps

NERC-funded PhD studentship at Sussex University, UK

Understanding sociality: group size and foraging rewards

The evolution of eusociality, in which some individuals forfeit their own reproduction and help others to reproduce, is a central problem in evolutionary biology. Together with cooperatively-breeding vertebrates, wasps and bees are ideal study systems, partly because they exhibit a wide range of social levels. Funding is secured for the studentship, which would focus initially on testing a potentially fundamental advantage of sociality in terms of foraging rewards. While some social insect foragers can recruit others to food patches, individuals in small social groups forage independently. Under independent foraging, day-to-day variation in the group's total foraging success should be smaller as the number of foragers (i.e. group size) increases: groups should have an advantage compared with lone individuals in terms of increased day-to-day reliability in foraging rewards. More reliable foraging rewards may allow groups to 'plan ahead' more successfully than lone individuals. For example, groups should be able to more closely match the number of offspring being reared to their more predictable food supply. Lone individuals, in contrast, should face large daily fluctuations in their foraging rewards. Lone individuals may be forced to abort excess offspring if short-term foraging success is unexpectedly low; or waste excess food if foraging is unexpectedly successful. Both effects should reduce their reproductive efficiency compared with groups.

The studentship will initially involve testing these ideas using wasps and bees, followed by subsequent work determined by the developing interests of the student. It is straightforward to record successful foraging events by observing or videoing social insect nests, and to carry out experimental manipulations. Experiments are likely to involve fieldwork trips abroad in Spain (Polistes paper wasps) and/or Malaysia (Liostenogaster hover wasps), as well as in the UK (halictine sweat bees), accompanied by other members of the research group. Note: the insects studied live in very small colonies (<5-10 individuals) and almost never sting humans!!

REQUIREMENTS: a student with an interest in behavioural/evolutionary ecology, who has or expects to receive at least a 2:1 degree and is a UK citizen. If you are a citizen of another European Union (EU) member state you will not generally be eligible for a stipend, unless you have spent the previous three years in the UK undertaking education (undergraduate study or masters) (see http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp for further eligibility details). The successful applicant will have a fitness level suitable for work in the field. A driving license would be useful. Because the work involves recording colour marks on individual animals, it would not be suitable for someone who is colour-blind.

SUPERVISION: the studentship will be co-supervised by Professor Jeremy Field (see http://www.sussex.ac.uk/biology/profile115853.html) and Professor David Waxman (see http://www.sussex.ac.uk/biology/profile2846.html), both members of the School of Life Sciences, Sussex University, UK. Together, they will provide complementary expertise to help the student develop his/her research in an interdisciplinary way. Sussex University is one of the leading research-led universities in the UK, with an international reputation for innovation and interdisciplinarity in research. The School of Life Sciences is a well-equipped and truly international research environment, providing excellent opportunities to interact with leading researchers and their groups. The School is probably the leading UK centre for research using social insects. Jeremy Field, Tom Collett and Francis Ratnieks are well-established specialists with international reputations. Related research areas in the School include behaviour, ecology, evolution, neuroscience, theoretical biology, genetics and genomics, and developmental biology.

APPLICATIONS

Applicants should email a covering letter and CV to Jeremy Field (j.field@sussex.ac.uk). The CV should include: 1. Contact details (including e-mail addresses) for the applicant and 2-3 referees who would be available to provide references during March/April 2009. 2. The applicant's availability for interview during April 2009.

Applicants must be available for interview at Sussex University, and review of applications will begin immediately and continue until the position is filled.

Informal enquiries: e-mail Jeremy Field (j.field@sussex.ac.uk)

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Professor Jeremy Field School of Life Sciences

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UZurich ComputationalEvolution

PhD thesis in computational evolutionary biology

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

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

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

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references.

Please include the word “COMP10” in the subject line. The application deadline is May 1, 2010.

Prof. A. Wagner

Christiane Gujan <gujan@bioc.uzh.ch>

UZurich ExperimentalEvolution

PhD thesis in experimental evolution

A Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The Wagner lab studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects involve laboratory evolution of yeast, E. coli and fruitflies, as well as in vitro evolution of ribozymes. A sample of the laboratory's research can be found at http:/-/www.bioc.uzh.ch/wagner/. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles. **

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will develop. The labs work is concept-driven instead of system-driven, and projects are not restricted to the model organisms mentioned above. A successful candidate will have substantial research experience with molecular biological techniques, acquired in research with an evolutionary orientation. State of the art experimental technology is available through the Functional Genomics Center Zurich, which provides platforms for ultra-high throughput sequencing, transcriptomics, proteomics, and metabolomics. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further. The position offers a highly competitive salary of up to three years on annually renewable contracts.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch: CV including publication list, a statement of research interests not exceeding three pages, including a sketch of an experimental evolution project, as well as three academic references. Please include the word “EXPEVOL10” in the subject line. The application deadline is May 1, 2010. The position is available immediately.

Prof. A. Wagner

Christiane Gujan <gujan@bioc.uzh.ch>

Jobs

ArizonaStateU Summer AvianColoration

SEEKING UNDERGRADUATE RESEARCH ASSISTANT FOR STUDY OF AVIAN COLORATION AND SEXUAL SIGNALING

We are seeking a qualified undergraduate to participate in a Research Experience for Undergraduates (REU) opportunity, funded by the National Science Foundation, to study coloration and sexual signaling in birds. The research experience will involve up to 10 weeks of full- time work during the summer of 2010 (approx. June-August) at Arizona State University. The REU student will work closely with Professor Kevin McGraw and Dr. Mat Giradeau (post-doctoral associate) on this project. The program includes a weekly stipend, and some travel funds will be available to help defray the cost of traveling to Tempe, Arizona.

The main research project will center on the relationships between dietary pigment access, oxidative stress, immunocompetence, and ornamental plumage coloration in house finches (Carpodacus mexicanus) The student will gain hands-on experience working with birds and will utilize a suite of biochemical, immunological, nutritional, and color- analysis techniques in the lab. In addition, the student will be involved in data entry, analysis, and interpretation. The student may also develop an independent project that dovetails with the main goals of the funded research.

We seek students with strong credentials, a general background in biology and chemistry, and an interest in ecological, evolutionary, physiological and/or immunological research. Preference will be given to students planning to attend graduate school in animal behavior or a related field. Women and ethic minority students are especially encouraged to apply.

Interested students should submit the following application materials electronically (as attachments, preferably in a single PDF) to kevin.mcgraw@asu.edu

i) curriculum vitae, ii) grades (unofficial transcripts are fine) and a list of relevant courses, iii) names and contact details for three references iv) a cover letter that describes any previous research and a brief statement explaining your interest in obtaining research experience in these areas.

Kevin McGraw <Kevin.McGraw@asu.edu>

BritishColumbia InvertSystematics

Curator, Invertebrate Zoology Full-Time Heritage Resources Officer R30 Victoria $67,177.34 - $76,911.00

Opportunity:

The Royal British Columbia Museum Corporation is the only organization in the world dedicated specifically to the preservation of, and education about, the human and natural history of British Columbia. Its mandate is to fulfill the Government's responsibilities for public trusteeship of the Provincial collections and exhibits. The collection is preserved for existing and future generations of British Columbians.

The Natural History Section of the Collections, Research and Access Branch has an excellent opportunity for a dynamic and creative person with a desire to share the Invertebrate Zoology collection with the world! Dividing their time between research, collection development and public programming, the successful applicant will demonstrate expertise in one taxonomic group of invertebrates relevant to British Columbia while having a good knowledge of other invertebrate groups for specimen identification and collection development purposes. The Curator will plan and participate in public programming through exhibit planning, popular wjavascript:SetCmd(cmdSend);riting and public speaking. As a key member of a team, the successful candidate will serve on a variety of committees within and outside the museum, and be a strong communicator. The Curator will be responsible for recruiting, training and directing the day-to-day activities of a vibrant group of volunteers, research associates, co-op students and contractors.

The ideal candidate will have a Doctorate degree in science relating to Invertebrate Zoology with an emphasis on taxonomy or systematics. In addition to being qualified for cross-appointments in universities, you will have practical experience in specimen identification. You must demonstrate experience in planning, completing and publishing scientific research. While experience working in a museum setting is not mandatory, it is considered an asset. As a member of an organization responsible for sharing the wonders of the museum, the successful candidate will be comfortable delivering presentations and providing information, identifications and expertise relating to Invertebrate Zoology and the museum across a wide diversity of audiences including government agencies, the media, the scientific and education community and the general public.

The taxonomic strengths of the existing RBCM invertebrate collection are: echinoderms, mollusks, polychaetes, sponges, decapods and land snails. The potential for regional partnerships between the museum and government or universities on the deep sea or other areas of investigation is significant and encouraged.

Please access the information at http://www.royalbcmuseum.bc.ca (click on About RBCM, then Employment Opportunities). Please quote: Competition RB2010:46576

Competition: RB2010:46576

Closing Date: 2010-04-09

Apply to: Business and Human Resource Services, 2nd Floor, 675 Belleville Street, Victoria, BC, V8W 9W2

Contact: Colleen Calverley

Phone: 250/387-2263

Fax: 250/387-0102

ccopley@royalbcmuseum.bc.ca

CornellCollege 2mnth instructor

Organismal Biologist Needed IMMEDIATELY:

Due to an illness, The Department fo Biology at Cornell College is suddenly in need of an instructor for a course schedule to begin April 5 2010. We may also need an instructor for a course to begin May 2. Cornell College classes are taught in blocks lasting three and one half weeks. Classes meet twice daily for a total of four to four and a half hours of lecture and lab per day. Our needs are for someone to teach one or two of the courses listed below. The first course listed in each block would be preferred, but exsting faculty could teach either course were we to find an exceptional applicant with a specialty in the alternative course topic.

Block 8 (April 5-28) Foundations: Organismal Biology (Introductory biology: Mendelian and population genetics, evolution, systematics, organisms, ecology, behavior) or Animal Behavior

Block 9 (May 2-26) Vertebrate Zoology or Conservation Biology

A doctorate is preferred, but PhD candidates in their final year are encouraged to apply. To apply, email your CV and a brief description of your teaching experience and have two letters of recommendation sent by email to:

Dr. Andy McCollum amccollum@cornellcollege.edu Department of Biology Cornell College Mount Vernon IA 52314

AMccollum@cornellcollege.edu

Corvallis Oregon BioLabTech

The USDA Forest Service, Pacific Northwest Research Station is looking to fill a Biological Science Laboratory Technician position (GS-0404-07; $38,790 per year) at the Forestry Sciences Laboratory in Corvallis, OR. This is a full-time, TERM position with a 13 month appointment. The position may be extended, dependent upon satisfactory job performance and the availability of funds. The vacancy announcement for this position is posted at the USAJOBS website (http://www.usajobs.opm.gov; control number 1819288). You can access this job quickly by selecting the ?advanced search? tab and typing the control number (1819288) in the keyword search field.

The incumbent will be part of the Forest Genetics Team, and funding for the position comes from by the US Forest Service and USDA-CSREES Plant Genome program. The position will provide research support for two studies: * Quantifying seasonal transcriptome variation and measuring seasonal growth in Douglas-fir. This study use Illumina-based RNA-Seq approaches to measure seasonal transcriptome changes in different provenances of Douglas-fir, with the goal of identifying gene networks that respond to climatic stress. The study also requires field work under a the full-range of

Oregon Coastal weather conditions. * Evaluating genetic diversity of Port-Orford Cedar and Alaska Yellow-Cedar, two conifers of regional concern in the Pacific Northwest. This study involves microsatellite development using massively parallel sequencing, and genetic screening of breeding populations and wild stands.

Applicants should possess training in biology, botany, microbiology, biochemistry, genetics or cell and molecular biology. Demonstrated experience in field-field based sampling methods, DNA and RNA sample preparation, and reference-guided and de-novo assembly of massively parallel DNA or RNA-Seq libraries is essential.

Interested applicants or those desiring further information may contact Rich Cronn (rcronn@fs.fed.us, 541-750-7291). USDA Forest Service is an equal opportunity employer. Only U.S. citizens may apply for this position.

Rich Cronn, Research Geneticist US Forest Service, Pacific NW Research Station 3200 SW Jefferson Way, Corvallis, OR 97331 541-750-7291 phone * 541-750-7329 fax * rcronn@fs.fed.us

Richard Cronn <rcronn@fs.fed.us>

CostaRica FieldAssist FrogVariation

A field assistant is needed to collaborate in the work that will be done in Costa Rica on the poison frog Oophaga granulifera.

This is part of aninternationalPhD project on the geographical variation in morphology, genetics and behaviour in the granular poison frog, based at the University of Veterinary Medicine (TiHo) of Hannover (Germany) and carried out in collaboration with the University of Cambridge, (UK).

The position is for May 2010.

The selected person will participate in the frogs catching, colour measurements using a spectrometer, calls recordingand tissue sampling.

The work involves many hours in the field. Tropical conditions are demandingand present potential dangers, thereforethe candidate shouldbe motivated, physically fit andnot worried by the possible encounters withvenomous snakes.

The salary is 500 dollars, food and accomodation have to be paid by the assistant.

If you are interested in the position please contact Oscar Brusa at oscar.brusa@tele2.it

oscar.brusa@tele2.it

ImperialCollege FieldTechnician

Fieldwork Technician Division of Biology, Silwood Park Campus Imperial College London Salary £23,450 - £26,020 per annum

All appointments will normally be made at the bottom of the salary range We are seeking to recruit a Fieldwork Technician who will be funded as part of an ERC Advanced Investigator grant of 2.1M awarded to Prof Tim Coulson. This position is available for five years, starting from 1 June 2010.

Working as part of a highly experienced team at the cutting edge of evolutionary research, you will provide technical support for research on how evolutionary and ecological processes influence the dynamics of heritable phenotypic traits and vice versa. You will assist in that part of the research project where we study the behaviour, ecology and dynamics of wood mice populations in the field. The work will involve small mammal trapping, marking, release, radio-tracking and help in maintaining a wireless sensor network which tracks individual mice living in the study area. This is an exceptional opportunity to participate in a major research project, for which extensive pilot data is already available, and for which funding has been secured for the duration of the project.

The successful candidate must have 2 A-Levels in relevant subjects, or equivalent vocational qualifications plus work experience preferably in a relevant technical/scientific role, enthusiasm for biological research, and sound laboratory and fieldwork skills.

You will be part of a thriving research group (www.bio-demography.org) in the Ecology and Evolution Section (http://www3.imperial.ac.uk/biology/research/ecologyandevolution) of the Division of Biology (http://www3.imperial.ac.uk/biology) and will be based at Silwood Park Campus in Berkshire (http://www3.imperial.ac.uk/silwoodparkcampus)

Informal inquiries (with CV) should be made to Prof Tim Coulson: t.coulson@Imperial.ac.uk Interviews will take place in mid April.

Committed to equality and valuing diversity. We are also an Athena Silver SWAN Award winner and a Stonewall Diversity Champion.

Closing Date 23 March 2010 (midnight GMT/BST)

How To Apply Our preferred method of application is online via https://www4.ad.ic.ac.uk/-OA_HTML/OA.jsp?akRegionCode=-IRC_VIS_VAC_DISPLAY_PAGE&akRegionApplicationId=800&OASF=IRC_VIS_VAC_DISPLAY&OAHP=-IRC_EXT_SITE_VISITOR_APPL&transactionid=-1243564724&retainAM=Y&addBreadCrumb=-RP&p_svid=16416&p_spid=835012&oapc=6&oas=-TOKZY_LTBM7RlTZUQ4A5Mg .Please download the application form and save to your computer. Once completed, please upload your application form prior to submitting your application. Should you have any queries please contact: Mrs Diana Anderson - 020 7594 2207 or email d.anderson@imperial.ac.uk Job description and personal information available via the above website.

Tim Coulson Professor of Population Biology Imperial College London Silwood Park Ascot Berkshire, SL5 7PY

Work website www.bio-demography.org www3.imperial.ac.uk/people/t.coulson

"Coulson, Tim N" <t.coulson@imperial.ac.uk>

ImperialCollege LabTech

Laboratory Technician Division of Biology, Silwood Park Campus, Imperial College London Salary £23,450 - £26,020 per annum

All appointments will normally be made at the bottom of the salary range We are seeking to recruit a Laboratory Technician which will be funded as part of an ERC Advanced Investigator grant of 2.1M awarded to Prof Tim Coulson. This position is available for five years, starting from 1 June 2010.

Working as part of a highly experienced team at the cutting edge of evolutionary research, you will provide technical support for a research project on how evolutionary and ecological processes influence the dynamics of heritable phenotypic traits and vice versa. You will assist in that part of the research project where we study the behaviour, composition and dynamics of bulb mite (Rhizoglyphus robini) populations in the laboratory. The work will mainly be laboratory based, although field work is planned for the future. This is an exceptional opportunity to participate in a major research project, for which extensive pilot data is already available, and for which funding has been secured for the duration of the project.

The successful candidate must have 2 A-Levels in relevant subjects, or equivalent vocational qualifications, plus work experience, preferably in a relevant technical/scientific role, enthusiasm for biological research, and sound laboratory and fieldwork skills.

You will be part of a thriving research group (www.bio-demography.org) in the Ecology and Evolution Section (http://www3.imperial.ac.uk/biology/-research/ecologyandevolution) of the Division of Biology (http://www3.imperial.ac.uk/biology) and will be based at Silwood Park in Berkshire (http://-www3.imperial.ac.uk/silwoodparkcampus).

Informal inquiries (with CV) should be made to Prof Tim Coulson: t.coulson@Imperial.ac.uk

Interviews will take place in mid April.

Committed to equality and valuing diversity. We are also an Athena Silver SWAN Award winner and a Stonewall Diversity Champion.

Closing Date 23 March 2010 (midnight GMT/BST)

How To Apply Our preferred method of application is online via https://www4.ad.ic.ac.uk/-OA_HTML/OA.jsp?akRegionCode=-IRC_VIS_VAC_DISPLAY_PAGE&akRegionApplicationId=800&OASF=IRC_VIS_VAC_DISPLAY&OAHP=-IRC_EXT_SITE_VISITOR_APPL&transactionid=-1243564724&retainAM=Y&addBreadCrumb=-RP&p_svid=16417&p_spid=835013&oapc=12&oas=-cs2yNErHioGoSPgOK7pcJw .Please download the following application form and save to your computer. Once completed, please upload your application form prior to submitting your application.

Should you have any queries please contact: Mrs Diana Anderson - 020 7594 2207 or email d.anderson@imperial.ac.uk

Job Description and Person Specification also available from the above website.

Tim Coulson Professor of Population Biology Imperial College London Silwood Park Ascot Berkshire, SL5 7PY

Work website www.bio-demography.org www3.imperial.ac.uk/people/t.coulson

"Coulson, Tim N" <t.coulson@imperial.ac.uk>

MaxPlack Leipzig ProgrammerBioinformatician

- Programmer/Bioinformatician -

There is an opening (fall 2010) for a programmer/bioinformatician with a strong interest in computational genomics to work in our research group at the Max Planck Institute for Evolutionary Anthropology (Department of Evolutionary Genetics). One main aim in the laboratory is the characterization of genes whose protein functions require the trace element selenium. These genes incorporate selenium in the form of selenocysteine, the 21st amino acid in the genetic code, and are known as selenoprotein genes. Building on our expertise in the computational identification and annotation of selenoprotein genes in eukaryotic genomes, the programmer/ bioinformatician will develop computational pipelines to annotate genes and other genomic features, analyze data from re-sequencing and comparative expression experiments and manage the relational database SelenoDB. We will aim to provide a comprehensive view of the selenoprotome's function and evolution to selenium researchers. Ample opportunities for the analysis of primate genomes in collaboration with other groups in the Department will exist.

We are seeking a motivated, well-organized and creative person. Previous research experience and knowledge of scripting languages and relational databases are advantadges. The programmer/bioinformatician will receive a payment according to Max Planck Institute rates. The working environment of the institute is English-speaking, and the members constitute a highly international group. The institute is in Leipzig, a pleasant city of 500,000 inhabitants situated two hours from Berlin and three hours from Prague. Applicants should send their CV, transcripts and name and address of two references (in PDF format) to Dr. Sergi Castellano (castellanos@janelia.hhmi.org).

Some articles of interest to candidates are:

S Castellano, AM Andrés, E Bosch, M Bayes, R Guigó and AG Clark Low exchangeability of selenocysteine, the 21st amino acid, in vertebrate proteins Molecular Biology and Evolution, 26, 2031-2040 (2009)

S Castellano, VN Gladyshev, R Guigó and MJ Berry SelenoDB 1.0: a database of selenoprotein genes, proteins and SECIS elements Nucleic Acids Research, 36, D339-D343 (2008)

S Castellano, AV Lobanov, C Chapple, S Novoselov, M Albrecht, D Hua, A Lescure, T Lengauer, A Krol, VN Gladyshev and R Guigó Diversity and functional plasticity of eukaryotic selenoproteins: identification and characterization of the SelJ family Proceedings of the National Academy of Sciences USA, 102, 16188-16193 (2005)

GV Kryukov, S Castellano, SV Novoselov, AV Lobanov, O Zehtab, R Guigó and VN Gladyshev Characterization of mammalian selenoproteomes Science, 300, 1439-1443 (2003)

S Castellano, N Morozova, M Morey, MJ Berry, F Serras, M Corominas and R Guigó in silico identification of novel selenoproteins in the Drosophila melanogaster genome EMBO reports, 2, 697-702 (2001)

– Sergi Castellano

East Lab, 2E.290 Janelia Farm Research Campus Howard Hughes Medical Institute 19700 Helix Drive Ashburn, VA 20147 (USA)

http://selab.janelia.org/people/castellanos Ph: 571 209 4000 ext. 7160 Fax: 571 209 4095

castellanos@janelia.hhmi.org

MPI Leipzig 5yr HomininSubsistence correction

The Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, offers the position of

Leader of a Max Planck Research Group on

* *

âHominin subsistenceâ

Over the last several million years, hominins have developed diverse dietary strategies to survive and expand in changing environments. From the origin of meat consumption to the intensification of resource use by Late Palaeolithic hunter-gatherers, we have seen that diet, and the more general term âsubsistence,â clearly involves the continuous interaction between environment, biology, and culture. New questions and models have arisen that address the relationship between this dietary evolution and the broader questions of the evolution of life histories, technological adaptations, and the social organization of hominins.

We are seeking a Max Planck Research Group Leader who can design a novel and well structured 5-year research project to explore hominin subsistence strategies. The call for research proposals is intentionally broad. We seek a group leader with an expertise in one of the related areas of research but who is encouraged to take a multidisciplinary approach to addressing the research question that they propose. This may include, for example, methods such as zooarchaeology, isotopic studies, or modelling, as well as related disciplines.

The Max Planck Institute for Evolutionary Anthropology has five departments, including the Department of Human Evolution (Director: Jean-Jacques Hublin), with which the Max Planck Research Group will be associated. Therefore, although this is an independent Research Group we would expect that the proposed project and team would interact with the Department of Human Evolution, and can use the extensive research facilities available (Further information may be obtained at http://www.eva.mpg.de/ and http://www.eva.mpg.de/evolution/.)

This is a fulltime research position. The salary will be at the W2 level on the German university scale, equivalent to an assistant/associate professor. There are associated funds for research scientists to work in the group, specifically funding for one post-doctoral scientist (13/14 TVöD) and two PhD students, as well as two technicians. Start-up funds for equipment are available, and a substantial yearly budget for operating costs will be provided. The appointment will be for a term of 5 years. Further information on the Max Planck Research Groups may be obtained at http://www.mpg.de/english/institutesProjectsFacilities/juniorResearchGroups/aboutJrg/index.html

Applicants should have demonstrated outstanding research potential and clear evidence of achievement. Applicants should have a Ph.D. obtained within the last 5 years.

The Max Planck Society is committed to employing more handicapped individuals and to increasing the share of women in areas where they are underrepresented, and therefore expressly encourages applications from such qualified individuals.

Applications should include a CV, a detailed research plan (max. 8 pages), and the names of three referees and must be received at the address below by *May 15, 2010*.

Max Planck Institute for Evolutionary Anthropology Personnel Department Deutscher Platz 6 04103 Leipzig Germany**

Carolyn Rowney <rowney@eva.mpg.de>

NESCent TrainingCoordinator

Training Coordinator and Bioinformatics Project Manager U.S. National Evolutionary Synthesis Center

A unique position is available for a training coordinator and bioinformatics project manager at the U.S. National Evolutionary Synthesis Center in Durham, North Carolina (NESCent). NESCent is a National Science Foundation funded research center managed by Duke University, the University of North Carolina at Chapel Hill and North Carolina State University on behalf of the international evolutionary biology community. NESCent facilitates synthetic research by bringing together diverse expertise, data, tools and concepts [1]. In addition to a resident population of 20-30 scientists, the Center hosts over 800 visitors a year. An informatics staff is on-site to support resident and visiting scientists' needs in high-performance computing, electronic collaboration, scientific software and databases; this includes custom software development for a limited number of high-impact projects. NESCent's training program includes a rotating series of open-application summer courses, ad -hoc short courses for resident scientists, and remote internships (including past participation in the Google Summer of Code).

The training coordinator and bioinformatics project manager will provide oversight to the Center's training activities. The incumbent will also serve as the interface between scientists and software developers at NESCent. The position provides extensive opportunities for collaboration and intellectual engagement with both NESCent-sponsored scientists and informatics staff; however, this is not an independent research position. The incumbent will report to the Director, while coordinating the work of a small informatics team and activities among the Center's science, education and informatics programs.

Responsibilities: 50% - Consult with sponsored scientists (including scientists in residence and working group participants) about informatics resources and needs. Manage software product development by gathering requirements from scientists, participating in conceptual design, monitoring implementation progress and product quality, facilitating communication between software developers and scientists, and researching software solutions.

25% - Oversee NESCent's course curriculum by identifying opportunities for onsite or online informatics courses that satisfy demand for advanced training of resident and visiting scientists, recruiting instructors, providing guidance to instructors in developing course syllabi, coordinating logistical and technical support requirements, conducting assessments, and serving as a liaison to course organizers at other institutions.

25% - Assisting in the management of NESCent's summer informatics intern program, by coordinating the recruitment, application & review process for students, communicating expectations to students and mentors, monitoring student progress, documenting student outcomes, and performing assessments.

Education: Required: M.S. in Biology, Bioinformatics, or a related field. Preferred: Ph.D. and two years postdoctoral experience in evolutionary biology, or an equivalent combination of relevant education and/or experience.

Experience: Required: Excellent communication, interpersonal, and organizational skills. Experience with computationally oriented scientific research. Preferred: At least two years in development of databases and open source software. Organization, coordination, development and delivery of courses and workshops appropriate for graduate-level participants.

Terms of Employment: Salary will be competitive and commensurate with experience. As a full-time employee, the incumbent will receive Duke University's benefits package (http://hr.duke.edu/benefits/main.html). The position is available immediately and will remain open until filled. The position is currently funded through November 2014, contingent on annual renewal of the Center by the NSF.

How to Apply: Please send a C.V., including contact information for three references, and a brief statement of interest to Allen Rodrigo, Director, NESCent, at a.rodrigo@nescent.org. Inquiries about suitability for the position are welcome. Duke University is an Equal Opportunity/Affirmative Action employer. Additional information about NESCent: http://www.nescent.org [1] Sidlauskas B, Ganapathy G, Hazkani-Covo E, Jenkins KP, Lapp H, McCall LW, Price S, Scherle R, Spaeth PA, Kidd DM (2009) Linking Big: The Continuing Promise of Evolutionary Synthesis. Evolution. http://dx.doi.org/10.1111/j.1558-5646.2009.00892.x tjv@bio.unc.edu tjv@bio.unc.edu

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OhioStateU FieldAssist PlantEvolution

Full-time Field Research Assistants (paid) are needed for research on the ecology and evolution of plant mating systems in Central Ohio. Research will focus on the response of plant morphology and mating patterns to availability of resources. Duties will include maintaining plant populations, collecting morphological data and seeds, as well as some easy building activities. Moderately strenuous activity will occur daily and we will be outside most days. Field research is conducted in small teams on Ohio State University's experimental farms in Columbus, OH and the surrounding area. Prior field experience is highly desirable; strong work ethic, meticulousness, and ability to work both independently and in small teams are required. The project offers research and learning experiences for Project Assistants, particularly with regard to the ecology and evolution of plant mating systems.

Desired dates of employment (35 hours/week): May 1 to September 1, 2010. Wage is commensurate with education and experience. Transportation to remote field sites will be provided.

Consideration of applications will begin on April 10th. Please submit via email a brief letter of application, a resume, and the names, phone numbers, and email addresses of three professional references to: Lesley Campbell, lgc@rice.edu, at Rice University.

Lesley Campbell <lgc1@rice.edu>

OklahomaStateU EvolutionaryBiol

Evolutionary Biologist V Tenure-track

As part of our continued growth in the areas of Environmental Stress and Ecology & Evolutionary Biology, the Department of Zoology at Oklahoma State University invites applications for a tenure-track, assistant professor in organismal (including humans) evolution. Applicants are expected to have a Ph.D., post-doctoral research experience, teaching experience, and demonstrated success in obtaining extramural funding. Responsibilities of this position will include establishing a vigorous, extramurally funded research program, successfully mentoring M.S. and Ph.D. students, and effectively teaching courses at the undergraduate and graduate level.

The Department of Zoology has a long history of research in conservation biology, ecology, evolution, physiology, and environmental toxicology, and a variety of partnerships with the Departments of Botany, Microbiology and Molecular Genetics, Biochemistry and Molecular Biology, Natural Resource Ecology and Management, the Oklahoma Cooperative Fish and Wildlife Research Unit, and the Center for Veterinary Health Sciences. More information can be found at http://zoology.okstate.edu . Applicants should submit a letter of application, curriculum vitae, separate statements of research interests and teaching philosophy, and three sample publications, by email (kristen.baum@okstate.edu; pdf preferred) or by standard mail, to Dr. Kristen Baum, Chair, Faculty Search Committee, Department of Zoology, Oklahoma State University, 501 Life Sciences West, Stillwater, OK 74078. Three letters of recommendation should be sent directly by the applicants references by standard mail to the address above. Application review will begin 15 April 2010, with employment beginning 1 January 2011. Filling of this position is contingent upon availability of funding. Oklahoma State University is an AA/EEO/E:Verify Employer committed to diversity. OSU:Stillwater is a tobacco:free campus.

Puni Jeyasingh Department of Zoology, 501 Life Sciences West, Oklahoma State University, Stillwater, OK 74078-3052. Phone: (405) 744-9634. Fax: (405) 744-7824. http://web.me.com/-punidan/Jeyasingh/Jeyasingh_Lab.html Puni Jeyasingh <puni.jeyasingh@okstate.edu>

Oslo HeadBotanicalGarden

Head of Botanical Garden

VACANCY FOR POSITION AS HEAD OF BOTANICAL GARDEN (SKO 1211) http://-www.admin.uio.no/opa/ledige-stillinger/2010/-teknadm/headBotanicalGarden-2009-16288.html available at the Natural History Museum, University of Oslo. The Natural History Museum (NHM) of the University of Oslo has a staff of around 150 engaged in research, curation of collections and teaching and supervision of students in botany, geology, palaeontology and zoology. With emphasis on the need to meet the demands of society for more information on the natural world, there exist plans for considerable development of the present Botanical Garden with the addition of a new greenhouse with expected building starting in 2011. The Botanical Garden has a staff of more than 20 including two head gardeners. This vacant position is for a leader of this group and one who will cooperate with others section leaders answerable to the Director of NHM.

Job description and responsibility

Scientific and administrative leader of the Botanical Garden including future planning Budget and personnel responsibility Responsibility for the scientific collections of the garden Aid in the planning of the new greenhouse Secure cooperation with other scientific sections at NMH Strengthen ties between the Botanical Garden and the association of friends of the garden

Requested qualifications

Professor/Associate Professor grade of scholarship, preferably in systematic botany Experience from an equivalent national or international position Documentation of experience of the areas mentioned in the above job description Leadership of a technical and scientific staff Documentation of fund raising ability and success in obtaining sponsored funding Ability to communicate verbally and in writing both in Norwegian and English

The applicant's merits, such as personal initiative, team spirit, ability to work independently or within a group and good humour, will be judged when ranking candidates for the position.

It should be noted that the University of Oslo reserves the right to all research results obtained during employment.

According to the law of public records §25:2, all information contained in the application can be made public even though the applicant requests anonymity.

For further information please contact: Director Arne Bjørlykke (tel: 22 85 16 43/ ++ 47 90 09 50 12; arne.bjorlykke@nhm.uio.no , Research director Fridtjof Mehlum (tel: 22 85 17 23; fridtjof.mehlum@nhm.uio.no or Personnel officer Hedda Ugletveit (tel: 22 85 18 19; hedda.ugletveit@nhm.uio.no .

Salary scale 66-78 (NOK. 518 200-667 100 (according to qualifications and experience)

Closing Date: March 23, 2010

Reference number 2009/16288

Application in 4 copies, marked with reference number, together with CV and references should be sent to:

University of Oslo, Natural History Museum, P.O. Box 1172 Blindern, N-0318 Oslo, Norway

An extended applicant form must be completed and submitted together with the application. This form is available at: http://www.admin.uio.no/opa/ledige-stillinger/english/soker-skjema_GBR.rtf Application papers will not be returned.

magnus.popp@nhm.uio.no magnus.popp@nhm.uio.no

Petersham MA 2SummerFieldTech Collections

Summer Fieldwork Opportunity for NEON - Two Field Technicians in Ecology/Evolution:

The National Ecological Observatory Network (NEON, Inc.) is a nonprofit science corporation dedicated to understanding how changes in climate, land use and invasive species impact ecology/evolution.

Two temporary Field Technicians are needed to collect at sites in the Northeast - located at the Harvard Forest in Petersham, MA.

The work schedule will be 3 days on/four days off with 8-10h days anticipated from June 7 - July 30.

Field technicians will install pitfall and mosquito traps, check, empty, and reset traps weekly, maintain traps and other field equipment. Technicians will carry a GPS unit and a PDA for data entry. This work will aid with the development of a site-specific collection in order to aid with the development of systematics tools.

Compensation is $12/hr plus mileage (reimbursed).

For a list of qualifications and to apply go to: www.neoninc.org . NEON Inc. is an Equal Opportunity Employer. Women, Minorities, Veterans and Disabled Persons are encouraged to apply.

Laura Reynolds Recruiter

NEON, Inc. (National Ecological Observatory Network) 5340 Airport Blvd. Boulder,CO 80301 PH: 720-746-4930

www.neoninc.org Laura Reynolds <lreynolds@neoninc.org>

SanDiego Zoo cytogenetics

San Diego Zoo's Institute for Conservation Research is seeking a Research Technician to establish fibroblast cell lines from avian taxa. The applicant selected for this position will be responsible for culturing and freezing somatic cells from a variety of avian species and karyotyping the derived cell lines. Applicants must have experience working in a tissue culture laboratory with demonstrated knowledge of cultured cell types, sterile technique, media development and preparation, culture and freezing of cells, microscopy and photo microscopy. Must have knowledge of standard laboratory procedures, safety practices, general lab maintenance and skill in use and basic maintenance of general laboratory equipment such as microscopes, centrifuges, incubators, biological hoods, water baths, balances, pipetors and pH meters. Knowledge of basic taxonomic nomenclature and clinical cytogenetic techniques preferred (standard, G-band and C-band techniques). Proficiency in Windows-based computer programs such as word processing and spreadsheets preferred. Applicants should have the ability to work cooperatively in a team environment, follow through on assignments and be detail oriented. This position is short term, funded by an NIH grant, and will last approximately 17 months - starting around March 28, 2010 through August 31, 2011. Application deadline is March 10, 2010. For more information or to apply go to: http://www.sandiegozoo.org/jobs/ oryder@ucsd.edu oryder@ucsd.edu

SantaClaraU 2 FullTimeLecturers EvolBiol

Subject to funding, the Biology Department of Santa Clara University invites applicants for two full-time lecturer positions starting in academic year 2010-2011. One position is for two years, the other for three years. Candidates should hold the PhD by the time of appointment and show evidence of excellence in teaching and research. Teaching load is seven courses. We are seeking experienced instructors with expertise in ecology and evolutionary biology. Teaching responsibilities will include: 1) participating in the ecology/evolution components of our introductory series for majors; 2) upper division in ecology, evolution, or related topics, involving hands-on laboratory or field experience and 3) contributing to the university core curriculum in either the natural sciences or in Science, Technology and Society. SCU does not sponsor any visa applications for this position. The successful candidate must be able to provide evidence of identity and legal authorization to work in the United States. Salary range $48,300 to $51,100, depending on teaching experience; eligible for benefits. Santa Clara University is a Catholic, Jesuit comprehensive university located in the Silicon Valley; the Biology Department is focused on undergraduate education.

Applications should include the following 1. Letter of interest outlining qualifications, teaching experience (including a statement describing experience working with people of diverse cultures and identities), and teaching philosophy. 2. Curriculum vitae 3. Names and contact information for three references. DEADLINE FOR APPLICATIONS April 6, 2010. Applications should be submitted electronically to Biology@SCU.edu. Please state Lecturer in Ecology and Evolutionary Biology in the subject line.

Thanks!

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

http://www.scu.edu/cas/biology/staffandfaculty/-JaniceEdgerly-Rooks.cfm Janice Edgerly-Rooks <jedgerlyrooks@scu.edu>

Stanford Next-GenSequencingTech HumanPopGen

Hi all,

We are looking to hire at least one bright, energetic, and enthusiastic technician at Stanford. The person will work closely with me and others in the lab on applying next-gen sequencing to problems in human population genetics and domestication genomics. Full details are below. Folks should feel free to email me with questions and potential queries. To apply, please go to the website (and read the full job description below):

Web page: http://jobs.stanford.edu/find_a_job.html Job ID: 37550 (enter as keyword for search)

Carlos

Carlos D. Bustamante, Professor Department of Genetics Stanford School of Medicine 300 Pasteur Drive Lane Building, Room L-301 Stanford, CA 94305-5120 Phone: +1-650-723-6361 Fax: +1-650-725-1534 cdbustam@stanford.edu http://med.stanford.edu/-profiles/frdActionServlet?choiceId=facProfile&fid=-15848 Administrative Assistant: Ms. Drina Adams Phone: 1-650-723-1073 Fax: 1-650-725-1534 drinaadams@stanford.edu

Web page: http://jobs.stanford.edu/find_a_job.html Job ID: 37550 (enter as keyword for search)

Life Science Research Assistant

Job ID: 37550 Job Location: School of Medicine Job Category: Life Science Research Salary: 2P2 Date Posted Mar 18, 2010

The Department of Genetics seeks a Life Science Research Assistant II. The LSRA will be involved in defined research projects and will be assigned a portion of the research project(s) to handle independently. S/he will be expected to make original scientific contributions. The LSRA is expected to develop novel protocols and procedures, and interpret and analyze the results. The position also entails lab management support such as ordering supplies and equipment, maintaining lab records, and adhering to safety regulations.

The focus of the position is the execution of experiments using high throughput sequencing technologies. Projects will include full genome sequencing, targeted sequencing using array capture, and RNAseq experiments. Applicants should have a strong desire to apply the latest genomics approaches and technologies to answer questions of biological importance and a willingness to work in a collaborative environment.

Qualifications:

âFour-year college degree required, field of study Biology, Chemistry, Biochemistry or related.

âTwo years experience and comprehensive understanding of biological sciences principles

âProficiency with the following techniques required: standard molecular biology techniques such as PCR and gel electrophoresis.

âGeneral computer skills and ability to quickly learn and master computer programs.

âStrong analytical skills and excellent judgment.

âMust be careful, well organized, able to work both independently and well with others, and the ability to work on deadlines with general guidance is essential.

Desired Qualifications: â Experience with high throughput DNA sequencing, including the creation of libraries for Illumina sequencing

â Experience with other sequencing technologies, such as SOLiD.

â Experience with techniques for targeted genome capture

â Experience with RNA isolation and the preparation of samples for RNAseq experiments

â A strong desire to master and apply a range of the latest sequencing technologies and genomic approaches to answer important biological questions

"Carlos D. Bustamante" <cdbustam@stanford.edu>

Stockholm FieldAssist ParasiteDynamics

A position has become available for a field assistant to work on a project studying climate impacts on parasite transmission dynamics for a period of 10 weeks this summer, in Sweden. The project is led by Prof. Greg Hurst, University of Liverpool.

The position would suit a graduate student planning on pursuing a career in ecological and/or evolutionary ecology research. Travel expenses can be covered for candidates applying from within Europe. Please see advertisement text below.

For informal enquiries & further information, please contact Dr Jon Ryder (jon.ryder@liv.ac.uk; Tel. +44 (0)151 795 4527), School of Biological Sciences, University of Liverpool. Applications (CV and covering letter) should be sent to Mary-Jo Hoare, School of Biological Sciences, University of Liverpool, Liverpool L69 7ZB (electronic applications to: mjhoare@liverpool.ac.uk). Applications will be received until the position is filled.

Summer 2010 Ecological Fieldwork in Sweden:

Climate impacts on the dynamics of a sexually-transmitted parasite of two-spot ladybird beetles

Duration: Approximately 10 weeks during the period June to August 2010.

Location: Stockholm, Sweden.

Nature of work: Working with Dr Jon Ryder and Mary-Jo Hoare, you will be monitoring populations of the two-spot ladybird, Adalia bipunctata, together with its sexually-transmitted mite, Coccipolipus hippodamiae. You will also be making measurements of meteorological, microclimatic and behavioural variables, and using field cages to record other aspects of parasite transmission and dynamics.

Skills, character, and experience required: Although previous field work experience is not essential, you should have a good grasp of basic ecology and entomology. Above all, you must be reliable, hard- working, and capable of showing initiative. The ability to work well in a small team is important, but you will also be required to spend a certain amount of time working independently. You also need to be physically fit and able to work long days.

Would suit: A good student or graduate seeking experience of ecological field-based research.

You will receive: Food, costs of travel and accommodation, research facilities, plus a modest stipend. You will also receive all necessary training and supervision.

More about the project: All work will take place within the city of Stockholm, where both ladybird and parasite are common. The field-work forms part of a three-year, NERC-funded project involving collaboration between Prof Greg Hurst (PI), Dr David Atkinson (both University of Liverpool), Prof Mike Boots (University of Sheffield), and Dr Rob Knell (Queen Mary, University of London). The project aims to investigate how thermal environment and density co-determine the dynamics of the ladybird-mite system in natural populations. The project includes laboratory and field measurements to calibrate epidemiological models being developed for this system.

Jon Ryder

Senior Research Associate School of Biological Sciences Biosciences Building Crown Street University of Liverpool Liverpool L69 7ZB

Tel: +44 (0)151 795 4528 Fax: +44 (0)151 795 4410 Email: Jon.Ryder@Liv.ac.uk

Jon Ryder <jon.ryder@liverpool.ac.uk>

UCaliforniaLosAngeles DirectorConservationScience

Director for Conservation Science UCLA

La Kretz Center for California Conservation Science

UCLA Institute of the Environment

UCLA is seeking to fill the position of Director for the new La Kretz Center for California Conservation Science. The La Kretz Center is operated by the UCLA Institute of the Environment, the Stunt Ranch Reserve and Division of Life Sciences and in cooperation with the National Park Service, California Department of Parks and Recreation, and the Mountains Recreation and Conservation Authority. Collaborating with both UCLA faculty and agency staff, the Director will work to promote and coordinate cross-disciplinary scientific research that informs and supports the environmental management of California^{1}s exceptional biodiversity and unique ecosystems. Specific responsibilities for the Director will be 1) to promote partnerships and collaborations with government agencies and private organizations and facilitate the development of new partnerships; 2) to carryout and encourage research relevant to the goals of the Center; 3) to seek funding to support the operation and expansion of the Center; 4) to assist in organizing workshops and conferences for the Center; 5) teach one course each year on the UCLA campus; and 5) to enhance opportunities for student research in conservation science and environmental outreach programs to the public. The Director will be housed with other Center staff in National Park Service facilities with additional space and administrative support at the UCLA Institute of the Environment. Minimum requirements for the position are a doctorate in a field related to conservation science and an established record of achievement and commitment to this field of study. The Director position is a non-tenure track academic position but presents opportunities for a possible appointment as an adjunct professor in a campus department. Applicants should submit application materials online to LaKretzCenter-Position@ioe.ucla.edu, including a cover letter, curriculum vitae, statements of research, teaching and interdisciplinary experience and interests, and the names and contact information for four references. Inquires about the position should be directed to Search Chair, Professor Phil Rundel (rundel@lifesci.ucla.edu). Additional questions about email submission of applications should be directed to Eileen Sir, Manager of the Institute of the Environment, at esir@ioe.ucla.edu. Women and minority applicants are encouraged to apply. UCLA is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of faculty and staff diversity.

Tom Smith <tbsmith@ucla.edu>

UCentralFlorida VisitingLecturer EvolutionaryBiol

The Department of Biology at the University of Central Florida seeks to hire a Visiting Lecturer to start August 2010. The position is renewable annually for a maximum of four years. The successful candidate must have the ability to teach Introductory Biology and Ecology to Biology majors. Preference will be given to candidates who are also able to teach undergraduate upper division and graduate courses related to Ecology, such as Animal Behavior and Behavioral Ecology. The successful applicant will have a Ph.D. in a relevant discipline from an accredited institution and a minimum of one-year teaching experience. Salary is negotiable commensurate with experience. A comprehensive benefits package is also offered. See http://biology.cos.ucf.edu/ for department details. All applicants must complete an application online at < http://www.jobswithucf.com >www.jobswithucf.com. For additional information contact Dr. Laurence von Kalm at lvonkalm@mail.ucf.edu.

Christopher L. Parkinson, Ph.D. Dept. of Biology University of Central Florida 4000 Central Florida Blvd. Orlando, FL 32816-2368 office: 407-823-4847 fax: 407-823-5769 http://biology.ucf.edu/~clp/ E-mail cparkins@mail.ucf.edu

Chris Parkinson <cparkins@mail.ucf.edu>

UGeorgia PlantRootEvolution

Associate Professor in Below Ground Ecology/Evolution

The Department of Plant Biology at the University of Georgia invites applications for the Haines Family Professorship in Below Ground Ecology. This new position will focus on the below ground component of plant ecology: plant roots and their interactions with their environment, other plants and soil organisms (including fungi, bacteria and herbivores), and soil processes (including nutrient and water cycling). We seek an individual who addresses fundamental ecological and evolutionary questions and who integrates field- and lab-based research approaches with molecular tools and techniques. The successful candidate will have a Ph.D. degree and a record of scientific productivity appropriate for appointment at the level of associate professor. S/he is expected to continue and expand a vigorous externally-funded research program and to teach and train undergraduate and graduate students. The Plant Biology Department encompasses a broad range of disciplines and has historical strengths in plant ecology, evolutionary biology and mycology (http://www.plantbio.uga.edu). We interact with numerous other ecologists, mycologists, and plant scientists across campus in the Odum School of Ecology, Warnell School of Forestry and Natural Resources, Departments of Plant Pathology, Crop and Soil Sciences, Genetics, Biochemistry and Molecular Biology, and on-campus branch of the USFS Southern Research Station. There is also the potential to utilize a wide range of off- campus facilities such as the UGA Marine Institute at Sapelo Island and its associated Sapelo Island Microbial Observatory, the Coweeta Hydrologic Lab and LTER, and the Savannah River Ecology Lab. To apply, the following should be submitted at http://www.plantbio.uga.edu/positions.html : (1) a single PDF file containing a cover letter, curriculum vitae, and short statements of research interests and teaching philosophy; (2) a single PDF file containing three reprints of research papers; (3) four letters of recommendation submitted by references. The search will remain open until the position is filled. Complete applications (including letters) received by March 25, 2010 are assured full consideration. The Franklin College of Arts and Sciences, its many units, and the University of Georgia are committed to increasing the diversity of its faculty and students, and sustaining a work and learning environment that is inclusive. Women, minorities and people with disabilities are encouraged to apply. The University is an EEO/AA institution.

Jim Leebens-Mack 4505 Miller Plant Scinces Department of Plant Biology University of Georgia Athens, GA 30602-7271

Phone: 706-583-5573 Fax: 706-542-1805 email: jleebensmack@plantbio.uga.edu url: http://www.plantbio.uga.edu/~jleebensmack/JLMmain.html jleebensmack@plantbio.uga.edu

UGuelph ResAssist PlantEvolution

Job Advertisement, Department of Integrative Biology, University of Guelph

Research Assistant, posted March 29 2010

The Caruso and Maherali Labs are seeking a full time Research Assistant in Plant Ecology and Evolutionary Biology.

The successful candidate will oversee field and greenhouse experiments designed to examine sex ratio evolution in wild plant populations, take part in other lab research projects in evolutionary ecology, and participate in day-to-day lab management.

We seek a candidate who can work independently and has some background in plant ecology and/or evolutionary biology, either through coursework or previous research. Background in plant reproductive biology or plant physiological ecology would be desirable, but is not essential.

The position is suitable for those who have recently completed an undergraduate degree in biology and are seeking additional research experience prior to entering graduate or professional programs. There will be opportunities to develop an independent project related to current research in our labs.

We are currently accepting applications, and will do so until the position is filled. The position will start in early August 2010. The initial appointment is for one year, but may be extended. Salary will be commensurate with experience, and will include benefits.

To apply, please submit a letter of interest, CV, and the contact information for three references to Christina (Chris) Caruso (carusoc@uoguelph.ca) or Hafiz Maherali (maherali@uoguelph.ca).

Christina M. (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 Canada 519-824-4120 x52030 carusoc@uoguelph.ca christinamariecaruso@gmail.com

christinamariecaruso@gmail.com

UManchester 3year Bioinformatics

Research Fellowship in Bioinformatic Approaches to Genetics & Development Salary £28,983 - £35,646 p.a.

The role will be broad-ranging involving data analysis of genome-wide primary experiments (carried out by

Manchester researchers), contributing to experimental design and bespoke downstream informatic analyses of all results. This could entail analysis of chromatin immunoprecipitation experiments (e.g. for histone modifications and transcription factors), RNA-seq and expression microarray, high- throughput sequencing data, and attendant proteomic analyses using mass spectrometry. The role therefore complements 'wet' experimental ones from a number of other research groups, and will require a collaborative approach to experimental working.

Within this role, there will be the protected opportunity to develop an individual career, apply for prestigious external senior fellowships, and prepare for a future independent research career as a principal investigator.

Informal enquiries may be addressed to: Professor Neil Hanley (for BRC overview of the position), Chair of Medicine, neil.hanley@manchester.ac.uk

Professor Simon Hubbard (for computational biology aspects of the position), Chair of Computational Biology, simon.hubbard@manchester.ac.uk Dr Andrew Devereaux (for clinical aspects of the position), Director of the National Genetics Reference Laboratory Manchester, andrew.devereaux@cmft.nhs.uk

Application forms and further particulars can be obtained at http://www.manchester.ac.uk/news/-vacancies If you are unable to go online you can request a hard copy of the details from Barbara Milnes, Tel: +44-161-275-1190. E-mail: barbara.milnes@manchester.ac.uk .

Closing date: 30 March 2010. Please quote reference MHS/10169.

david.robertson@manchester.ac.uk

UMontpellier 3 Biol

Three Associate Professor positions are available at the University of Montpellier, France. Deadline for application is March 25, 2010. It is necessary to be relatively fluent in french.

In order to apply, candidates first need to have gone through a "qualification step" last winter or any of the previous 4 years. If you have not applied to this step, you will not be allowed to apply to these positions in 2011, but you are encouraged to go for this qualification step next winter, in order to be able to apply to similar positions next year (I can give you more information about this if you want). If you have (successfully) gone through this qualification step in the last 4 years, you may go to https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/emplois_publies.html for further information about application.

Below are linked to descriptions (in french) of each Ass. Prof. positions (teaching + research), as well as people to contact.

Position 1. Biostatistics and quantitative genetics : https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/ListesPostesPublies/-ANTEE/2010_1/0341088Y/FOPC_0341088Y_212.pdf Position 2. Conservation Biology of Vertebrates : https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/ListesPostesPublies/-ANTEE/2010_1/0341088Y/FOPC_0341088Y_423.pdf Position 3. Aquatic (Plant) Ecology : https:/-/www.galaxie.enseignementsup-recherche.gouv.fr/-ensup/ListesPostesPublies/ANTEE/2010_1/-0341088Y/FOPC_0341088Y_980.pdf We also have - a Full Professorship in Aquatic animal ecophysiology: https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/ListesPostesPublies/-ANTEE/2010_1/0341088Y/FOPC_0341088Y_625.pdf - A full Professorship in Paleontology and the origins of modern mammals : https://-www.galaxie.enseignementsup-recherche.gouv.fr/-ensup/ListesPostesPublies/ANTEE/2010_1/-0341088Y/FOPC_0341088Y_675.pdf Best

Isabelle Olivieri

Isabelle Olivieri <Isabelle.Olivieri@univ-montp2.fr>

UniversidadAustraldeChile 3 EvolBiology

Curricula competition to appoint 3 full time Academic positions, with degree of PhD, assigned to the Faculty of Sciences, to support the PhD Program in Systematic and Ecology (SISTECOL) in the areas (1) Population and/or Community Ecology, (2) Evolutionary Biology, and (3) Plant Molecular Systematic.

Position 1 - PhD possessing consolidate trajectory, leading multidisciplinary groups and carrying out research in Population and/or Community Ecology, mainly on population dynamics in managed and productive ecosystems, and/or bio-resources management, in marine and/or limnology areas.

Position 2 - PhD carrying out research in Evolutionary Biology. Desirably, the applicant should have expertise studying experimentally the interface between evolutionary biology and development biology (Evo-Devo), using approximations coming from the population biology, development biology, molecular evolution and/or evolutionary genetics.

Position 3 - PhD carrying out research in Plant Systematic, possessing demonstrable expertise using modern molecular tools, being able to conduct evolutionary, phylogenetic and/or biogeography studies, either at a population, species and/or taxonomic group level, emphasizing higher plants.

General Responsibilities for the 3 positions: The academics to be hired are expected to carry out, in the short run, the following activities:

1. Supervision of PhD students, with an active participation in SISTECOL through counseling students and directing PhD theses.

2. Cutting-edge scientific research, through ISI publications, and obtaining national competitive research grants (FONDECYT or similar).

3. Associative scientific research, through national and international cooperation grants.

4. Undergraduate and postgraduate teaching, coordinating courses in their respective areas and collaborating in other courses.

5. University management, including willingness to participate in committees or work groups, to take academic-administrative positions, and/or to take part in academic management projects.

Application requirements:

- To be in the possession of the degree of PhDr at the moment of being contracted, obtained through an accredited program, either national or international.

- A postdoctoral training is desirable.

- To pass an exam of Psychological Evaluation.

BENEFITS

Full time contract in an academic category in agreement with their antecedents. Remuneration in agreement with the academic category the applicant is contracted in. Operational expenses during the first three years of the contract are also contemplated.

Antecedents required for application:

- To accredit degree of PhD.

- To submit a CV and a copy of their most relevant ISI publications to the position they are applying.

- Two reference letters issued by remarkable scientists, either Chilean or foreigners.

- To explain the motivations for their applications by written.

Availability to take possession of the position from May 10th, 2010.

Procedure for the selection and assessment of submitted antecedents:

Antecedents will be evaluated by an ad hoc committee. An academic presentation and/or an interview may be asked to some of the applicants. The antecedents from this process will then be submitted to the final approval of MECESUP 2 with the advising of the Counseling for Advanced Human Capital (Consejo de Capital Humano Avanzado). The University keeps to itself the right of declaring the application deserted either totally or partially, without the obligation to express the reason for such determination.

Deadline for Application and Antecedents Delivery: MARCH 26th, 2010

Submit antecedents to:

Direccion de Personal, Concurso № 005, Universidad Austral de Chile, POBox 567, Valdivia, Chile.

Deadline for results delivery: April 30th, 2010

Name and address of the person responsible for answering questions and/or delivering information:

Dr. Christian Figueroa Caro, Instituto de Ecología y Evolución, Facultad de Ciencias, Universidad Austral de Chile, Casilla 567, Valdivia, Chile.

Telephone number: (+56) (63) 221 449.

Email: christianfigueroa@uach.cl

Christian C. Figueroa Associate Professor Director Center for Research on Plant-Insect Interactions - iCROP Universidad Austral de Chile Instituto de Ecología y Evolución Casilla 567, Valdivia Phones: +56 63 22 1449 (direct) +56 63 221344 (secretary and fax) www.uach.cl; www.ecolevol.cl; www.icrop.cl

christianfigueroa@uach.cl christianfigueroa@uach.cl

UNorthCarolina Wilmington NatHistoryAssistCurator

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

Assistant Curator of Natural History Collections, UNC-Wilmington

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

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

Organizational and effective verbal communication skills, basic computer knowledge, database management, and related skills are required. Applicants with a minimum MS or MA degree in biology or a related discipline and a strong background in plant taxonomy are especially encouraged to apply. Previous experience with Specify is preferable. To apply, complete the online application process at http://consensus.uncw.edu< https://mail.uncw.edu/exchweb/bin/redir.asp?URL=http://consensus.uncw.edu/ > by electronically submitting separately (1) a letter of application including a statement of collection-based experience and research interests, (2) a curriculum vitae, and (3) contact information for three professional references. MS Word or PDF attachments are preferred. For questions about the position, contact Paul E. Hosier, Search Chair, hosier@uncw.edu or (910) 962-2642. For questions about the online application process, contact Ms. Tracie Chadwick, chadwickt@uncw.edu or (910) 962-3536. The application process will close on 15 February 2010. UNCW actively fosters a diverse and inclusive working and learning environment and is an equal opportunity employer. Qualified men and women from all racial, ethnic, or other minority groups are strongly encouraged to apply.

Thanks,

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

"Van Tuinen, Marcel" <vantuinenm@uncw.edu>

UNotreDame ResTech Genomics

Research technician (genomics, molecular ecology) at University of Notre Dame

Position Description: We seek a temporary, full-time research technician at the Center for Aquatic Conservation at the University of Notre Dame. The position starts May, 2010 (exact start date flexible) and currently has funding through August, 2010. There is the possibility of additional funding beyond August. The technician will perform molecular analyses of field samples, operate and maintain laboratory equipment, prepare solutions and order laboratory reagents. Occasional field sampling may be required.

Qualifications: The successful candidate will be expected to independently perform basic molecular biology techniques such as DNA extraction, PCR, gel electrophoresis, and DNA gel extraction for sequencing. Candidate should also be able to demonstrate experience with proper documentation, data reporting practices, and general organizational skills. Previous experience performing molecular techniques are preferred. A background check is required before hiring.

Pay rate: Position pay is $12-$15 per hour, depending on qualifications.

Contact: For inquiries, email Andrew Mahon (amahon@nd.edu). To apply, send electronic resume, cover letter, and 3 references to Joanna McNulty (mcnulty.9@nd.edu), Program Coordinator for the Center for Aquatic Conservation at the University of Notre Dame.

Closing Date: Applications will be considered as received until April 15, 2010.

Michelle.L.Budny.4@nd.edu

USFWS WashingtonState ConservationGenetics

The Abernathy Fish Technology Center (AFTC), Longview, Washington, provides applied fishery research and development capabilities for the U.S. Fish and Wildlife Service (Service) Pacific and Pacific Southwest Regions (CA, ID, NV, OR, and WA). AFTC currently maintains active Applied Research Programs in the fields of Nutrition, Ecological Physiology, and Conservation Genetics. The Applied Research Programs assist restoration and recovery efforts by scientific development and evaluation of new methods, concepts, systems, and approaches for use by various Fish and Wildlife Management Offices, Fish Health Centers, National Fish Hatcheries, other programs such as Ecological Services, National Wildlife Refuges, and Law Enforcement, and various external partners such as state and other federal agencies, tribal governments, and non-governmental organizations. For further information about AFTC and our research programs, please see the following web site: http://www.fws.gov/-aftc/ The Conservation Genetics Program currently has three open positions. The first is a permanent GS7/9 lab manager position. For a position description please see the following at USAJobs.

http://jobview.usajobs.gov/GetJob.aspx?JobID=-86354132&aid=86594022-9310&WT.mc_n=125 The other two positions are for Term GS9/11 fish biologist/geneticists. The position description and application information can be found at:

http://jobview.usajobs.gov/-GetJob.aspx?JobID=86684328&JobTitle=-Fish+Biologist+(Genetics)+TERM&q=&where=longview%2c+wa&brd=3876&vw=b&FedEmp=N&FedPub=Y&x=0&y=0&
03-08+00%3a03%3a00

Denise Hawkins Regional Geneticist U.S. Fish & Wildlife Service Abernathy Fish Technology Center 1440 Abernathy Creek Rd. Longview, WA, 98632 Phone: (360)425-6072 x339 Fax: (360)636-1855

Denise_Hawkins@fws.gov

UWisconsin Madison SystemsBiology

Open Rank Position in Systems Biology

University of Wisconsin, Madison

The Wisconsin Institute for Discovery (WID) at the University of Wisconsin-Madison (www.discovery.wisc.edu) invites applications for faculty openings in Systems Biology. Our interests encompass (but are not limited to): (i) Quantitative Experimental Biology - development and application of new measures of biological entities (e.g. molecules, viruses, microbes), including their levels, functions, activities, and interactions; (ii) Computational Biology - integration of diverse 'omic' and additional data to advance predictive models of how viruses, cells, or whole organisms function and interact; (iii) Evolutionary Biology - development of new experimental, mathematical or computational approaches to better understand how viruses, cells or organisms evolve and co-evolve. Areas of special interest include: virus-host and microbe-host interactions (beneficial or pathogenic), innate and adaptive immunity, and ecological and evolutionary dynamics. Opportunities are available at the Assistant, Associate or Full Professor level. Successful candidates will occupy space in a new state-of-the-art and centrally-located WID research facility specifically designed to spark and support cross-disciplinary collaborations. WID is the public half of an exciting public-private pair of Institutes that will promote basic research and facilitate the translation of new discoveries to practice. Each successful candidate will be appointed to the department of the University that most appropriately matches her/his experience and interests. S/He will be expected to develop a vigorous, independent research program; attract and maintain extramural funding for her/his research program; teach undergraduate and/or graduate courses; develop new course(s) in her/his area of expertise as appropriate; supervise graduate and postgraduate research; participate in faculty governance activities in the department, college and/or University; and actively engage with the national and international scientific community.

Additional Information: The University of Wisconsin-Madison is a world-class academic institution with an international reputation for basic, applied and cross-disciplinary research. It attracts scholars and students at all levels from around the world. Nationally, UW-Madison ranks fourth among all U.S. universities for research and development expenditures, exceeding $950 million annually. The University has a deep culture of collaborative interdisciplinary research, reflected recently by major grants such as the $150 million DOE Great Lakes Bioenergy Research Center award (2007) and the $50 million NIH Translational Medicine award (2007). Interdisciplinary and translational mega-centers that are positioning UW at the forefront of collaborative research include the Microbial Sciences Building (2007), the School of Medicine and Public Health's Interdisciplinary Research Complex (2008), and the Wisconsin Institute for Discovery (opening Fall 2010). Of special relevance to the Systems Biology theme, the University is the home of internationally renowned centers, institutes and laboratories that are defining the frontiers of Genomics Science, Molecular Virology, Microbial Pathogenesis & Host Responses, High Throughput Computing, and Optical and Computational Instrumentation. Finally, UW-Madison is the home of nationally recognized pre-doctoral and post-doctoral training programs in Biotechnology, Computation and Informatics in Biology and Medicine, Microbiology, Microbial Symbiosis, and Virology.

PVL http://www.ohr.wisc.edu/pvl/pv_063855.html We are accepting applications on-line http://newfac.sysbio.discovery.wisc.edu Inquires about these opportunities may be addressed to:

JOHN YIN WISCONSIN INSTITUTE FOR DISCOVERY THEME AREA: SYSTEMS BIOLOGY Visit our website: http://newfac.sysbio.discovery.wisc.edu Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

https://mywebspace.wisc.edu/carollee/web/Lee/Lee.html Carol Eunmi Lee <carollee@wisc.edu>

WildlifeInstIndia 1YearResearchAssociate WildlifeConservatoin

For more information, please contact: Dr. S. P. Goyal (goyalsp@wii.gov.in)

Research Associate One

Essential Qualifications:

a. M.Sc. in Biotechnology/ / Molecular Ecology/Animal Genetics Or M.V.Sc. in Animal Genetics

b.Ph.D. in Molecular Biology/Animal Genetics

Desirable Qualification/Experiences: b. Working experience in electrophoresis and molecular genetics using PCR based techniques, PCR-RFLP and DNA sequencing/ developing species specific characteristics

c.Good knowledge in biostatistics and multivariate techniques for use in DNA and animal genetics

d.Any other academic qualification related to work.

Job Requirements: e.R.A. is required to work under supervision of Nodal Officer, Wildlife Forensic Cell for developing DNA based techniques and protocols for dealing wildlife offence cases

f.To prepare protocols for identifying species from biological materials seized under wildlife offences

g.Establish liaison with national and international forensic laboratories

h.To provide scientific input and assistance in organizing workshop by WII and other organizations

i.To maintain proper record and files of all wildlife forensic cases

j.To prepare annual requirement of equipment, glass wares, chemicals, plastic wares and maintain proper stock entries of these.

k.To collect reference samples , and other work assigned by Nodal Officer

Duration: One year

fishtiaq2001@yahoo.com

Other

454 Sequencing facilities

Hi all,

can anyone recommend a US core facility for 454 sequencing? We want to do one full run using GS FLX (non-titanium) long-read chemistry (= 250bp av. reads), and the sstDNA library prep has already been done... so just emPCR titration & shotgun sequencing for this particular project. Main considerations would be (1) cost, and (2) turn-around time. Any suggestions would be much appreciated.

cheers, Ryan

email: ryan.garrick@yale.edu

454 sequencing facilities answers

Hi all,

here's a compilation of responses to my question about 454 sequencing facilities.

cheers, Ryan

Original post:

can anyone recommend a US core facility for 454 sequencing? We want to do one full run using GS

FLX (non-titanium) long-read chemistry (= 250bp av. reads), and the sstDNA library prep has already been done... so just emPCR titration & shotgun sequencing for this particular project. Main considerations would be (1) cost, and (2) turn-around time. Any suggestions would be much appreciated.

General outcome:

(1) Seem to be looking at $US10-12K for a full plate run (incl. titration), but library prep will add another $500+.

(2) minimum 10-14 days, up to 4 weeks in some cases. If have want to do just a 1/2 plate or less, will need to wait for someone else with similarly-sized project, so that the plate can be shared

(3) worth noting that Roche/454 are rapidly phasing out the non-titanium option, so regaents will become harder to come by soon. This also means that if you want to run only a 1/2 plate with this older chemistry, you might end up waiting a long time for a partner to share that other 1/2 of the plate with you.

Interesting website:

Google map of sequencing facilities in the URL below and you can do limited searches for 454 sequencers (tick box on the right): http://pathogenomics.bham.ac.uk/hts/ Non-exhaustive list (thanks to all for suggestions!): * Note that prices, where given, are not necessarily directly comparable. I apologise for any errors that I may have made.

EnGenCore (recommended by a number of people, incl. Roche/454 Life Sciences) University of South Carolina Columbia, SC 29208, USA http://engencore.sc.edu/ * US11.7K full plate

VBI Core Lab Virginia Bioinformatics Institute Washington Street Blacksburg, VA 24061, USA http://www.vbi.vt.edu/core/ * US11.8K full plate

Macrogen Korea http://www.macrogen.co.kr/eng/ngs/ngs_main.jsp * US$12K full plate, first library prep free, further preps US$500

454 Life Sciences Branford, CT 06405, USA http://454.com/contact-us/request-sequencing-services.asp * US20K full plate (user must NOT do library prep)

Genome Sequencing Laboratory New Mexico State University http://biology-web.nmsu.edu/houde/conspirators.htm * US11K full plate

Emory GRA Genome Center, Emory University School of Medicine 201 Dowman Drive. Atlanta, Georgia 30322 USA http://www.corelabs.emory.edu/labs/gra_genome_center/index.html http://www.corelabs.emory.edu/labs/gra_genome_center/rates.html * US10.2K full plate

Purdue Genomics Core Facility Purdue University West Lafayette, IN 47907 http://www.genomics.purdue.edu/~core/ * US15K full plate

High-Throughput Sequencing and Genotyping Unit University of Illinois 1201 W. Gregory Drive, Urbana, IL 61801 http://www.biotech.uiuc.edu/centers/Keck/Highthroughput/ * US9.4K full plate

Institute for Genome Sciences & Policy (IGSP) Duke University CIEMAS Durham, NC 27708, USA http://www.genome.duke.edu/cores/sequencing Indiana University, Center for Genomics and Bioinformatics http://cgb.indiana.edu/services/genome_sequencing/ IBEST DNA Sequencing Analysis Core University of Idaho Life Science South, Moscow, Idaho 83843 http://www.ibest.uidaho.edu/home/research_facilities.php Genome sequencing core University of Virginia Charlottesville, VA. 22904 http://faculty.virginia.edu/454seq/ Institute for Genome Sciences University of Maryland School of Medicine http://www.igs.umaryland.edu/454.php ryan.garrick@yale.edu

ABI7900HT vs BioradCFX384

Hi All,

We're about to invest in a real time PCR system and have been looking at ABI's 7900HT (fast 384 wells) and Bio-rad's CFX384. We would primarily use the system for SNP validation and low to medium thoughput SNP genotyping. In addition, we aim to do some quantitative PCR. It would be nice to hear from users of these systems about the pros and cons and how they compare.

Thanks

Jens

wodans12@yahoo.se

Alternative to Futuyma Textbook Recommendation

Hi, everyone:

I have been using Futuyma to teach my Evolutionary Biology course thus far. Personally, I like the breadth of topics in Futuyma but I have found that it is a little too advanced for my students and I skip 1/3 or more of the sections for that reason. All of the other books I've looked at - example: Kardong's "Introduction to Biological Evolution" is too basic for what I would like to do. Ideally, I'd like to find something intermediate between Futuyma and one of these ultra-basic texts - with a somewhat smaller price tag as well.

Once I have some feedback I'll send a summary of what I learn back to the list. Thanks in advance for any recommendations that get passed along. You can email me directly at:

pmack@as.muw.edu

Paul

Paul Mack, Ph.D Assistant Professor of Biology Department of Sciences and Mathematics Mississippi University for Women 1100 College Street, MUW-100 Columbus, MS 39701 662-329-4987

Paul Mack <PMack@as.muw.edu>

Annotating Haplotypes

My last two postings to the EvolDir have proven extremely helpful, so I thought I would try another. This one is in the spirit of "the only really stupid question is the one that's not asked." I have never seen clear instructions on how to indicate haplotype frequencies in the various DNA file formats (FASTA, NEXUS, PHYLIP, etc.). When I want to load both haplotype sequence and frequency information into a program like DNAsp, TCS, etc. I've typically been simply making multiple entries of the same sequence. So, if there are three copies of "Haplotype 1" in a population, I write its sequence (and its name) 3 times. But, as the numbers get bigger, this seems so incredibly clumsy to me, that I "know" there must be a better way of doing it.../

Any hints would be much appreciated.

Bruce J. Turner Dept. Biol. Sci. VIRGINIA TECH Blacksburg, VA 24061 USA

"Bruce J. Turner, Dept. Biol. Sci., VPISU, Blacksburg, VA 240" <fishgen@vt.edu>

Ant body mass data

Dear colleagues,

A correction: I am searching for data on body mass (fresh, dry) on sexuals for the species below.

I would infinitely appreciate it if anyone would be able to supply a source for body mass data on these ants (below). Personal unpublished data would also be fine. Many thanks in advance,

Best regards,

Else Fjerdingstad

Dinoponera quadriceps

Neivamyrmex nigrescens

Eciton burchellii

Dorylus (Anomma) molestus

Aenictus laeviceps

Pachycondyla inversa

Platythyrea punctata

Gnamptogenys striatula

Ectatomma ruidum

– Else J. Fjerdingstad, Ph.D. Assistant Professor of Biology

Queens College, CUNY 65-30 Kissena Blvd Flushing, NY 11367 USA Email: Else.Fjerdingstad@qc.cuny.edu http://qcpages.qc.edu/Biology/Fjerdingstad/-Fjerdingstad.html — Esse quam videri

E Fjerdingstad <efjerdingstad@gmail.com>

Assignment tests with GeneClass2

Dear all,

we are trying to assign individuals to potential populations of origin with the GeneClass2 software, but for some reason unknown to us GeneClass does not accept our file with the to-be-assigned individuals. We have tried Genepop and Genetix files, and the whole file (as for self-assignment purposes) is working fine, but as soon as we delete all pops except the individuals to be assigned it does not work any more. We have not found any reference input files for individuals to be assigned so we do not know exactly how they should look. Perhaps someone can help us on this or even provide a working infile.

Any feedback will be highly appreciated.

Yours sincerely,

Frank Zachos

PD Dr. habil. Frank E. Zachos Zoological Institute Christian-Albrechts-University Kiel Olshausenstrasse 40 (postal address) 24118 Kiel, Germany Tel.: +49 / (0)431 - 8804529 Fax: +49 /(0)431 - 8801132

Frank Zachos <fzachos@zoologie.uni-kiel.de>

Assignment tests with GeneClass2 answers

Dear all,

with respect to my recent query concerning the GeneClass2 software I was using to carry out assignment tests I have received a couple of well-informed responses.

My main problem was that the software did not accept my file containing the to-be-assigned individuals. This held irrespective of whether I used a Genepop or Genetix format (both of which are supported by GeneClass2).

The advice that finally made the software run was to add a .dat extension to the files. The software then immediately accepted the infiles. However, when I re-downloaded the software, it even accepted the files without this extension. So, eventually it might have been to do with my computer, too.

Anyway, thank you very much out there for sharing your experiences with me. Should anyone need a working infile, he or she is welcome to contact me.

All the best,

Frank

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fzachos@zoologie.uni-kiel.de

Automated DNA extraction

Dear members,

Ill be happy if any of you can give some piece of advice about your experience with equipments for automated DNA extraction (like Promega's Maxwell 16 System) and systems to destroy hard tissues. We are currently working with insect legs and manual homogenizing is far from efficient.

Thanks in advance. Best wishes, Romina

Dra. Romina Piccinali Laboratorio de Eco-Epidemiología Facultad de Ciencias Exactas y Naturales Universidad de Buenos Aires Argentina Tel/Fax +54-11-4576-3318

E-mail: rpicci@ege.fcen.uba.ar

Bern Switzerland FieldAssist BirdEvolution

We are looking for an enthusiastic field assistant (European nationality) who is interested in working in a field experiment on Great tits in Bern, Switzerland. The work will start immediately and last until the end of June 2010. In the experiment we will study the influence of parasites on immune and stress response of the host. The great tits are a good system to study the effect of ectoparasites on life-history traits since they readily accept nest boxes making them easy to manipulate and follow from egg laying to offspring fledging.

The successful candidate will be involved in all the aspects of the work, including ringing the birds, counting fleas, conducting recordings, and measuring body indices of the birds. Motivation is very important as the work is hard and demanding, may take place in changing weather and requires long hours at times. Accommodation and transportation within Europe will be provided. Some financial assistance will also be available to cover living expenses. Candidates must hold a valid European driving license. For further details please contact Michèle Wegmann at michele.wegmann@iee.unibe.ch or Bea Vögeli at beatrice.voegeli@iee.unibe.ch or at + 41 31 631 3018.

Michèle Wegmann <michele.wegmann@gmail.com>

BFast SNP users

Hello,

Looking for anyone with experience using bfast to analyze SNPs in SOLiD data who is interested in chatting about parameter choices, etc.

Thanks much! Marta

Marta L. Wayne, PhD Associate Professor P.O. Box 118525 Department of Biology University of Florida Gainesville, FL 32611-8525 (courier: B30 Bartram Hall) vox: 352-392-9925 fax: 352-392-3704 http://www.biology.ufl.edu/People/faculty/mlwayne.aspx mlwayne@ufl.edu

Commercial PlantDNA extraction

Dear Evoldir

I will be processing a moderately large number of plant tissue samples for DNA extraction in the near future. I'm new to the US and would like to find out if there are any commercial plant DNA extraction services available here, particularly that would service Louisiana. Any additional feedback on price, turn-around time and DNA quality/quantity would be greatly appreciated.

Many thanks Kym Ottewell

kymott@gmail.com

DNA extraction answers

Dear Evol-members, Thank you very much to all of you that sent me suggestions about your experience with automated DNA extraction machines and tissue homogenization. Below, I copy the answers and my original question.

Best, Romina

My original inquiry:

Dear members,

Ill be happy if any of you can give some piece of advice about your experience with equipments for automated DNA extraction (like Promega's Maxwell 16 System) and systems to destroy hard tissues. We are currently working with insect legs and manual homogenizing is far from efficient.

Thanks in advance. Best wishes, Romina

Answers:

1) Hi Romina - If you are looking for an inexpensive way to go - check our hour homemade version, very easy to make and extremely effective.

For the earliest and rudimentary version see - http://www.polyploid.net/machacadora/machacadora.html Donovan

2) Hi Romina,Your email was passed onto me from Professor Wetherall. For hard tissues like insect legs or whole insects we use a method called ANDE which has been used by several agricultural labs for nondestructive DNA extraction for PCR purposes only - it is not suitable if you want good quality DNA.

more information can be found at http://www.ande.com.au/ regards

David

3) Dear Romina

We extract from insects using the qiagen blood and tissue kit (both tubes and 96 well plates), but have used a variety of kits. Presently we also use a plate extraction kit from zygem. We do not homogenise tissue we incubate either whole insects, or parts of them (e.g. legs) in the extraction buffer with proteinase K, and then remove the body parts before continuing with the extraction. This works fine, thus there is little need for you to homogenise tissue.

Cheers Brent

4) Hi Romina, We used qiagen animal tissue extraction kit. It works well with insect legs.

Qixin

5) Hello Romina, In response to your email below : we use a TissueLysser from Qiagen, and to extract DNA and RNA from leaf tissue it is very efficient...

Best wishes, Raquel Carvalho

6) Hi Romina,

I work on ants, and we homogenize using an electric power drill that you can buy in a hardware store. Just stick in the usual pestle instead of the drill bit, and you're set to go.

We are using the Qiagen kits, which work very well.

best, Beth

7) Hi Romina In plants, we freeze the tissue in liquid nitrogen, and grind by adding a metal bead and shaking. This should work with insect parts too

You can do this in 96 well plate format using the Geno/Grinder 2000 (or newer 2010 version) or the Qiagen Tissue Lyser

These machines don't do the DNA extraction, but just grind the tissue. It works with very hard tissues and takes about 5 minutes or less

diana

8) Dear Romina,

In our facility we use Biomek FX robot for semi-automated DNA extraction (elution is done manually, to minimize chances of contamination). Please find attached my papers and detailed protocol for DNA extraction which is suitable for insects. For insects you don't actually need tissue homogenization, simply use overnight incubation at 56C. Biomek robots are quite sophisticated, but the software is intuitive.

For plants we use similar protocol (see attached paper), but use Tissue Lyser and stainless steel beads for grinding.

Please let me know if you have more questions.

Best regards, Nataly

9) Dear Romina

I tested the Maxwell 16 on tough Eucalyptus leaves and it did not crush them very well. The Retsch mixer mill works well for most eucalypt leaves though (after they have been frozen in liquid nitrogen).

The Promega reps (at least in Australia) are very nice and might lend you a machine and give you a kit to test the protocol in your species of interest.

Good luck Rebecca

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rpicci@ege.fcen.uba.ar rpicci@ege.fcen.uba.ar

Duplicate sequence eliminator

Does anyone know of a program, preferably one in the public domain, that can go through a list of nucleotide sequences and identify (and remove) duplicates? Occasionally, one of the analysis programs I use identifies a duplicate in the middle of an analysis, but I would prefer to clean up the list first. It seems to me that an alignment program ought to be able to do this, but I don't recall one that does...

Bruce J. Turner Dept. Biol. Sci. VIRGINIA TECH Blacksburg, VA 24061 USA

"Bruce J. Turner, Dept. Biol. Sci., VPISU, Blacksburg, VA 240" <fishgen@vt.edu>

Evolution 2010 MSI FacultyTravelAward

Evolution 2010 MSI Faculty Travel Award

Are you a biologist at a minority-serving institution? Apply now for a travel award to attend Evolution 2010 in Portland, OR.

The National Evolutionary Synthesis Center (NESCent), with support from the Society for the Study of Evolution (SSE), is pleased to announce a travel award for faculty from Minority Serving Institutions (MSIs) to attend Evolution 2010 V the annual meeting of SSE, SSB (Society of Systematic Biologists) and ASN (American Society of Naturalists) V to be held in Portland, OR from June 25-29, 2010.

If you are a faculty member at an MSI, HBCU or other institution with significant enrollment of underrepresented minority students, you are encouraged to apply. Funds are available to cover conference registration, travel, food and lodging for up to three individuals.

This award is intended to provide MSI faculty with an opportunity to present original research in evolution, systematic biology, evolutionary genomics/informatics or other disciplines typically represented at the SSE/SSB/ASN meetings. As such, your application must include a talk/poster title. (Abstracts are not required to apply.) In addition, you will be asked to provide a brief (1 page) statement describing how this award will contribute to your professional/scientific development, as well as provide benefit to your students and institution.

To apply, please go to:

http://www.nescent.org/eog/-2010facultytravelaward.php Application Deadline: March 31st, 2010 (Awards will be announced by April 9th, 2010)

For more information, please contact Dr. Jory Weintraub (jory@nescent.org)

Jory P. Weintraub, PhD Science Education and Outreach Program Manager National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200 Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Web: www.nescent.org

Jory Weintraub <jory@unc.edu>

Evolutionary Comparative Anatomy Textbook Recommendation

Hi, All:

I will be teaching a Comparative Anatomy course for the first time this coming fall and would like to structure it so that it has a very strong evolutionary emphasis. I'm wondering if anyone has done something similar and has a textbook they could recommend. I have a copy of Kardong's "Vertebrates: Comparative Anatomy, Function, Evolution" (4th edition) that could work but would like to hear of other possibilities.

Once I have some feedback I'll send a summary of what I learn back to the list.

Many thanks!

Paul

Paul Mack, Ph.D Assistant Professor of Biology Department of Sciences and Mathematics Mississippi University for Women 1100 College Street, MUW-100 Columbus, MS 39701 662-329-4987

Paul Mack <PMack@as.muw.edu>

France VolFieldAssist SwampTurtleEvolution

Field assistant in evolutionary ecology of European swamp turtles

We are looking for a voluntary field assistant to participate in a conservation project on European swamp turtles (Emys orbicularis), starting as soon as possible and lasting until July 2010, at the Research Station Petite Camargue Alsacienne in France (www.camargue.unibas.ch).

The work will include observation and localisation of aquatic turtles living in the nature reserve, capturing the turtles, observing breeding behaviour and locating nests. The applicant is expected to stay for the entire field season from the end of March until the end of July.

The field site is situated in the nature reserve Petite Camargue Alsacienne in France, about 10 km north of Basel (Switzerland). We cannot cover travel expenses, but we offer free accommodation and use of the infrastructure at the research station. The assistant will receive 350 Euros per month to cover living expenses.

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

Christian Rust <christian_rust@hotmail.com>

GeneMapperSoftware in Windows7

Hello all

I finally installed GeneMapper v3.5 in a Windows2000 virtual machine, over a Windows7 operative system, and it works well (at least until now).

Some colleges gave me some advices about it:

- The software can cause major troubles even when run with the right operating system and on an AB certified computer. So is better to get a computer dedicated to this work if you do not want crashes and data loss

- You should load your data files in the same operative system where you are running the software. It makes it run faster.

- And an alternative to GeneMapper is a software that Dr. F.Palero has developed recently. It reads the .fsa files using PeakScanner (free- download) and get the peaks by means of a simple file where you can set the features of your microsatellites.

It allows you to define the bin set automatically with AlleloBin or manually using R. It is called P2EMA and you can download it for free from http://sourceforge.net/projects/p2ema/ There you could download also PeakScanner and R. It hasn't been tested yet in Windows7 but it works well in WindowsXP, and, according to Microsoft, the softwares that run in WindowsXP should work in Windows7 too.

If you want to know more about it you can contact with Dr.F.Palero fpalero@ist.ac.at

Thanks,

Inés Sánchez-Donoso PhD Student ines.sanchezdonoso@ub.edu

Animal Biology Department Faculty of Biology Barcelona University Spain

Inés Sánchez Donoso <ines.sanchezdonoso@gmail.com>

Herpetology teaching specimens

I am developing a herpetology course at Tulane University and need to put together a collection of preserved specimens to use in conjunction with the laboratory portion of the course. Tulane had a teaching collection long ago but after years of non-use, it was donated to another university.

With this in mind, I am wondering if there are other herpetology teaching collections going unused that people wouldn't mind donating to help me get Tulane's new collection started? Any leads and any reptile or amphibian material would be appreciated. I'm more than happy to arrange for shipping or pick-up.

Thank you! Cori Richards-Zawacki

–

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

Assistant Professor Department of Ecology and Evolutionary Biology Tulane University, New Orleans, Louisiana

"At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?" - Ralph Waldo Emerson

coririchards@gmail.com

LERN group selection debate online

Dear all

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

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

- Stuart West Professor of Evolutionary Biology, University of Oxford

- Herbert Gintis Professor of Economics, Santa Fe Institute, University of Siena, and Central European University

- Samir Okasha Professor of Philosophy of Science, University of Bristol

- Mark Pagel Professor of Biology, University of Reading

Best wishes

Gillian

Gillian Pepper MSc Student - Evolutionary Psychology Brunel University

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ht08ggp1@brunel.ac.uk ht08ggp1@brunel.ac.uk

Lyon SMBE 2010 UndergradTravelAwards

SMBE UNDERGRADUATE MENTORING AND DIVERSITY TRAVEL AWARDS

2010 ANNUAL MEETING OF THE SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION

July 4-8, Lyon, France

CONFERENCE WEBSITE

http://smbe2010.univ-lyon1.fr/ DEADLINE FOR RECEIPT OF NOMINATIONS/APPLICATIONS: April 10, 2010

PROGRAM OUTLINE

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students to participate in a Mentoring and Diversity Program. Five of these positions will be reserved for undergraduates from traditionally underrepresented groups in our scientific discipline.

The goals of this program are: (1) to provide students with the opportunity to experience the excitement of attending and presenting at an international scientific conference, (2) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field, and (3) to promote diversity at the SMBE annual meeting.

To achieve these goals, each recipient of an SMBE Undergraduate Mentoring and Diversity Program Award will be paired with two mentors, one a senior graduate student and the other a postdoctoral fellow or faculty member. Mentors will serve as contact points for the students, attend some sessions with the students, and, more generally, explain the “goings-on” at a multiday scientific conference in order to minimize the anxiety often felt by first-time conference attendees. The mentors will also facilitate connections to graduate students, postdoctoral fellows and faculty members.

ELIGIBILITY

Candidates must currently be enrolled as undergraduate students (Bachelor’s level degree) or have graduated within the last 6 months at the time of application. Some awards will be reserved for undergraduates from traditionally underrepresented groups in our scientific discipline.

CONFERENCE PARTICIPATION

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

AWARDS

Ten awards will be given. Award recipients residing in Europe will receive US $1,000 to be used to help cover the cost of airfare, accommodation, and meeting registration. All other recipients will receive US $1,500. Each participant will also receive an online student subscription to the journal Molecular Biology and Evolution for the year of 2011.

APPLICATION

1. Faculty members may nominate undergraduates by sending a brief letter of recommendation and the abstract of the work to be presented at the poster session. The single PDF file should be sent to Dr. Dan Graur (dgraur[at]uh.edu).

OR

2. Students may apply for the award themselves by providing information on their background, academic status, the email address of their supervisor, and an abstract of the work to be presented at the poster session. The single PDF file should be sent to Dr. Dan Graur (dgraur[at]uh.edu).

TRADITIONALLY UNDERREPRESENTED GROUPS

Applications for one of the awards reserved for undergraduates from traditionally underrepresented groups should contain a brief statement of eligibility for these awards.

DEADLINE

The deadline for receipt of nominations/applications is April 10, 2010.

dgraur@gmail.com

Moulis France VolFieldAssist LizardPopulations

Field Assistant Landscape effects on common lizard population connectivity La *S*tation d’*E*cologie *E*xperimentale du CNRS à *M*oulis.

We seek a field assistant to participate in a BiodivERsA funded project (Tenlamas) starting on the 20^th June 2010 until the 20^th August 2010. The goal of the project is to test the utility of current models of population connectivity using the common lizard. The field assistant will contribute to the collection of data for a landscape genetic study of population connectivity in the Cevenne, France. They will also be responsible for behavioural experiments designed to investigate habitat preferences of the common lizard. No salary is associated with this position but accommodation will be provided.

This position is ideal for candidates who are studying biology and have an interest in gaining practical experience of field biology and behavioural experimentation. The ideal candidate should: be self motivated with an eye for detail; have a reasonable level of physical fitness; have an interest in behavioural ecology and/or population ecology; be able and willing to communicate in both French and English.

To apply please send a CV and cover letter to the address below (preferably by e-mail) describing your qualifications for the position, but most importantly why you are interested in the position and what you hope to gain from it. Closing date for applications is the 2^nd April 2010. Candidates will be contacted by the 16^th april 2010

Dr Colin Bleay, Station d'Ecologie Experimentale du CNRS 09200 Moulis France.

Colin.Bleay@EcoEx-moulis.cnrs.fr

MrBayes positive loglikelihood values

Dear members, Im currently running a MrBayes phylogenetic analysis of an insect mitochondrial gene (COI) and the following problem happened to me several times. After several generations of standard deviation of split frequencies around 0.005 (which seems to show that convergence is close) the likelihood value of the cold chain switches from a negative value around -1576 to a value of 21786.283 and convergence gets impossible to achieve. A warning saying: WARNING: In LIKE_EPSILON - for division 0 char 7 has like = 0.000000000000000000000000000000 also starts to appear from time to time. Has anyone experienced a problem like that? A tried to increase the number of generations, the number of heated chains, to decrease the temp value and to switch to a more realistic model, as suggested, but nothing seems to work Has anybody a good piece of advice? Thanks in advance, Romina

Dra. Romina Piccinali Laboratorio de Eco-Epidemiología Departamento de Ecología, Genética y Evolución Facultad de Ciencias Exactas y Naturales Universidad de Buenos Aires Argentina E-mail: rpicci@ege.fcen.uba.ar Tel: 4576-3318 / 4576-3300 int. 223

rpicci@ege.fcen.uba.ar rpicci@ege.fcen.uba.ar

MSI Faculty Evolution 2010

Are you a biologist at a minority-serving institution? Apply now for a travel award to attend Evolution 2010 in Portland, OR.

The National Evolutionary Synthesis Center (NESCent), with support from the Society for the Study of Evolution (SSE), is pleased to announce a travel award for faculty from Minority Serving Institutions (MSIs) to attend Evolution 2010 V the annual meeting of SSE, SSB (Society of Systematic Biologists) and ASN (American Society of Naturalists) V to be held in Portland, OR from June 25-29, 2010.

If you are a faculty member at an MSI, HBCU or other institution with significant enrollment of underrepresented minority students, you are encouraged to apply. Funds are available to cover conference registration, travel, food and lodging for up to three individuals.

This award is intended to provide MSI faculty with an opportunity to present original research in evolution, systematic biology, evolutionary genomics/informatics or other disciplines typically represented at the SSE/SSB/ASN meetings. As such, your application must include a talk/poster title. (Abstracts are not required to apply.) In addition, you will be asked to provide a brief (1 page) statement describing how this award will contribute to your professional/scientific development, as well as provide benefit to your students and institution.

To apply, please go to:

http://www.nescent.org/eog/-2010facultytravelaward.php Application Deadline: March 31st, 2010 (Awards will be announced by April 9th, 2010)

For more information, please contact Dr. Jory Weintraub (jory@nescent.org)

Jory P. Weintraub, PhD Science Education and Outreach Program Manager National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200 Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Web: www.nescent.org

Jory Weintraub <jory@unc.edu>

NESCent Phyloinformatics Summer of code

*** Please disseminate widely at your local institutions, including *** *** posting to message and job boards, so that we reach as many *** *** students as possible

PHYLOINFORMATICS SUMMER OF CODE 2010

http://hackathon.nescent.org/-Phyloinformatics_Summer_of_Code_2010 The Phyloinformatics Summer of Code program provides a unique opportunity for undergraduate, masters, and PhD students to obtain hands-on experience writing and extending open-source software for evolutionary informatics under the mentorship of experienced developers from around the world. The program is the participation of the US National Evolutionary Synthesis Center (NESCent) as a mentoring organization in the Google Summer of Code(tm) (http://code.google.com/soc/).

Students in the program will receive a stipend from Google (and possibly more importantly, a T-shirt solely available to successful participants), and may work from their home, or home institution, for the duration of the 3 month program. Each student will have at least one dedicated mentor to show them the ropes and help them complete their project.

NESCent is particularly targeting students interested in both evolutionary biology and software development. Initial project ideas are listed on the website. These range from phylogenetics pipeline development to a user interface for MIAPA-driven annotation of experiments, interactive animations of gene tree evolution, and rendering phylogenies on Google Earth. All project ideas are flexible and many can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

TO APPLY: Apply online at the Google Summer of Code website (http://socghop.appspot.com/), where you will also find GSoC program rules and eligibility requirements. The 12-day application period for students opens on Monday March 29th and runs through Friday, April 9th, 2010.

INQUIRIES: phylosoc {at} nescent {dot} org. We strongly encourage all interested students to get in touch with us with their ideas as early on as possible.

2010 NESCent Phyloinformatics Summer of Code: http://hackathon.nescent.net/-Phyloinformatics_Summer_of_Code_2010 Google Summer of Code FAQ: http://socghop.appspot.com/-document/show/program/google/gsoc2010/faqs DataONE Summer 2010 Internship Program (managed separately, and different from GSoC; postdocs also eligible): http://d1-lab.appspot.com/ Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center http://nescent.org hlapp@nescent.org

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NESCent Phyloinformatics Summer of code corrections

The Call for Student applications that I sent on Thursday has two errors. In the event anyone got confused, this is about soliciting student applications to the *2010* program (the original email said 2009).

Also, the Ideas page URL at the bottom of the email was wrong, the one given at the top is correct though. In the event that someone wanted to print out the announcement in order to post to a job or message board, I'm including the corrected version below.

Sorry about the inconvenience.

-hilmar

*** Please disseminate widely at your local institutions, including *** *** posting to message and job boards, so that we reach as many *** *** students as possible. ***

PHYLOINFORMATICS SUMMER OF CODE 2010

http://hackathon.nescent.org/-Phyloinformatics_Summer_of_Code_2010 The Phyloinformatics Summer of Code program provides a unique opportunity for undergraduate, masters, and PhD students to obtain hands-on experience writing and extending open-source software for evolutionary informatics under the mentorship of experienced developers from around the world. The program is the participation of the US National Evolutionary Synthesis Center (NESCent) as a mentoring organization in the Google Summer of Code(tm) (http://code.google.com/soc/).

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2010 NESCent Phyloinformatics Summer of Code: http://hackathon.nescent.org/Phyloinformatics_Summer_of_Code_2010 Google Summer of Code FAQ: http://socghop.appspot.com/document/show/program/google/gsoc2010/faqs DataONE Summer 2010 Internship Program (managed separately, and different from GSoC; postdocs also eligible): http://d1-lab.appspot.com/ Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center http://nescent.org hlapp@nescent.org

NGS biodiversity software

CANGS: a user friendly tool for processing and analyzing 454 data in biodiversity studies

Features:

- primer clipping - quality filtering - filtering of rare sequences (singletons, doubletons etc.) - grouping sequences according to barcodes - a special algorithm to account for indels caused by the 454 technology during primer clipping - assigns species names to sequences - measures overlap between different groups - provides input files for commonly used rarefaction analysis software

executables and a manual are available at: http://i122server.vu-wien.ac.at/pop/software.html
more details can be found at: http://www.biomedcentral.com/content/pdf/1756-0500-3-3.pdf Christian Schlötterer Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://i122server.vu-wien.ac.at/pop schlotc@gmail.com

NSF Dimensions of Biodiversity,FAQposted

I call your attention to NSF[1]s Dimensions of Biodiversity initiative (http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446&org=BIO&from=home) and the new FAQ just posted on our website.

[3]The Dimensions of Biodiversity initiative seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding of the diversity of life on Earth. This campaign will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Successful proposals should integrate these three dimensions to understand interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, in innovative or novel ways, to understand the roles of biodiversity in critical ecological and evolutionary processes.[2]

Letter of IntentDeadline Date:May 7, 2010 Full ProposalDeadline Date:June 8, 2010

George W. Gilchrist, Ph.D. Program Officer, Evolutionary Processes Cluster Division of Environment Biology National Science Foundation 4201 Wilson Blvd, Suite 635s Arlington, VA 22230 Phone: 703.292.7138 Fax: 703.292.9064 Email: ggilchrist@nsf.gov

George Gilchrist <ggilchri@nsf.gov>

Parental genotype reconstruction

Hi, Has anyone written a script to choose the most likely genotypes of the two parents of a full-sibship from the genotypes of those siblings? Here I want to prespecify the sibships and just reconstruct the most likely parental genotypes at each locus. Thanks, Mike

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

blouinm@science.oregonstate.edu

Phyloseminar JensLagergren Mon29

On March 29th, phyloseminar.org will present Jens Lagergren speaking on “Probabilistic analysis of gene families with respect with gene duplication, gene loss, and lateral gene transfer.” Abstract below.

NOTE: the seminar will begin at 10h PST, which is three hours earlier than the previous seminars.

This is 13h Eastern Standard Time, 19h Central European Time, and 6h in Christchurch and Auckland!

Here’s the abstract:

Incongruences between gene trees and corresponding species trees are common. Gene duplication, gene loss, and lateral gene transfer are three types of evolutionary events that can cause such incongruences. I will first describe a probabilistic process that contains standard models of nucleotide substitutions (i.e., such that underly probabilistic methods for phylogenetic tree reconstruction) as well as gene duplication and gene loss. This process takes place in a given species tree and can be used to reconstruct a gene tree for a gene family of interest and simultaneously reconcile the gene tree with the species tree. I will describe the algorithms available for this model and also describe how they perform on biological data compared to competing methods. Finally, I will describe an extension of this model that also contains lateral gene transfer and show how it performs on synthetic data.

Hope to see you there!

Erick

ematsen@gmail.com

POP7 and Genotyper

Dear Evoldir members,

Nowadays, we are analyzed our microsatellite fragments with POP4 and genotyping using GENOTYPER software. However, coming soon we are going to begin to analyzed our microsatellite fragments with POP7. Are there any problem to analyze fragments runs in POP7 with GENOTYPER?

Thank in advance, Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología Facultad de Ciencias del Mar Campus de Tafira Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain Phone: (+34) 928 45 45 43 Fax: (+34) 928 45 29 22

canariensis750@hotmail.com

PratherLectures EOWilson Apr5-8

Professor Edward O. Wilson will be delivering this year’s John M. Prather Lectures in Biology at Harvard University on April 5, 6 & 7. This series of distinguished public lectures is a capstone event to mark his 55 year career in biology at Harvard.

The first of the three talks, “Biodiversity and the Future of Biology”, will be held at 6:00pm on Monday, April 5th, at Sanders Theatre, followed by a reception and book signing at the Harvard Museum of Natural History. Because of the expected turnout, all attendees are required to have advance tickets for the April 5th lecture. The second and third lectures will be held at 4:00pm on April 6 & 7 in Science Center B, and will not be ticketed. His lecture on April 6th is entitled “The Superorganism,” and on April 7th, “Consilience.”

If you are interested in obtaining tickets to the public lecture on April 5th, or have any further questions about attending the Prather series, please contact Jeannette Everritt at 617-495-5891 or jeverritt@oeb.harvard.edu.

Naomi Pierce <naomi.pierce@googlemail.com>

Protect Lake Baikal petition

Dear colleagues,

It has not been widely publicized in the news, but there has been a very unfortunate turn of events for Lake Baikal, the largest and the most ancient lake on the planet and one of the UNESCO World Nature Heritage Sites. On January 13, the Russian government made several changes in the list of activities prohibited in the area of Lake Baikal that allowed the reopening of the Baikalsk pulp and paper mill, the main air and water polluter in the region. This decision is very unpopular in Russia, but the opposition is being suppressed (e.g., http://www.www.greengrants.org/-breakingnews.php?news_id=271). Furthermore, the government is propagating the myth that there is no scientific evidence for the negative effect of the mill on Lake Baikal. I am trying to gather support from the scientific community in order to convince Russian President Dmitry Medvedev to revert the changes in the regulation. I posted an open letter at http:/-/www.ipetitions.com/petition/baikal/ and ask you to sign it.

Thank you very much in advance, Dennis Lavrov

Dennis V. Lavrov, Assistant Professor Department of Ecology, Evolution, and Organismal Biology, Iowa State University, 343A Bessey Hall, Ames, IA 50011 phone: (515) 294-9091; fax: (515) 294-1337 http://www.eeob.iastate.edu/faculty/LavrovD/ Dennis Lavrov <dlavrov@iastate.edu>

Q Value software help

In the past, I've used the q value software package to control the false discovery rate when making large number of pairwise comparisons of gene frequencies or Fst values (I'm one of those who feel that the typical Bonferroni "correction" is too conservative for preliminary surveys). However, I can't get the latest versions of the software to run on any of my computers, MAC OS 10.4.x, 10.5.x, or Windows XP Professional. In every case, the program loads the P values from a text file, but then "hangs" at the "Execute" stage. In each case, I believe that I have the correct version of R (the statistical package that supports the Q value calculations) installed and running, with the appropriate interface also. However, I'm no "R" expert by any means, and I could be making some obvious mistake that I'm (not so blissfully) unaware of...

I would appreciate knowing if there is anyone out there successfully running "Q value" on machines like mine, and if so, can I get some advice? I have been unable to contact any Q value support groups. Does the LINUX version work better?

Thanks to all.

Bruce J. Turner Dept. Biol. Sci. VIRGINIA TECH Blacksburg, VA 24061 USA

"Bruce J. Turner, Dept. Biol. Sci., VPISU, Blacksburg, VA 240" <fishgen@vt.edu>

Royal Society LifeCycles

Royal Society Publishing has just published 'From polyphenism to complex metazoan life cycles' compiled and edited by Giuseppe Fusco and Alessandro Minelli. See - http://rstb.royalsocietypublishing.org/-site/2010/metazoa.xhtml for further details or you can go straight to the issue contents which are freely available online until the end of February 2010 at http://rstb.royalsocietypublishing.org/-content/365/1540.toc The print issue is available at the special price of Â£47.50. You can order this online via the above web page (enter special code TB1540 when prompted) or, alternatively, you can contact debbie.vaughan@royalsociety.org

All Royal Society content (65,000+ articles dating back to 1665) is FREE to access until 28 February 2010 in celebration of the Royal Society's 350th anniversary (http://royalsocietypublishing.org/seefurther)

Felicity Davie Tou-can Marketing The Holly 42 Heath Hill Road South Crowthorne Berkshire RG45 7BW

Tel. +44 (0)1344 466600 Fax. +44 (0)1344 466601 E-mail: felicity@tou-can.co.uk www.tou-can.co.uk felicity@tou-can.co.uk felicity@tou-can.co.uk

Sampling tall trees

Dear evoldir memebers,

We are working with a palm species (Phoenix canariensis), and we are interested in take samples of leaves, as weel as, fruits. Nowadays, we are using a pruning pole (4m) with a scissors in one end. However, it is not enough to take samples from fruits. Have anybody develop or known a alternative method to take samples from the tall trees?

Thank in advance,

Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología Facultad de Ciencias del Mar Campus de Tafira Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain Phone: (+34) 928 45 45 43 Fax: (+34) 928 45 29 22 email: mgonzalez@proyinves.ulpgc.es

canariensis750@hotmail.com

Sanetra Kaufman contact

Dear Colleagues,

I would terribly much like to get hold of my former postdoc peers, Drs. Matthias Sanetra from Germany and French Dr. Bernard Kaufmann, to ask questions on unpublished datasets, that I would much like to cite.

Extensive googling has not allowed me to find a working email address. Both are experts in social evolution and population genetics of ants, and did postdocs in the late Professor Ross Crozier's Lab in Australia.

If you know of a working contact email for either one, or both, please reply directly to me.

Many thanks in advance for any and all assistance,

Best regards,

Else Fjerdingstad

– Else J. Fjerdingstad, Ph.D. Assistant Professor of Biology

Queens College, CUNY 65-30 Kissena Blvd Flushing, NY 11367 USA Email: Else.Fjerdingstad@qc.cuny.edu http://qcpages.qc.edu/Biology/Fjerdingstad/-Fjerdingstad.html efjerdingstad@gmail.com

SMBE Call for Undergrad Mentors

CALL FOR MENTORS SMBE UNDERGRADUATE MENTORING AND DIVERSITY PROGRAM 2010 ANNUAL MEETING OF THE SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION

July 4-8, Lyon, France

CONFERENCE WEBSITE http://smbe2010.univ-lyon1.fr/ PROGRAM OUTLINE

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

To achieve these goals, each recipient of an SMBE Undergraduate Mentoring and Diversity Program Award will be paired with two mentors, one a senior graduate student; the other a postdoctoral fellow or faculty member.

Mentor activities will include:

1. Attending some conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the "goings-on" at a multi-day scientific conference in order to minimize the anxiety often felt by first-time conference attendees..

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

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

4. Attending the poster session and SBME Undergraduate Mentoring and Diversity Program Award recep-

tion with the student.

WE ARE SEEKING INDIVIDUALS INTERESTED IN BEING A MENTOR

If you are interested in mentoring an undergraduate at this year's SMBE meeting in Lyon, please email Dan Graur (dgraur[at]uh.edu).

SMBE <info@smbe.org>

SNP genotyping companies answers

Hello everybody, I posted a question a few weeks ago regarding a company /an institution that does SNP genotyping for reasonable prices and as some people asked me to post the answers, here they are. My original question is posted below. Thanks a lot to all who responded, your comments were very helpful! By the way: we have not decided yet which offer to take, so there is no final judgement from my side. But it seems that the actual price is going to be like 12,000 Euros at least - if you go for a company. Best, Katharina

— Hi all, Does anyone know (and recommend) a company (or any other institution) that genotypes homemade SNPs for a reasonable price? We have fish DNA of at least 2-400 individuals and would like to genotype around 100 SNPs (already developed) in them. The offers we got so far range around at least 20,000 Euros, which overspends our budget... Happy for any suggestion, Katharina

Answers:

Someone suggested to contact

Maribel Riveiro, riveirom@dnalandmarks.ca - www.dnalandmarks.ca

http://www.kbiosciences.co.uk – they were recommended from several people and seem to be not too expensive – and they have a cost calculator at their web site

Applied Biosystems Open array platform – seems like they design the primers for you and prep the plate and all you have to do is bring your samples and load the machine...

https://products.appliedbiosystems.com/ab/en/US/adirect/ab?cmd=catNavigate2&catID=605780&tab=DetailInfo

Two reasonably priced facilities inCanada:

1.Sick Kids Hospital inToronto http://www.tcag.ca/dnaSequencingSynthesis.html

2. McGill / GenomeQuebec Innovation Centre

http://www.genomequebecplatforms.com/mcgill/services/genotyping/index.aspx?l=e

'We have always found Sick Kids to be cheaper and more willing to work on smaller scale projects'

MassARRAY system by Sequenom, f.ex.implemented in

CIGENE,Norway, contact "Paul Ragnar Berg"<paul.berg@umb.no> or

http://www.ncl.ac.uk/ihg/research/facilities/flx/sequenom.htm http://www.src.sk.ca/html/research_technology/ag_bio/genserve_lab/about_us/index.cfm

New Mexico State University, Roche-454 FLX Genome Sequencer, contact Peter Houde

genomics@biology.nmsu.edu

http://biology-web.nmsu.edu/houde/conspirators.htm

maybe try new technologies likehttp://www.raindancetechnologies.com/ for cheaper genotyping

MTT Agrifood ResearchFinland, ask Johanna Vilkki

University of Wisconsin – see website, but they charge 48.5% overhead to external clients (http://www.biotech.wisc.edu/ServicesResearch/DNA/DNASeq/Genotyping.asp)

v.lucchini@ngbgenetics.com - offer the analysis of 96 SNPs in 480 samples for around 13.000 euro. The laboratory is certified ISO 17025.

–

Katharina Oetjen PhD student

Institute for Evolution and Biodiversity Westfälische Wilhelms-Universität Hüfferstr. 1 48149 Münster

Tel.: +49 (0) 251 83 21652 Fax: +49 (0) 251 83 24668 Email: oetjen@uni-muenster.de

http://www.uni-muenster.de/Evolution.PlantEvolEcol/People/Katharina/ oetjen@uni-muenster.de

Software Combining P-values

Dear Colleagues,

This short message to announce the release of the article and companion software : MultiTest V.1.2, a program to binomially combine independent tests and performance comparison with other related methods on proportional data Thierry De Meeûs, Jean-François Guégan and Anatoly T Teriokhin BMC Bioinformatics 2009, 10:443 (23 December 2009) http://www.biomedcentral.com/1471-2105/10/443 . This software implements a new procedure based on the binomial allowing getting a global P-value out of a series of independent tests, alternative to Fisher's Chi-square, Goudet's SGM and Stouffer's Z. It is freely accessible from a link in the article or at http://gemi.mpl.ird.fr/SiteSGASS/SiteTDM/ProgMeeusGB.html . It is with great sorrow that we also have to inform you of the death of our friend and co-author of this work Anatoly Teriokhin, Professor at Moscow Lomonosov University, who passed away at the beginning of year 2010. He successively got two red position fellowships at CNRS in our team several years ago, and we started then on different collaborative projects. Without him these works, and in particular the one announced here, would never had existed. It has been a great privilege to work with him.

Thierry De Meeûs and Jean-François Guégan

Thierry de Meeûs DR2 CNRS, Mis à disposition à l'IRD, UMR 177 IRD-CIRAD "Trypanosomoses"

Adresse Centre International de Recherche-Développement sur l'Elevage en zone Subhumide (CIRDES), N559, rue 5.31, 01 BP 454, Bobo-Dioulasso 01, Burkina-Faso.

Tel: (+226) 20 97 00 94 Fax: 20-97-23-20 Cell: (+226) 76 86 40 88

Cell France: (0)6 19 83 52 60 http://gemi.mpl.ird.fr/SiteSGASS/SiteTDM/TdeMeeus.html Ancienne adresse Génétique et Evolution des Maladies Infectieuses UMR CNRS/IRD 2724, UR IRD 165 Equipe: Structures Génétiques et Adaptation dans les Systèmes Symbiotiques (SGASS) Centre IRD de Montpellier 911 Avenue d'Agropolis, B.P. 64501 34394 Montpellier Cedex 5, France. Secrétariat: +33 (0)467 41 61 97 Fax: +33 (0)467 41 62 99

thierry.demeeus@mpl.ird.fr

Software GeoPhyloBuilder ArcGIS

GeoPhyloBuilder v1.1 for ArcGIS is now available. GeoPhyloBuilder is an add-on for ESRI's ArcGIS geographical infromation system that builds 3D spatial trees from a tree file and associated geographical data. v1.1 supports two new methods for node positioning based on minimum convex polygon centroids and the centroids of overlap and disjunction between sister nodes.

The installation file, VB.net source code and reference manual can be downloaded from http://sourceforge.net/projects/geophylobuilder/ . Project web pages https://www.nescent.org/wg_EvoViz/GeoPhyloBuilder#Software_Information David M. Kidd

Research Associate Center for Population Biology Silwood Park Campus Imperial College London 0207 594 2470

d.kidd@imperial.ac.uk

"Kidd, David M" <d.kidd@imperial.ac.uk>

Software Poptree2

Dear All:

We are pleased to announce the availability of the new Windows-interfaced computer program package POPTREE2 (http://www.med.kagawa-u.ac.jp/~genomelb/takezaki/poptree2/index.html). POPTREE2 computes various genetic distance measures and constructs phylogenetic trees of populations or closely related species from allele frequency data by using the neighbor-joining method and UPGMA. Bootstrap tests can be performed for phylogenetic trees. POPTREE2 also computes heterozygosities and Gst, measures of the extent of genetic variation in a population and genetic differentiation among subdivided population. All the computation can be done through a simple Windows-interface and phylogenetic trees can be displayed and changed in a publishable form in the same Windows-interface.

The distance measures that can be computed are (i) Da distance (Nei et al. 1983), (ii) Nei's standard genetic distance (Dst) (Nei 1972), (iii) Fst* distance (Latter 1972), (iv) delta mu square distance (Goldstein et al. 1995), and (v) Dsw distance (Shriver et al. 1995). Delta mu square distance and Dsw distance can be used only for microsatellite DNA data, in which alleles are represented by the number of repeats, whereas Da, Dst, and Fst* can be used for any kind of allele frequency data. Dst and Fst*, heterozygosities, and Gst are computed by the original method without sample size bias correction as well as with bias correction. The details of the computational methods are available in the user guide of POPTREE2. The command-line versions of POPTREE for DOS and UNIX (POPTREE version 1) are also available.

The instructions for using POPTREE2 have been published in Molecular Biology and Evolution 27:747-752.

Best regards,

Naoko Takezaki

Life Science Research Center, Kagawa University, Kagawa 760-0793, Japan

Masatoshi Nei

Department of Biology and Institute of Molecular Evolutionary Genetics, Pennsylvania State University, University Park, PA 16802, USA

Koichiro Tamura

Department of Biological Sciences, Tokyo Metropolitan University, Tokyo 192-0397, Japan

takezaki@med.kagawa-u.ac.jp

Software QDD microsatellite analysis

We are happy to announce the official release of QDD: a user-friendly program to select microsatellite markers and design primers from large sequencing projects.

QDD is designed to treat all bioinformatics steps from raw sequences till obtaining PCR primers: Sorting sequences by tag, removing adapters/vectors, detection of microsatellites, detection of redundancy/possible mobile element association, selection of sequences with target microsatellites and sufficiently long nanosatellite-free flanking regions, and primer design.

The program can be run both under Linux and Windows in an a easy to use command line option, the windows version is supported by a Graphical User Interface.

executables and a manual are available at: http://www.univ-provence.fr/gsite/Local/egee/dir/meglecz/QDD.html more details can be found at: http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btp670?

Jean-François Martin Centre de Biologie et Gestion des Populations (CBGP) Montpellier SupAgro Campus International de Baillarguet CS 30 016 34 988 Montferrier sur Lez Cedex

tél: 00 33 (0)4 99 62 33 20 fax : 00 33 (0)4 99 62 33 45 mail: martinjf@supagro.inra.fr

Jean-François Martin <martinjf@supagro.inra.fr>

Software TreeBASE

We are pleased to release a new version of TreeBASE – a database of phylogenetic knowledge: http://www.treebase.org. TreeBASE is designed to serve as a digital archive of phylogenetic data reported in peer-reviewed scientific publications.

Improvements include:

- Richer annotation of metadata (journal DOIs, specimen georeferences, Genbank accession numbers, etc) - A mapping between taxon labels and taxonomic names in uBio and NCBI for improved normalization of names - The ability to visualize and edit trees using Phylowidget - The ability to search on tree topology - Data are delivered in several serializations, including NEXUS and NeXML - A special URL gives journal editors and reviewers anonymous advanced access to data - Programmatic access to the data using the PhyloWS API.

Objects in TreeBASE (e.g. studies, trees, matrices) can now be referenced with persistent and resolvable URIs that serve as both globally unique identification numbers and resource locators. These URLs can be included in the PDF of a journal article or on a researcher's website – so access to matrices and trees is only a click away. Queries expressed in PhyloWS syntax return results in RDF as RSS 1.0 feeds, which means that users can set their favorite RSS Reader to fetch all new TreeBASE studies that satisfy a particular query (e.g. return all studies published in "Systematic Biology," or return all trees that include "Homo sapiens," etc).

For the short term, we will be busy patching bugs and making fixes. In the longer term we plan to continue extending our API (e.g. providing URIs to clades, subtrees, etc) and adding classifications to allow searching on higher ranks.

Below is our press release.

The TreeBASE Team.

Database gives researchers access to the latest findings about the tree of life

Durham, NC - A vastly improved phylogenetics database gives scientists and educators access to state-of-the-art knowledge about the evolutionary relationships among living things.

TreeBASE a database designed to help scientists store, share, and study evolutionary trees was first developed in the mid-1990s as way to archive the vast amounts of phylogenetic information accumulating in the literature.

"Phylogenies were being published at an explosive rate," said Bill Piel of Yale University. "What we needed was a database where we could compile them so people could use them later."

The database allows researchers to archive and retrieve published phylogenetic trees and data from different studies. "People can store sequence alignments, morphological character sets, and the resulting phylogenetic trees - all in digital form. They can also be recovered and reanalyzed or combined with other data," Piel said.

Since the first prototype was developed, researchers have contributed more than 6,500 trees from over 2400 articles, describing the relationships among well over 60,000 taxa. A variety of journals now require their authors to deposit phylogenetic data in TreeBASE, and peer reviewers are given anonymous access to the data prior to publication.

Years of work have gone into improving and upgrading the original version. "At some point we knew we had to make it bigger and better," said Michael Donoghue of Yale University. Now, a team of biologists and computer scientists is releasing a new version that is completely rebuilt. With this upgrade, the database is poised to become an increasingly valuable community resource for a number of fields, including conservation biology, biogeography, and education, developers say.

"We have introduced a wide variety of features that simply didn't exist before," said Val Tannen at the University of Pennsylvania. "In terms of data deposition and how users interact with it, it has taken a huge leap forward," Donoghue added.

Much richer information can now be stored. "Trees can contain information such as the length of each branch, which is important for studying the timing of evolutionary events," Piel explained. The database also has an improved system for making sure that information such as taxonomic names and DNA sequence IDs match those found in other sources.

Researchers will be able to take advantage of a more user-friendly interface and more advanced search techniques. "There are things you can query now that you couldn't before," said Piel. "For example, you can search for trees that share a certain topology."

"The visualization tools have also received a major upgrade," he added. "For example, now users can dynamically manipulate and zoom in and out of large trees."

A number of advanced features have been introduced that will, says Piel, "allow bioinformaticians to do new and creative things with the data without being blocked by the user interface." These include support for new machine-readable phylogenetic data exchange and web service standards.

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SouthAfrica VolFieldAssist MuridEvolution

Volunteers needed as field assistants for the project:

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

>From May 2010 onwards

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to evolution, ecology and behavior before starting an MsC or PhD project.

Project: We study the evolutionary and ecological reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers are also expected to help with maintenance of the research station (water pump, solar power, etc.)

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1000 (around 100 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 120 Euro) per month applies. 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 300 - 400 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for volunteers to start in May 2010 and especially for the period June to December 2010. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@ieu.uzh.ch.

More information under < http://www.stripedmouse.com/ > www.stripedmouse.com

Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin Research Assistant, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

PD Dr. Carsten Schradin Research Associate, Institute of Evolutionary Biology and Environmental Studies Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486 Fax: +41 - (0)44 635 5490

(Tel. secretary: +41 - (0)44 635 5271)

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

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

visit < http://www.stripedmouse.com/ > http://www.stripedmouse.com

Carsten Schradin <carsten.schradin@ieu.uzh.ch>

SSB Graduate Student Research Awards

Society of Systematic Biology Graduate Student Research Award

The Society of Systematic Biologists (SSB) announces the 2010 annual Graduate Student Research Award competition. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: http://systbio.org/?q=node/6). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards will range between $1,200 - $2000 and approximately seven to nine awards will be made. The list of awardees below includes examples of successful proposals for you to download.

How to apply All application materials must be in electronic format. Applicants and their recommenders are required to use pdf format, rather than Word or some other application, to minimize difficulties in file transfer. Applicants should send all materials (except letters of reference) in a SINGLE pdf file. Letters of recommendation should be sent separately by the referees in pdf format or in the text of an e-mail; please include the FULL NAME OF APPLICANT in recommendation letters.

Applicants must submit

1. a curriculum vitae (one page) 2. brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3. budget and budget justification (1 page) 4. and arrange for two letters of recommendation; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. PLEASE INCLUDE APPLICANT'S CONTACT E-MAIL ADDRESS AT THE TOP OF THE APPLICATION ITSELF. Both Masters and Ph.D. students in their FIRST TWO YEARS are eligible. Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

Please email all application materials and queries to SSB Awards Committee ssb-apps@life.uiuc.edu . IN THE SUBJECT LINE OF THE E-MAIL, PLEASE INDICATE "Student Research" FOLLOWED BY FIRST INITIAL AND LAST NAME.

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2010.

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Society of Systematic Biology Award Available

Ernst Mayr Award (Graduate Student Award)

The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meetings of the Society of Systematic Biologists. The award consists of $1000 and a set of available back issues of Systematic Biology.

Who is Eligible. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to: http://systbio.org/?q=node/6). Previous Mayr award winners are not eligible.

Application Procedure. Applications should be sent to the current SSB Awards Committee Chair (Sydney Cameron), at ssb-apps@life.illinois.edu. E-mail submissions are required. IN THE SUBJECT LINE OF THE E-MAIL, please indicate the SSB award category as "Mayr Award" followed by first name initial and last name.

Applicants should: 1. Submit a 400-word abstract of their talk to the SSB Mayr Awards Commitee (ssb-apps@life.illinois.edu) by NO LATER THAN 19 APRIL, preferably before the deadline. All candidates will be notified of their participation status no later than 26 April. 2. Register for the meeting using the meeting registration process (http://www.evolutionsociety.org/SSE2010/). When you login to the Evolution 2010 Presentation Submission site and submit your title and keywords, you will be given an option to declare your candidacy for the SSB Ernst Mayr Award. Please note that deadline for submission of presentation titles for Evolution 2010 is 19 April.

Judging. Based on the submitted abstracts, the Mayr Awards Committee (appointed by the Awards Chair) will select a maximum of 15 applicants for

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SSE International Travel Awards

The Society for the Study of Evolution (SSE) announces International Travel Awards for 2010, to foster international relationships between evolution societies and SSE members with particular focus on students and young scientists. The committee sponsors annually a series of activities/awards to reach this goal: international travel awards for meeting attendance, international symposia awards, and other international events awards. For details and eligibility requirements, see the SSE awards webpage (http://www.evolutionsociety.org/awards.asp#sseic). Deadline for application is March 31, 2010.

Judy Stone <jstone@colby.edu>

SSE logo

Dear Society for the Study of Evolution Members,

The Society is going to update its logo. We'd like your thoughts, ideas and concepts before we start the design process.

When you think of evolution, what does it look like? Feel like?

What picture would you paint to tell someone about SSE?

Are there specific things you feel need to be incorporated in an SSE logo?

If you're artistic and/or simply have a great design idea, please send it in to WDahl@EvolutionSociety.org. If we select your concept, we'll give you next year's membership and a print subscription to Evolution.

Deadline is April 1, 2010.

Thank you for your time and consideration! We look forward to seeing what you have to say.

Sincerely,

Bill

William M Dahl Society for the Study of Evolution 4475 Castleman Avenue St. Louis, MO 63110

PO Box 299 St. Louis, MO 63166-0299

WDahl@EvolutionSociety.org Ph: 314-577-9566, FAX: 314-577-9515 http://www.evolutionsociety.org/ The Society for the Study of Evolution was founded in March, 1946. The objectives of the Society for the Study of Evolution are the promotion of the study of organic evolution and the integration of the various fields of science concerned with evolution. The Society publishes the scientific journal Evolution and holds annual meetings in which scientific findings on evolutionary biology are presented and discussed.

Bill Dahl <wdahl@botany.org>

Teaching evidences of evolution

Dear friends,

I am teaching Evolution for Biology students and I need material (books, PDF articles, pictures, etc.) to teach about EVIDENCES of evolution.

My idea is to show very easy and strong evidences like the fossil record with simple forms appearing first in the strata (whales are not present firstly but invertebrates) and molecules becoming more complex from invertebrates to vertebrates.

Thanks for any suggestions and material and I feel that we need to produce more educational material about this subject like movies and slide sets!!!

Prof. Dr. J. C. VOLTOLINI Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br Website do grupo de pesquisa ECOMAM: http://jcvoltol.sites.uol.com.br/ Fotos de Projetos e Cursos: http://jcvoltol.fotoblog.uol.com.br/ Amostra de um Curso de Campo de Ecologia: http://trabiju.blogspot.com/ Currículo Lattes: http://lattes.cnpq.br/8137155809735635 Fotos Artísticas: http://voltolini.fotos.net.br/texturas 'Siamo tutti angeli con un'ala e possiamo volare soltanto se ciabbracciamo'

jcvoltol@uol.com.br

Treeview for WindowsVista and above

I've had various reports that my (now ancient) phylogeny-viewing program TreeView won't install on Microsoft Windows Vista and/or Windows 7. I suspect this is due to the installer I used to bundle the program, not TreeView itself. I've created a new installer, available from http://taxonomy.zoology.gla.ac.uk/rod/treeview.html (see the link labelled "Version for Windows Vista and later") that should install TreeView on Vista (and Windows 7, although I've not had a chance to test on a Windows 7 machine).

I hope those users that have had trouble with TreeView on recent versions of Windows will now be able to install the program.

Regards

Rod

Roderic Page Professor of Taxonomy DEEB, FBLS Graham Kerr Building University of Glasgow Glasgow G12 8QQ, UK

Email: r.page@bio.gla.ac.uk Tel: +44 141 330 4778 Fax: +44 141 330 2792 AIM: rodpage1962@aim.com Facebook: http://www.facebook.com/profile.php?id=-1112517192 Twitter: http://twitter.com/rdmpage Blog: http://iphylo.blogspot.com Home page: http://taxonomy.zoology.gla.ac.uk/rod/rod.html r.page@bio.gla.ac.uk r.page@bio.gla.ac.uk

TV program Evolution Sex

I'm a producer for a science television company in the UK, and I'm on the lookout for a female, American evolutionary biologist to front a possible tv programme about the evolution of sex. If anyone is interested, or can recommend anyone, I would be very grateful of you could contact me off-list at e.newton@hotmail.co.uk

Many thanks, Liz

Liz Newton BSc (Hons) MSc Freelance Science Writer / Film-maker e.newton@hotmail.co.uk 07796 033 490

liznewtonmedia.googlepages.com

http://www.youtube.com/user/molehillmedia Liz Newton <e.newton@hotmail.co.uk>

UNotreDame UndergradResearch SpeciationBiology

GLOBES SUMMER 2010 UNDERGRADUATE RESEARCH PROGRAM UNIVERSITY OF NOTRE DAME

June 1 - August 6, 2010

The Program: The GLOBES (Global Linkages of Biology, the Environment, and Society) program at the University of Notre Dame is pleased to sponsor a Research Experience for Undergraduates (REU) program during the summer of 2010. Funded by an NSF-IGERT training grant, GLOBES undergraduate research fellowships provide an exciting opportunity to be involved in cutting-edge research with the intent of providing real world solutions to environmental and human health issues. Research projects mentored by GLOBES faculty and students include speciation biology, ecological genetics and the evolutionary consequences of climate change.

Program Activities: The program consists of 10 weeks of full-time research, developed and mentored by GLOBES fellows and faculty. Applicants are encouraged to contact faculty and fellows about potential projects before submitting applications (go to website http://globes.nd.edu). Other activities include a weekly seminar program and journal club, regular research lab meetings, workshops on career choices in the sciences, research ethics, problem solving, and scientific writing. Lastly, participants have the opportunity to give formal presentations at the end of the summer REU Symposium.

Support: The award consists of a $4200 stipend and includes housing on campus, meals, lab supplies and travel (up to $500).

Eligibility: Current sophomores and juniors, who are U.S. citizens or permanent residents, are eligible to apply; exceptionally well qualified freshmen may be considered. Women, minority students, students with disabilities, and students from small colleges are encouraged to apply.

Application Materials: Priority will be given to applications postmarked by February 12, 2010. Application forms can be found at globes.nd.edu and must include (1) a cover letter stating your career goals and research interests; (2) a completed application form; (3), an official transcript, and (4) two recommendation letters from science faculty. Incomplete applications will not be considered.

Selection: Preference will be given to sophomores and juniors whose primary interest is a research career, and who will likely pursue a Ph.D. Award notifications will occur in late March/early April.

Send Application Materials to: Virginia Anderson, GLOBES Administrative Coordinator University of Notre Dame Department of Biological Sciences Notre Dame, Indiana 46556-0369 Phone: (574) 631-3287 Email: g.anderso@nd.edu

If you need to express mail, only send via FedEx or UPS, not the US post office.

Ginna Anderson GLOBES Program University of Notre Dame Department of Biological Sciences Rm 180 Galvin PH: 574-631-3287 EMail: g.anderso@nd.edu Mail to: P.O. Box 369 Notre Dame, Indiana 46556 Web: http://globes.nd.edu Ginna Anderson <g.anderso@nd.edu>

Vol Field assist Great tits Switzerland

I am seeking an enthusiastic candidate with a European nationality interested in assisting a field experiment on Great tits in Bern, Switzerland. The work is to start immediately and last until the end of June 2010. In the experiment we will study the influence of avian predators, through maternal effects, on life-history traits of Great tits, and possible additional effects on the ectoparasites of the tits. The great tits are a good system to examine the effects of predators and ectoparasites on life-history of birds since they readily accept nest boxes making them easy to manipulate and follow from egg laying to offspring fledging. The successful candidate will be involved in all the aspects of the work, including ringing the birds, simulating predators, conducting behavioral observations and recordings, and more. Applicants with a BSc/Msc in Biology/Ecology and with bird handling experience would have an advantage. However, motivation will play a key role: the work is hard and demanding, may take place in changing weather and requires long hours at times. Motivated applicants could develop their own individual research on a topic related to the program and their own interests, and if particularly motivated could be involved in the publications. Accommodation and transportation within Europe will be provided. Some financial assistance will also be available to cover living expenses.

Candidates must hold a valid European driving license. For further details please contact Michael Coslovsky at m.coslovsky@students.unibe.ch or at + 41 31 631 3019.

m.coslovsky@students.unibe.ch

PostDocs

AMNH NewYork 2 HostPathogens

Postdoctoral Positions at the American Museum of Natural History (AMNH)

Two positions available June 1, 2010 to work on a grant-funded project studying the biological, systematic, and computational challenges presented by phylogenetic reconstruction of host-pathogen systems. The project will involve the development of analytical approaches and their implementation in

POY [using C and OCAML] http://research.amnh.org/scicomp/research/projects/invertebrate-zoology/poy?q=projects/poy.php and Supramap http://supramap.osu.edu/sm/supramap/home Applicants should have experience in systematics, biogeography, host-pathogen systems, and/or computational biology. Ph.D. required in biology, computer science, or related fields.

Varón A., Vinh L., Wheeler W.C. (2010). POY version 4: phylogenetic analysis using dynamic homologies. Cladistics. 26: 72-85.

Janies, D., T. Treseder, B. Alexandrov, F. Habib, J. Chen, R. Ferreira, Ümit atalyürek, A. Varón, W.C. Wheeler. in press. The Supramap project: Linking pathogen genomes with geography to fight emergent infectious diseases. Cladistics.

Janies, D., A. Hill, R. Guralnick, F. Habib, E. Waltari, W.C. Wheeler (2007) Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1). Systematic Biology. 56:321-9.

Interested parties should contact:

Ward Wheeler

Division of Invertebrate Zoology

American Museum of Natural History

wheeler@amnh.org

crowley@amnh.org

Athens Extinctions

*PostDoc Position *

Project - *Predicting extinctions on islands: a multi-scale assessment*± (2010-2013. (FCT- PTDC/BIA-BEC/100182/2008)

Creative and motivated candidates are invited to apply for a three-year Postdoctoral Scientist position, at the Azorean Biodiversity Group, *University of Azores* for participation in a collaborative project between Paulo A. V. Borges, Kostas Triantis (University of Azores), Aris Parmakelis (University of Athens) and Robert Whittaker (Biodiversity Research Group, Oxford University Centre for the Environment).

This project will investigate the dynamics of species extinction in Azorean endemic arthropods. The project will be conducted in 13 fragments of primary forest in seven Azorean islands. The primary method of investigation will be analysis of genetic diversity of populations in large and small fragments, but the project will also include the modelling of abundance and distribution data of endemic species sampled sequentially from 1999/2000 and onwards, as well as the samplings to be obtained during the project.

Candidates should hold a Ph.D. in a pertinent field; entomological experience is desirable but not mandatory. The ideal candidate would have excellent skills in statistics, handling of large data sets, stochastic/mechanistic and/or prognostic modelling and an interest in combining molecular and ecological research to analyse past and future arthropod biodiversity trends. The project will require extensive field work in the summer and some travel to the University of Oxford and Athens.

Starting salary will be 1495æ/month (2245æ/month when working in Athens or Oxford).

Please send a CV, a brief statement of research interests, and the names and contact information for two references to Paulo Borges, pborges@uac.pt. Review of applicants will begin on March 1 and will continue until the post is filled. We would like the post-doc to start on or before May 1, 2010.

ARIS PARMAKELIS, MSc., PhD. DEPARTMENT OF ECOLOGY AND TAXONOMY FACULTY OF BIOLOGY NATIONAL & KAPODISTRIAN UNIVERSITY OF ATHENS PANEPISTHMIOUPOLI ZOGRAFOU, GR-15784, ATHENS, GREECE Tel.: ++302107274736 aparmakel@biol.uoa.gr

Aristeidis Parmakelis <aparmakel@biol.uoa.gr>

Barcelona HumanPopulationGenetics

Postdoctoral Fellowship at the Universitat Autònoma de Barcelona (Barcelona, Spain).

Molecular Anthropology, Human Population Genetics or Human Biology

Profile of the task: - The candidate must have a strong background in human population genetics, molecular biology and statistical analysis. - Bioinformatics skills are also considered as a merit. - Proactive person who feels comfortable working in a team.

Working conditions: - Postdoctoral Fellowship of one year, extendable to another year, under the supervision of Dr. Maria Pilar Aluja, in the Biological Anthropology Unit. - Full time. - Gross Salary (including taxes): 26,639.00 per year, in 14 monthly payments. - Starting date: Immediately

Requests: Those interested should - Have obtained his PhD after 1 July 1998 in a university different from Universitat Autònoma de Barcelona. - In the case of having a PhD from the Universitat Autònoma de Barcelona, the candidate must show that he/she has made a stay in another university or research center for at least 2 years. - Send by email a Curriculum Vitae and two references letters.

Documents can be sent via e_mail to: d.bave @ uab.es MariaPilar.Aluja @ uab.es

Deadline: until April 14, 2010

Prof. Maria Pilar Aluja, Ph.D. Directora Del Dpt. Biología Animal, Biología Vegetal y d'Ecología Fac. Biociències Universitat Autònoma de Barcelona 08193 Bellaterra SPAIN Phone: + 34 935811911 Fax: + 34 935811321 email: mariapilar.aluja@uab.cat www.uab.es Cristina Pereira Santos (PhD) Professor Lector Unitat Antropologia Biològica Dep. Biologia Animal, Biologia Vegetal i Ecologia Facultat Biociències Edifici C Universitat Autònoma de Barcelona 08193 Cerdanyola del Vallès, BARCELONA (SPAIN)

Tel.: 34 93 5811503 Fax: 34 93 5811321 cristina.santos@uab.es

Cristina Pereira Santos <cristina.santos@uab.cat>

Barcelona SkinMetagenomics

A two-year postdoc position is available at the Institute of Evolutionary Biology (IBE), UPF-CSIC, Barcelona (http://www.ibe.upf-csic.es/ ; www.prbb.org), under the supervision of Francesc Calafell. The successful candidate will join a project in skin metagenomics: we are analyzing by ultrasequencing the microbial communities in human skin by themselves and in relation to the onset of psoriasis. We are looking for a Ph.D. in bioinformatics, genetics, or evolutionary biology, with a strong background in sequence analysis: assembly, alignment, tree construction, evolutionary analysis of sequences. Programming in PERL and other languages is a requirement. We seek a positive, analytical, proactive persone who feels comfortable working in a team.

Please send by April 30th a CV, a letter of intent and two references to:

Francesc Calafell, Ph D IBE, Institute of Evolutionary Biology (UPF-CSIC) CEXS-UPF-PRBB C/ Dr. Aiguader 88 08003 Barcelona, Catalonia, Spain

Tel: +34 93 3160842 Fax: +34 93 3160901

Email: francesc.calafell@upf.edu

BigelowLabs Maine Phylogenomics

January 14, 2010

Position Description

Post-doctoral position in bioinformatics / phylogenomics Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, Maine

A full-time post-doctoral position is available in the lab of Dr. Hwan Su Yoon at Bigelow Laboratory for Ocean Sciences in West Boothbay Harbor, Maine. This position involves participation in an NSF-funded project, "RedToL: Phylogenetic and Genomic Approaches to Reconstructing the Red Algal (Rhodophyta) Tree of Life" to study phylogenetic relationships of red algae using multi-gene dataset, and plastid genomes and transcriptome sequence data. Therefore, a post-doc with a strong background in evolutionary genomics, molecular evolution, bioinformatics, or genome analysis is requested to start in March 2010. Primary duties include plastid DNA isolation, EST library construction, phylogenomics and bioinformatics analysis. Candidate with a Ph.D. degree in evolutionary genomics, computational biology or a relevant field is required. Experience with next generation sequence analysis (454, Illumina, or SOLiD) is desirable. Funding is available for three years.

Applicants should send their CV, a letter of intent describing candidate's motivation, qualifications, skills, and experience relevant to this position, and contact information for two references to jobs@bigelow.org. Please reference #PD10-1 in the subject line. For full consideration, the application should be received by January 31st, 2010. Bigelow Laboratory is an Equal Opportunity Employer.

Jane Gardner <jgardner@bigelow.org>

BrighamYoungU GWAS Alzheimers

A postdoctoral researcher is sought to participate in analyses of genome-wide association studies (GWAS) of Alzheimer's disease and related quantitative traits. This position (1-2 years, extension possible) will be available in the Kauwe Lab (http://kauwelab.byu.edu) in the Department of Biology at Brigham Young University (located in Provo, Utah). The starting date is Sept. 1, 2010.

Potential analyses would include but not be limited to association analyses of qualitative and quantitative traits, haplotyping and examining gene-gene and gene-environment interactions. There will be opportunities for collaborative research with statisticians and computational biologists here at BYU and with collaborators at several other institutions.

Candidates should have substantial statistical (or mathematical) expertise, strong programming skills in a computer language (eg. SAS, PERL and/or R), and hold a PhD in statistical genetics, computational biology, bioinformatics or other related areas. Previous experience in GWAS or microarray analysis, quantitative genetics, or computational biology is preferred. Salary and benefits will follow the NIH pay scale.

Applicants should email a curriculum vitae and statement of research interests by email to Dr. John Kauwe (Kauwe@byu.edu). Evaluation of applications will begin on May 3rd, 2010.

kcrandallbyu@gmail.com

Clermont-Ferrand France BacterialGenomeEvolution

We are looking for candidates interested in bacterial genome evolution, for a postdoctoral position at the Laboratory of Animal Epidemiology of the INRA (the French National Institute for Agricultural Research), which is located in the neighbourhood of Clermont-Ferrand, in the center of France.

The postdoc will have to develop and to use appropriate population genetic tools to study the genomic diversity of closely related bacterial species within the genus Borrelia. The dataset was obtained using a resequencing approach based on next-generation sequencing methods. The aim of the project is to get a better understanding in how horizontal transfers and selective pressures shaped the diversity of this model system, which is invovled in Lyme disease.

The main activity of the postdoc will be the development and the implementation of sequence analyses. She or he will interact with biologists, informaticians and statiscticians involved in the project. A strong experience in sequence analysis, simulation of sequence evolution and programming, testified by publications in peer-reviewed journals, is therefore expected. Previous experience with genome-scaled data will be appreciated.

The contract would preferentially start by the 2nd of Mai 2010. it would be established for 24 month and the net salary will be 1800 euros per month. It is founded by the European Regional Development Fund which supports the development of the Auvergne region.

Please contact Xavier Bailly (xavier.bailly@clermont.inra.fr) for questions and applications. Apllications may include a detailed CV, pdfs of publications, a summary of on-going projects and letters of support sent separately.

Xavier Bailly Unité d'Epidemiologie Animale INRA de Clermont-Ferrand-Theix 63122 Saint Genes Champanelle France

tel: 33 (0)4 73 62 46 95 fax: 33 (0)4 73 62 41 48

http://www.clermont.inra.fr/epidemiologie_animale xbailly@clermont.inra.fr xbailly@clermont.inra.fr

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DurhamU DeepSeaPopulationGenetics

Molecular Ecology Job in Durham:

School of Biological & Biomedical Sciences, Durham University, UK

PDRA in Population Genetics in the Deep Sea at the Mid-Atlantic Ridge (Fixed Term)

£29,853 per annum

A 17-month post-doctoral position is available in the Molecular Ecology Group at the University of Durham, Durham, UK. Funding is from NERC and in affiliation with the ECOMAR consortium and MARECO (part of the census of marine life). The project will involve population genetic comparisons of amphipod species collected either side of the mid-Atlantic ridge and either side of the sub-polar front at a depth of 1500-2500m. There will also be some work on deep-sea shark species from putative populations in the North Atlantic. The broader objective is to better understand the processes involved in the structuring of populations in the deep-sea environment, especially in the context of life history characteristics. This follows on from earlier work on the same project investigating the population genetics of four deep-sea fish species with distinct life history characteristics, and the phylogenetic radiation of invertebrate species at the mid-Atlantic ridge, including amphipod species. The labwork will be facilitated by a full-time technician. The firm start date is 1 August, 2010. The successful applicant will have a PhD and extensive experience with population genetic lab and computer analyses. Application materials should include a c.v. and cover letter submitted through the web site given below, and two letters of reference sent to a.r.hoelzel@dur.ac.uk by the referees.

Closing Date: 19 April 2010 Vacancy Reference: 3713

Further details of the post and an application form are available on our website (https://jobs.dur.ac.uk) or Tel: 0191 334 6499; fax: 0191 334 6504.

a.r.hoelzel@durham.ac.uk

FieldMuseumNatHist BiodiversityInformatics

Postdoctoral Position in Biodiversity Informatics

A postdoctoral research position in biodiversity informatics is available at the Field Museum of Natural History's Biodiversity Synthesis Center (synthesis.eol.org), part of the Encyclopedia of Life Project (eol.org). The mission of BioSynC is to advance biodiversity science associated with the EOL along three lines: (1) accelerating the pace of scientific discovery and advances in large-scale synthesis in biodiversity and evolution with the use of bioinformatics tools; (2) providing a central location for scientific working groups to convene and explore synthetic biodiversity analyses; and (3) supporting the growth of EOL content and cross-disciplinary use of biodiversity information for scientific purposes.

Responsibilities: The successful candidate will be expected to carry out original research in biodiversity and evolution in one or more areas that blend biology with information technology (e.g., taxonomy and informatics of diverse organisms, phylogenetics of large species groups, computational biology, visualization of complex biological data, or web mobilization of images or collections data in biodiversity). In addition, our postdocs are expected to contribute to the incorporation of biodiversity information into the EOL, e.g., by convening and coordinating synthesis groups to develop informatics tools and protocols, collaborative grant writing, hosting training workshops, and collaborating with our partner EOL institutions in such areas as Education and Informatics.

Qualifications: PhD in a relevant scientific field such as biology or evolution; expertise in computer programming or bioinformatics; interest in group leadership and synthesis of ideas from multiple disciplines; excellent organizational skills and attention to detail.

Workplace: BioSynC is a newly renovated space in the Field Museum of Natural History, Chicago, IL. FMNH has an active and dynamic biodiversity research community, with extensive links to local universities, and the successful candidate will have to the opportunity to interact with a broad range of evolutionary biologists in a cosmopolitan setting.

The position is a full time appointment, two years in duration, with possibility for renewal. Salary is in the same range as NSF postdoctoral fellowships. Applications are currently being accepted, with a target date of April 15, 2010.

Please send application materials (CV, cover letter, and contact information of three references) or inquiries by email to biosync@fieldmuseum.org. A quality cover letter will be specific about the independent research the applicant plans to accomplish, the broader outreach goals of their plan, and how their work will integrate with the Encyclopedia of Life project.

karen.cranston@gmail.com

HarvardU PlantEvolution

Harvard University Department of Organismic and Evolutionary Biology Plant Evolutionary Biology Postdoctoral Fellow or Research Assistant with Professor Charles Davis

Duties & Responsibilities

* *The postdoctoral fellow or research assistant will work under the supervision of the faculty member and will conduct experiments involving the evolution of vascular plants, with a focus on the molecular genetics and phylogeography of arctic and alpine plants. Research will be directed primarily at examining the effects of Quaternary climate cycles of plants distributed in Arctic-Alpine systems. Uncovering which historic events had the largest genetic consequences for arctic and alpine floras during the Quaternary will greatly aid in our understanding of the role that climate change has played in species evolution. Additional responsibilities will include helping to understand plant phylogeny, biogeography, and mechanisms of horizontal gene transfer in plants.

Lab management will include the purchase of lab supplies and equipment, maintenance of commonly used lab stocks, upkeep of tissue samples, and general paperwork related to university protocols (e.g., inventory of chemicals). The individual is expected to maintain accurate and timely lab books, attend lab meetings, and perform other related duties as required. For more information on the Davis laboratory contact Charles Davis at cdavis@oeb.harvard.edu, and please visit our website at http://www.people.fas.harvard.edu/-˜ccdavis/ .

Required Education, Experience, Skills

* *Applicants must possess at least a college degree with a preferred major in biology. They should have the ability to conduct DNA/RNA extractions, PCR, gel electrophoresis, cloning of PCR products, and sequencing. Analytical skills should include PCR primer design, DNA sequence alignment, and phylogenetic methods. Experience with bioinformatics are preferred. Excellent communication (oral and written) skills, enthusiasm and ability to work in team environment with demonstrated skills and experience in molecular techniques are required.

Harvard University is an equal opportunity/affirmative action employer.

Applications will be accepted until March 21, 2010.

Christopher Preheim <cpreheim@oeb.harvard.edu>

ImperialCollege EvolutionaryDynamics

Division of Biology Faculty of Natural Sciences

Research Associate in Population Biology

Salary: Â£26,720- Â£33,080 per annum

A Research Associate position is available for five years from 1 June 2010 to research links between ecological and evolutionary dynamics. Details of the job description can be downloaded from www.bio-demography.org . The post is funded as part of an ERC Advanced Investigator grant of 2.1M over five years to Prof Tim Coulson. The post will be based in the Division of Biology at Silwood Park Campus, Division of Biology, Imperial College London.

The successful candidate will work on developing and applying methods to link population dynamics with the dynamics of phenotypic traits, genotypes and alleles. The position is the theoretical part of a larger project titled Linking Ecological and Evolutionary Dynamics in Theory, in the Laboratory and in the Field. As well as working with Tim Coulson, the position will involve close collaboration with Dr Isabel Smallegange who will be conducting laboratory work on experimental evolution in bulb mites and Dr Aurelio Malo who will be collecting extensive observational data on wood mice using recently developed wireless sensor technology for tracking wildlife. The bulb mite and wood mouse systems have been running for eighteen months. This is an excellent opportunity to be involved in the development of a major research project.

The successful candidate will have a PhD (or equivalent) in Population Biology, Evolutionary Ecology, Mathematical Biosciences, or a related field. You will also have a background in developing or applying theory and in writing and publishing papers in leading journals in the field. Experience of working as part of a multi-disciplinary team is desirable. There will be opportunities to participate in fieldwork on the wood mice and/or lab work on the bulb mites if desired.

You will be part of a thriving research group (www.bio-demography.org) in the Ecology and Evolution Section (http://www3.imperial.ac.uk/biology/-research/ecologyandevolution) of the Division of Biology (http://www3.imperial.ac.uk/biology) and will be based at Silwood Park (http://www3.imperial.ac.uk/-silwoodparkcampus)

Informal inquiries (with CV) to Prof Tim Coulson: t.coulson@Imperial.ac.uk

This position has a start date of 1 June 2010.

Our preferred method of application is online via our website http://www3.imperial.ac.uk/employment (please select Job Searchâthen enter the job title or NS2010049JT into Keywords. Please complete and upload an application form as directed.

Alternatively, if you are unable to apply online, please contact Mrs Diana Anderson on 020 7594 2207 or emaild.anderson@imperial.ac.uk to request an application form.

Closing date: 23 March 2010

Interviews will take place in late March/early April

Committed to equality and valuing diversity. We are also an Athena Silver SWAN Award winner and a Stonewall Diversity Champion

Tim Coulson Professor of Population Biology Imperial College London Silwood Park Ascot Berkshire, SL5 7PY

Work website www.bio-demography.org www3.imperial.ac.uk/people/t.coulson

"Coulson, Tim N" <t.coulson@imperial.ac.uk>

JagiellonianU EcologyEvolutionaryBiology

Institute of Environmental Sciences at the Jagiellonian University, Kraków, Poland (www.eko.uj.edu.pl)

20-month fellowship programme for strongly motivated scientists with a PhD degree in Biology, Ecology or related field, with net-fellowship 3200 PLN per month plus social benefits, realized in one of the research groups at the Institute of Environmental Sciences and a monthly internship at the universities in Europe and the U.S.

Candidates are required to contact IES Staff to discuss potential research project prior to the application.

Application deadline: 30 April 2010

Detailed information are available at:

www.eko.uj.edu.pl/ecology < http://-www.eko.uj.edu.pl/ecology >

Project co-financed by the European Union under the European Social Fund

"ecology@uj.edu.pl" <ecology@uj.edu.pl>

London ConservationGenetics

Conservation Genetics PDRA

This is a postdoctoral position for a scientist who wants to contribute to a the task of putting Conservation Genetics to practical use- i.e. to make the expertise of Conservation Geneticists available to conservation managers and policy makers. They will work as part of a European Union funded consortium, CONGRESS (Conservation of Genetic Resources for Effective Species Survival).

The PDRA's role will be to seek out and evaluate the relevant information needed by conservation managers if they are to make effective use of the advances in genetic technology, population and conservation genetics. The PDRA will identify examples of best practice, guidance and new innovations, in particular tools that European policy makers can use to incorporate genetic biodiversity into their policy framework.

The PDRA will work to School of Biological and Chemical Sciences to populate a database with information and examples that meet the standards and objectives developed by the consortium. Candidates for this position should have a PhD in a relevant field or equivalent professional experience demonstrating excellent skills that will allow them to evaluate conservation genetics research, the quality of data, methods (including those exploiting new sequencing technologies) and analytical approaches.

This is a full-time post for 18 months or a part-time post for 36 months. Salary is in the range of £33,659 per annum (full-time). The salary is inclusive of London Allowance. Benefits include 30 days annual leave and a final salary pension scheme.

For further details please contact r.a.nichols@qmul.ac.uk

Richard Nichols Professor of Evolutionary Genetics Web http://webspace.qmul.ac.uk/ranichols/-research.htm

Madrid PlantVirusCoevolution

*_POSTDOCTORAL POSITION AVAILABLE_*

Research topic: *Mechanisms of tolerance of plants to virus infection*. Recent work in the group has been directed at developing /Arabidopsis thaliana/ as a system for the study of plant-virus co-evolution. Results have shown the relevance of tolerance as a defence response to viruses and, hence, its potential role in plant-virus co-evolution. Analyses of natural variation (RILs) have allowed identification of QTLs determining tolerance to virus infection in Arabidopsis. *Research will focus on the analysis of candidate genes for tolerance to virus infection and on the molecular mechanisms of tolerance*.

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Period: 3 or 4 years, starting any time from now

Conditions: Contract conditions will be equivalent to those of the Spanish “Juan de la Cierva” Programme either funded by this programme or directly through the research group.

Requisites: Experience in plant-pathogen co-evolution or/and molecular evolution.

INTERESTED CANDIDATES PLEASE CONTACT Prof. *FERNANDO GARCÍA-ARENAL *PREFERABLY BEFORE FEBRUARY 28^th 2010

fernando.garciaarenal@upm.es

Publications of the group related to the topic:

Pagán, I., Alonso-Blanco, C. & García-Arenal, F. 2007 The relationship of within-host multiplication and virulence in a plant-virus system. /PLoS ONE /2, 2786.

Pagán, I., Alonso-Blanco, C. & García-Arenal, F. 2008 Host responses in life-history traits and tolerance to virus infection in /Arabidopsis thaliana./ /PLoS Pathog/. 4, e1000124.

Pagán, I., Alonso-Blanco, C. & García-Arenal, F. 2009 Differential tolerance to direct and indirect density-dependent costs of viral infection in /Arabidopsis thaliana/. /PLoS Pathog./ 5, e1000531.

*Fernando García-Arenal * *Professor* *Director, Centro de Biotecnología y Genómica de Plantas UPM - INIA* Campus de Montegancedo Autopista M40, Km38 28223 Pozuelo de Alarcón Madrid

T: + 34 91 336 4550/4539 F: + 34 91 715 77 21 E –mail: fernando.garciaarenal@upm.es

fernando garcia arenal

fernando.garciaarenal@upm.es

MaxPlanck Ploen YeastNaturalHistory

Postdoctoral position: ecology and natural history of wild Saccharomyces paradoxus yeast

Max Planck Institute for Evolutionary Biology, Ploen, Germany

Experimental Evolution group, led by Duncan Greig

We are looking for an ecologist or evolutionary biologist interested in studying the ecology of yeast in the wild. Saccharomyces cerevisiae is a research âsuper-modelâ, particularly for genetics, but increasingly for evolutionary biology. However, very little is known about its life in its natural habitat. Saccharomyces paradoxus, an undomesticated relative of S. cerevisiae, is readily isolated from the bark and leaves of oak trees. The aim of this project is to study the growth, life cycle, and dispersal of Saccharomyces paradoxus in oak and in surrounding soil, water, and insects. We are interested in the microbial community in which S. paradoxus lives and in reconstructing its natural environment in the laboratory for future experiments. Although practical experience with yeast or other microbes would be useful, it is not essential, and we would consider applications from well-qualified theoretical ecologists or evolutionists interested in moving into the lab. In addition to studying the natural history and ecology of wild Saccharomyces, the group also uses yeast in laboratory experiments on social interactions, sexual selection, and speciation.

The Max Planck Institute for Evolutionary Biology is a well-funded, expanding, and vibrant research institution, with superb facilities. It is located in Ploen, an attractive small town surrounded by lakes, a few kilometres from the Baltic coast. Neighbouring larger towns are Kiel and Lubeck, and the international airport at Hamburg is 80km away. Further information on the institute can be found at:

http://www.evolbio.mpg.de/english/index.html The position is potentially suitable for any level of postdoc and will initially be funded for two years, with an extension for an additional year if appropriate. There is no deadline for application â applications will be considered until the position is filled. Funding is available immediately, and comes in two forms depending on nationality. Foreigners can receive between 2100 and 3000 Euro per month, depending on experience, which is free from income taxes and social insurance contributions. Germans receive a similar grant, calculated according to several factors such as age, marital and family status.

Contact d.greig@evolbio.mpg.de for more information or to apply. Applications should comprise a letter describing the candidateâs research interests and relevant experience, a CV, a list of publications, and contact information for three referees.

Duncan Greig Max Planck Research Group Leader Max Planck Institute for Evolutionary Biology August Thienemann Str. 2 24306 Plön Germany

Telephone: +49 4522 763 234

Duncan Greig <d.greig@evolbio.mpg.de>

McMasterU StatisticalPopGenetics

McMaster University Analysis of Barcoding Data

Location: McMaster University Hamilton Canada

Project Title: Statistical Population Genetic Analysis of Barcoding data

Description: The projects involve developing new methods and/or using pre-existing bioinformatics tools for the analysis of gene sequence data. Candidates for the Postdoctoral Fellowship must have completed a Ph.D. in the field of statistical genetics, theoretical population genetics, molecular evolution or a related discipline. Experience in molecular evolution or population genetics, statistical analysis and/or bioinformatics/computer programming are required.

To apply: Send a complete CV, a description of your research achievements and interests, and the names of at least two referees via email to Golding@McMaster.CA. Include a subject header that clearly states “Application for Barcoding Postdoc”.

The postdoctoral fellowship would run for two years with the possibility of extensions.

Brian Golding Department of Biology McMaster University 1280 Main Street West Hamilton, Ontario, L8S 4K1

Tel: 905-525-9140 ext 24829 FAX: 905-522-6066

E-mail: Golding@McMaster.CA

Montpellier TheoreticalGenetics

We are looking for candidates for a postdoctoral position in theoretical ecology and genetics, based at the Institut des Sciences de l'Evolution, Montpellier France.

The postdoctoral fellow will contribute to a theoretical project aiming at understanding the role of migration and adaptation in the demographic responses of species to global change, including for instance the effect of climate warming and fragmentation. Our aim is to formulate model predictions in ways amenable to empirical testing, in particular in microcosm experiments using bacteria and paramecia. The main activity of the postdoctoral fellow will be theory development but she/or he will interact with empiricists and could participate to the design of experiments. The postdoctoral fellow will be included in a larger national network collaborating on a project concerned about the evolutionary responses to global change, including research teams in Montpellier, Paris and Grenoble (France), funded by the French research funding agency ANR (Project EVORANGE DECISION N2009 PEXT 01101).

Conditions for eligibility: - The candidate should have defended her or his PhD for less than two years and have no previous research experience in our lab - Strong experience in modelling, mathematics and simulations is absolutely required, as well as training in evolutionary biology and ecology, testified by publications in peer-reviewed journals. - Familiarity with quantitative genetics will be appreciated

Working conditions: - The contract could start anytime from now on but preferentially not after September 2010. - The net salary would be 2000 euros per month. - The contract will be established for one year, renewable once. - The work will be based at the Institut des Sciences de l'Evolution (CNRS-Université Montpellier2), Montpellier France. The main contact there will be Ophélie Ronce.

How to apply: Send BEFORE April 5th the following information through e-mail to ophelie.ronce@univ-montp2.fr: - one detailed CV - pdfs of publications - a summary of on-going projects - two letters of support sent separately

Please contact Ophélie Ronce (ophelie.ronce@univ-montp2.fr) for more details .

Ophelie Ronce Genetique et Environnement cc 65 Institut des Sciences de l'Evolution de Montpellier UMR 5554 Universite Montpellier II, Place Eugene Bataillon 34095 Montpellier cedex 5

tel: 33 (0)4 67 14 32 50 fax: 33 (0)4 67 14 36 22

NOTE THE NEW E-MAIL ADRESS: ophelie.ronce@univ-montp2.fr

http://www.isem.cnrs.fr/ Ophélie Ronce <ophelie.ronce@univ-montp2.fr>

OregonStateU PopulationDynamics

POSTDOCTORAL SCHOLAR: Landscape genetics of aquatic populations. The Department of Zoology, Oregon State University seeks candidates for a postdoctoral position, start date of 15 May 2010 (negotiable). As part of the Lytle lab (http://www.science.oregonstate.edu/lytlelab), the appointee will use molecular methods to understand how stream hydrology influences the population dynamics of multiple species of desert aquatic insects and amphibians. The molecular work will complement other projects in the research group pertaining to behavioral evolution, evolutionary theory, and conservation biology, and so an interest in cross-disciplinary collaboration is desirable. The appointee will also collaborate with co-PI Julian Olden at U. Washington and the Blouin genetics lab at OSU. Although based primarily in Oregon, the project will include some fieldwork in desert regions of Arizona. Candidates should have a Ph.D. or equivalent in evolutionary biology, ecology, genetics, or a related discipline, as well as experience with relevant statistical and computational methods. Candidates with experience in microsatellite development and analysis are especially encouraged to apply. Salary is $38,000 to $42,000 per year plus benefits (depending on experience), renewable annually at discretion of hiring supervisor for up to 3 years. For full consideration apply by 31 March 2010. Email a letter of application, CV, and contact information for three references to:

Dr. David A. Lytle, lytleda@oregonstate.edu (Dept. of Zoology, Oregon State University, Corvallis OR 97331). OSU is an AA/EOE.

lytleda@oregonstate.edu lytleda@oregonstate.edu

Oxford BacterialGenomeEvolution

We are recruiting a Postdoctoral Scientist to join the group of Dr. Daniel Wilson. The group is principally engaged in the activities of the UKCRC Consortium Modernising Medical Microbiology (www.modmedmicro.ac.uk), an ambitious project with the goal of revolutionising approaches to tracing and tracking clinically important micro-organisms in near-to- real time using whole genome sequencing technologies. The aim is to elucidate the evolution and epidemiology of four medically important pathogens, namely Mycobacterium tuberculosis, Staphylococcus aureus, Clostridium difficile and norovirus through the application and development of statistical analyses.

Postdoctoral Scientist Salary Scale for University Grade 7: £28,983 - £35,646 p.a. Candidates holding a PhD and experience in statistical inference, computationally intensive methods or population genetics and a programming language such as C++ are sought to be responsible for designing and implementing analyses of whole genome population data. You will need to work well independently and in a team, have good written and verbal skills and a publication record. Excellent applicants from non-genetics backgrounds are also welcomed. This post is funded by the UK CRC and is initially available for up to 2 years. Please quote reference HB-10-006-DW.

An application form and a job description are available from the Personnel Officer, Room 5800, Experimental Medicine Division, Nuffield Dept of Clinical Medicine, John Radcliffe Hospital, Oxford OX3 9DU, by phone (+44 1865 220528), email (personnel@ndm.ox.ac.uk) or online (www.expmedndm.ox.ac.uk). The closing date for applications is Friday, 2 April 2010.

Daniel Wilson <daniel.wilson@ndm.ox.ac.uk>

Paris SelectionInVertebrateGenomes

Two post-doctoral positions are available in the DYOGEN group at the Ecole Normale Supérieure (ENS) in Paris.

Position 1: Funded by a European project, the research topic involves the reconstruction of ancestral regulatory circuits in vertebrates, with a particular emphasis on the human X chromosome and genes involved in neurological disorders. The project will benefit from a wealth of data and methods already developped in the laboratory on ancestral genome reconstructions (e.g. Genomicus athttp://www.dyogen.ens.fr/genomicus). The ideal candidate will be familiar with large genomic datasets, the construction of phylogenetic relationships, and will be familiar with Linux/Unix and a programming language (ideally Python). The 2-year position is to be filled as soon as a suitable candidate has been found.

Position 2: The research subject will address the problem of identifying signatures of positive selection in vertebrate genomes using SNPs collected from genome sequencing projects. The project will benefit from methods already developped in the laboratory (Enard et al. Plos Genetics 6(2): e1000840). The exact questions to be investigated will depend on the candidate's interest and experience, but possible avenues include a focus on co-occurences of candidate genes involved in human diseases, with the possibility of resequencing DNA from affected individuals. The 2-year position is to be filled as soon as a suitable candidate has been found.

Both positions offer competitive salaries according to experience. The DYOGEN lab (http://-www.biologie.ens.fr/dyogen) benefits from substantial computing facilities and belongs to the Biology Institute of the Ecole Normale Supérieure (IBENS) in the centre of Paris near the jardin du Luxembourg. The Institute is composed of 35 research groups focusing on subjects related to functional and evolutionary genomics, neurobiology and development.

Interested candidates should send a CV, potential starting dates and the names of at least two references to:

dyogen-jobs@biologie.ens.fr

Hugues Roest Crollius Dyogen Group CNRS UMR8197 Institut de Biologie de l'Ecole Normale Supérieure (IBENS) 46 rue d'Ulm, 75230 Paris Cedex 05 tél: +33 (0)1 44 32 23 70

hrc@ens.fr hrc@ens.fr

PennStateU Adaptation

An NSF-funded postdoctoral position is available immediately in the laboratory of Tracy Langkilde (< http://homes.bio.psu.edu/people/faculty/langkilde/ >) at The Pennsylvania State University. The aim of this project is to understand the ecology and evolution of adaptive responses to rapid global change.

The main duties of the postdoc will be to conduct field and lab experiments and surveys aimed at unraveling the causes and consequences of changes in lizard anti-predator behavior following the invasion of red imported fire ants. The postdoc will be expected to play an important role in developing this research, in collaboration with the lab manager and graduate and undergraduate students involved in the project.

The successful candidate will have a PhD in behavioral ecology, ecology, evolutionary biology or a related field. Previous extensive field experience and publication of papers in leading journals in the field is a must. Candidates with prior experience in mark-recapture, population genetics, and research in reptilian systems are especially encouraged to apply.

The postdoc will be based at the University Park campus of Penn State. Field research trips totaling up to 3 months per year will be conducted in semi-remote locations throughout the Southeastern USA. A valid driver's license and willingness to drive long distances is required.

Target start date is April 1, 2010, with the first field trip taking place in early May 2010. The initial contract is for one year; with possible extensions up to three years pending satisfactory performance and available funding.

Interested applicants should send pdfs with CV, a short (less than one page) statement of research interests and experience, and contact information of three references to <mailto:tll30@psu.edu>, indicating “postdoctoral position”âin the subject line. The review of applications will begin immediately and continue until the position is filled.

Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

naf11@psu.edu naf11@psu.edu

RutgersU StatisticalPopGenetics

Postdoctoral Position in Statistical Population Genetics at Rutgers University

A postdoctoral position in population genetics is available in the lab of Jody Hey, at Rutgers University. The research will involve adapting coalescent models to problems in population divergence, as well as developing statistical methods for fitting divergence models to data sets. These methods will be used to study problems in the divergence of human populations, as well as in other systems.

Candidates with research experience in any the following will be considered:

- Population Genetics Theory - Coalescent modeling - The use of stochastic methods for likelihood and Bayesian computation (e.g. MCMC, Gibbs Sampling etc) - Statistical Phylogeography - Divergence Population Genetics

In addition candidates should have experience in programming using C/C++ or a similar low-level language.

The position can begin as early as Summer, 2010.

Applications should email a CV and any other relevant information to Jody Hey hey@biology.rutgers.edu

The Hey lab is on the Busch Campus of Rutgers University. This is in central New Jersey, just outside of the city of New Brunswick - a small cosmopolitan city within commuting distance (by car or train) of Manhattan.

Jody Hey Professor, Department of Genetics Rutgers University Nelson Biological Labs (rm B326) 604 Allison Rd. Piscataway, NJ 08854-8082

732-445-5272 http://genfaculty.rutgers.edu/hey/home hey@biology.rutgers.edu

“Hey, Jody” <Hey@Biology.Rutgers.Edu>

SanDiegoZoo ConservationGenetics

Job: Post-doctoral Fellow at San Diego Zoo

The San Diego Zoo invites applications for a 4-year post-doctoral research fellow to research, develop, model, and test various strategies for genetically managing herd or group-living species. The focus of the research will be to meet the management needs of the Al Ain Wildlife Park and Resort (AWRP) in Abu Dhabi, U.A.E. The AWRP currently maintains large breeding groups of antelope, including a number of species recognized by the IUCN as either Critically Endangered or Extinct in the Wild. Traditional, pedigree-based methods used to manage the genetics of many zoo populations have proven difficult to implement for herd species at the AWRP and elsewhere because pedigrees are unknown and specific breeding pairs can not be controlled. Furthermore, many of the antelope species maintained by the AWRP have projected or ongoing reintroduction programs utilizing AWPR stock. Thus, the AWRP is looking for innovative methods for managing the genetics of these populations that incorporate reintroduction efforts. Focal species for this research include Arabian oryx, scimitar horned oryx, and addax.

Qualified applicants will have a strong background in population genetics, math, modeling or animal breeding/herd management. Basic computer programming skills will be necessary for modeling and testing different management strategies; applicants without programming skills will be considered but must be willing to learn those skills during the first year of research. Some experience with field work, herd management and international travel are preferred.

EOE ALL EMPLOYMENT IS CONTINGENT UPON PASSING A DRUG SCREEN.

SOME EMPLOYMENT IS CONTIGENT UPON PASSING A PRE PLACEMENT PHYSICAL The post-doctoral fellow will be located primarily at the San Diego Zoo, but will be required to spend several weeks at the AWRP three or four times a year. The application deadline is April 30, 2010. For more information or to apply go to: http://www.sandiegozoo.org/jobs/ All applications must go to this web site. Do not mail Dr. Mandoza.

Rosemary Mendoza Human Resources Representative

San Diego Zoo P.O. Box 120551 San Diego, CA 92112-0551 Office: (619) 231- 1515 X4583 Fax: (619) 744-3326 rmendoza@sandiegozoo.org

Rosemary Mendoza <RMendoza@sandiegozoo.org>

UAntwerp BirdParasite

Call for applicants on bird-parasite research

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

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

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

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

If you are interested or need further information, contact Prof. Erik Matthysen at erik.matthysen@ua.ac.be

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

Groenenborgerlaan 171, 2020 Antwerpen +32 3 265 3464

erik.matthysen@ua.ac.be

UArizona EvolutionaryBiol

Postdoctoral Positions Available: Research Associate Arizona Research Laboratories, University of Arizona, Tucson, AZ NIH-Training Program: Postdoctoral Excellence in Research and Teaching (PERT)

The Postdoctoral Excellence in Research and Teaching (PERT) Program is a comprehensive program which offers up to three years of support to outstanding candidates seeking advanced postdoctoral research training, teacher training and student mentorship opportunities in preparation for an academic career in biomedical and life sciences. Funded by NIGMS through an IRACDA (Institutional Research and Career Development Award) training grant, the PERT program also fosters ties between research-intensive institutions and minority-serving institutions. PERT trainees may select from over thirty-six faculty research mentors at the University of Arizona, representing a broad range of disciplines in biomedicine, bioengineering, genetics, biochemistry, neurobiology, evolutionary biology, molecular/cellular biology, physiology and behavior. The program stresses the use of model organisms for biomedical and life sciences research. The program is administered through the Arizona Research Laboratories Center for Insect Science and is partnered with a Minority Serving Institution, Pima Community College, (http://www.pima.edu/program/biology/. Starting salary, based on the NIH NRSA scale, will be $37,368 for program participants with less than one year of postdoctoral experience. An annual allowance for research supplies and travel is also included. Positions are dependent upon continued funding. Additional information about the Center for Insect Science and the PERT program is available at http://cis.arl.arizona.edu/PERT .Qualifications: Applicants must have, as of the beginning date of the appointment, a Ph.D. in a related field from an accredited institution and must be U.S. citizens or permanent residents. Applicants should have no more than two previous years of postdoctoral experience at the time of application.

Application: All applicants must apply electronically through the University of Arizona's Career Track website at: https://www.uacareertrack.com, citing Job #44851. All applications are to include:

–a letter of interest with a statement explaining how the PERT program will assist the applicant in his/her research and career goals.

–a CV

–a three to six page research proposal developed with the intended PERT faculty research mentor describing the project to be undertaken during the training period

–three letters of reference

–a letter of support from the intended faculty research mentor

Potential applicants are encouraged to contact relevant Program Faculty as soon as possible to discuss research projects and the application process. Original letters of reference and the letter from the proposed faculty research mentor should be mailed to: PERT, Center for Insect Science, 1007 E. Lowell Street, University of Arizona, Tucson, AZ 85721-0106. Emailed letters will be accepted only if accompanied by an electronic signature. The letter of interest, CV and research proposal should be submitted online through the UA Career Track website listed above. Review of applications begins June 1, 2010. As an equal opportunity and affirmative action employer, the University of Arizona recognizes the power of a diverse community and encourages applications from individuals with varied experiences and backgrounds. Please contact Teresa Kudrna for more information, tkudrna@email.arizona.edu, 520-621-4923. –

Teresa Kudrna Program Coordinator, Sr. PERT Program Center for Insect Science 1007 E. Lowell Street, Room 227 Tucson, AZ 85721 Telephone: 520-621-4923 Fax: 520-621-2590 Email: tkudrna@email.arizona.edu

Teresa Kudrna <tkudrna@email.arizona.edu>

UCalgary Biodiversity

POSTDOCTORAL POSITION in Pollination and Biodiversity, combined appointment through Departments of Biological Sciences at University of Calgary and Simon Fraser University.

As part of the NSERC-funded Canadian Pollinators Initiative (CANPOLIN), researchers Jana Vamosi [http://homepages.ucalgary.ca/~jvamosi/] and Elizabeth Elle [http://www.sfu.ca/biology/faculty/elle/] invite applications for a two-year postdoctoral position requiring skills in pollination research. Individuals with experience in the development of datasets from disparate sources, considerable capacity for independent research, and strong quantitative abilities are preferred. Taxonomic skills in both plants and insects are a plus. The successful applicant will be responsible for developing and analyzing a dataset of pollination in native and nonnative Canadian plant species, and for helping to coordinate the efforts of ~20 researchers situated throughout Canada, all studying the abundance and diversity of pollinators and how they affect pollination within native and agroecosystems.This appointment is shared between University of Calgary and Simon Fraser University, but it is expected that the successful applicant will perform the majority of their responsibilities at the University of Calgary. The NSERC-CANPOLIN network is a consortium of 50 researchers in pollination biology and provides many collaborative opportunities [see http://www.uoguelph.ca/canpolin/ for more details]. To apply, please arrange to have a curriculum vitae, statement of research interests and plans, copies of two publications, and contact information for three references sent by email to Jana Vamosi [jvamosi@ucalgary.ca] and Elizabeth Elle [elizabeth_elle@sfu.ca] or by post to: Jana Vamosi, Department of Biological Sciences, University of Calgary, 2500 University Dr. NW, Calgary AB T2N1N4, Canada. Review of applications will begin on Feb 1, 2010 and continue until a suitable candidate is identified. Starting date is anticipated to be this spring or summer and is contingent on release of network funds. Salary and benefits will be competitive with NSERC postdoctoral fellowships and may include some additional funding for travel related to fulfilling responsibilities to CANPOLIN. Equity is a University policy; women, aboriginal peoples, members of visible minorities and persons with disabilities are encouraged to apply.

jvamosi@ucalgary.ca

UCalifornia LosAngeles MarinePopulationGenetics

We are advertising for a POST-DOCTORAL Position in Marine Molecular Ecology as part of an collaborative NSF Funded PIRE research project (http://sci.odu.edu/impa/ctpire.html) between Old Dominion University, UCLA and Duke University.The appointment is for one year (renewable up to 2 years maximum) beginning in summer of 2010 depending on availability. This position involves participation in an NSF-funded project to examine the population genetic and phylogeographic patterns of marine species in the Indo-Malay-Philippine archipelago and offers an excellent opportunity to develop a long-term research program in the world's most diverse marine environments. The successful candidate will be expected to live full time in Indonesia and potentially the Philippines and Malaysia planning and carrying out field sampling trips, and supervising the operations of a molecular laboratory. In addition, the successful candidate will be expected to teach a course in molecular ecology, supervise and mentor both American and foreign graduate and undergraduate students in the laboratory and field, maintain the project website, and take a prominent role in administering the project. All analyses, and research authorship, will be in collaboration with host country scientists, so the successful candidate will have a major role in developing collaborative projects with foreign scientists and students as well as obtaining all necessary research permits from foreign governments. While there are significant teaching and administrative responsibilities, the patient and flexible candidate will find good opportunities to develop related independent research activities. Applicants must have a PhD and be US citizens at the time of employment. While the position is funded through Old Dominion University, the successful candidate will work closely with both Kent Carpenter (Old Dominion University) and Paul Barber (UCLA). Please submit electronic copies of curriculum vitae, statement of interest, and the names, telephone numbers, and addresses (postal and email) of three references to: Kent E. Carpenter, kcarpent@odu.edu and Paul Barber paulbarber@ucla.edu. Review of applications will begin immediately and will continue until a suitable candidate is found. Women and minorities are encouraged to apply. Old Dominion University is an Affirmative Action/Equal Opportunity Employer and requires compliance with the Immigration Reform and Control Act of 1986

Dr. Paul H. Barber Department of Ecology and Evolutionary Biology 621 Charles E. Young Dr. South University of California Los Angeles Los Angeles, CA 90095 Phone: 310-794-5349 Fax: 310-206-3987 http://www.eeb.ucla.edu/Faculty/Barber The Diversity Project: http://www.eeb.ucla.edu/Faculty/-Barber/Intro.htm Coral Triangle PIRE Project: http://sci.odu.edu/impa/ctpire.html PEERS: http:/-/www.ugeducation.ucla.edu/urc-care/progpeers.htm Paul Barber <paulbarber@ucla.edu>

UEdinburgh DrosophilaLowRecombination

A postdoctoral position is available to work on a 3-year grant "Molecular evolution and variation in genomic regions with low recombination" to Brian Charlesworth, Insitute of Evolutionary Biology, University of Edinburgh, UK (Brian.Charlesworth@ed.ac.uk). The project involves the use of high-throughput sequencing technology to study DNA sequence variation and evolution in regions of the Drosophila genome with low rates of recombination, and comparative analyses of sequences in databases. Knowledge of evolutionary genetics and experience with DNA sequencing and computational methods for analysing sequence variation and evolution is essential. Familiarity with Drosophila genetics and genomics is desirable.

brian.charlesworth@ed.ac.uk

UGeneva PopGenomics GeneExpression

Post-doc positions in Population Genomics of gene expression in Geneva Two or more post-doc positions are available starting immediately or in the Fall 2010 in the group of Emmanouil (Manolis) Dermitzakis at the Department of Genetic Medicine and Development at the University of Geneva Medical School in Switzerland.

The selected candidates will work on projects on population genomics of human gene expression using next generation RNA sequence data (see Montgomery et al., Nature 2010) from various tissues in large samples and/or on quantitative genetics of cellular phenotypes such as chromatin modifications and protein abundance. Inferences will be linked with disease genetic studies through the various collaborations of the group with GWAS studies. The group has access to large computational (e.g. VITAL-IT at CIG in Lausanne), next generation sequencing and other high-throughput experimental facilities.

Candidates should have a background in one or more of the areas of computational biology, population genetics, bioinformatics and very good skills in programming.

The Department is highly interactive with many groups working on human genomics. The group has many national international collaborations on this and related projects. The positions are funded by grants from the Swiss National Science Foundation an endowment from the Louis-Jeantet Foundation and/or pending grant applications.

Interested applicants should send their CV and short statement of research interests to: emmanouil.dermitzakis@unige.ch

Some recent work from our group is listed below: Montgomery SB et al.. Transcriptome genetics using second generation sequencing in a Caucasian population. Nature. 2010 Mar 10. [Epub ahead of print]

Dermitzakis ET, Clark AG. Genetics. Life after GWA studies. Science. 2009 Oct 9;326(5950):239-40

Dimas AS, et al.. Common regulatory variation impacts gene expression in a cell type-dependent manner. Science. 2009 Sep 4;325(5945):1246-50.

Stranger et al. Relative impact of nucleotide and copy number variation on gene expression phenotypes. Science. 2007 Feb 9;315(5813):848-53.

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Emmanouil (Manolis) Dermitzakis, PhD Professor Department of Genetic Medicine and Development University of Geneva Medical School 1 Rue Michel-Servet Geneva 1211 Switzerland

Email: emmanouil.dermitzakis@unige.ch Tel: +41 (0) 22 379 5483 Fax: +41 (0) 22 379 5706

Admin assistant: Ancilla Stefani, Tel: +41 22 379 5551 e-mail: Ancilla.Stefani@unige.ch

Emmanouil.Dermitzakis@unige.ch

UGroningen SpatialModelling

At the Centre for Ecological and Evolutionary Studies of the University of Groningen a PostDoc position is available in the project Modelling the ecological implications of the spread of genes from transgenic crop into wild relatives. The project is financed by the Dutch Science Foundation in the context of the focal programme ERGO that was launched to assess the ecological implications of the introduction of transgenic crops. In the project computer models will be developed to investigate under what conditions and to what extent gene flow involving transgenes will substantially affect the population ecology and evolution of wild relatives. The main objective is to predict the dispersal pattern and invasion prospects of a transgene on basis of the genetics and life history of the plant species involved. This modelling project is part of a larger project comprising several experimental studies on the wild lettuce species Lactuca serriola. The models will therefore be developed in close interaction with other ecologists and population geneticists, and the model predictions will be validated with existing data.

Further information on the project can be found on the website www.rug.nl/biol/theobio or obtained from the two supervisors of the project, Kuke Bijlsma (r.bijlsma@rug.nl; Tel: +31 50 363 2117) and Franjo Weissing (f.j.weissing@rug.nl; Tel: +31 50 363 2131).

joke.bakker@rug.nl

UGuelph MarineBiodiversity

Postdoctoral position in Marine Biodiversity analysis through Next-Gen sequencing

Biodiversity Institute of Ontario, University of Guelph

A postdoctoral position is available to work with Dirk Steinke and Mehrdad Hajibabaei at the Biodiversity Institute of Ontario, on developing molecular biodiversity approaches based on Next-Gen sequencing platforms.

The position is part of the Marine Barcoding of Life (MarBOL) project that is affiliated with the Census of Marine Life and the International Barcode of Life Project (iBOL) and focuses on comparative ecosystem analysis by massive parallel sequencing of ecosystem samples from different oceanic regions. The candidate will contribute to the data generation and the design of probabilistic algorithms to analyze the sequence data generated.

This position involves working in a dynamic team equipped with cutting edge technologies including an in house 454FLX platform (and access to other Next-Gen sequencing platforms) and excellent molecular and computational infrastructure. Candidates for this position should have a strong background in bioinformatics (including experience in scripting languages such as python). Experience in molecular evolutionary biology and phylogenetics is also desirable.

The position is initially offered for one year with the possibility of renewal. Please send a complete CV, including names and contact information of three references, and a brief description of research interests to Dirk Steinke (dsteinke@uoguelph.ca). As the position is available immediately, the review process will commence as applications are received.

Dr. Dirk Steinke Lead Scientist Barcoding of Marine Life Biodiversity Institute of Ontario University of Guelph 50 Stone Road East Guelph, Ontario N1G 2W1 Canada tel. 1-519-824-4120 ext. 53759 fax 1-519-767-1656 eMail: dsteinke@uoguelph.ca

dsteinke@uoguelph.ca

UGuelph MedicalBarcoding

We are currently seeking a qualified postdoc candidate to be named on a MITACS Elevate Strategic Fellowships Program proposal aimed at developing next-generation DNA sequencing approaches for DNA barcoding of medically relevant species (pathogens, parasites, and disease vectors). The proposal is in review, but we now must identify a specific individual who would receive the award if the application is successful. If the proposal is funded, the candidate will work within the HealthBOL project at the Biodiversity Institute of Ontario (University of Guelph).

http://www1.mitacs.ca/main.php?mid=-10000560&pid=479 The fellowship is for one year, renewable for a second year.

NOTE THE FOLLOWING: At the time of application, be residents of Ontario* or citizens/permanent residents of Canada planning to move to Ontario and must have defended their doctoral thesis by September 1, 2010.

*A resident of Ontario is defined as someone who has resided in Ontario for a period of twelve consecutive months immediately prior to the start of the program.

Expertise in next-generation sequencing (especially 454) and medical and/or molecular diagnostics is critical.

Ontario residents and other eligible candidates with relevant expertise should contact Dr. Tara Gariepy, HealthBOL project manager, at tgariepy@uoguelph.ca as soon as possible. A candidate must be identified by March 31, so time is very short.

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

rgregory@uoguelph.ca

UHouston ExperimentalEvolution

Post-doctoral position in experimental evolution:

Applications are invited for a postdoctoral position in the lab of Tim Cooper at the University of Houston.

The successful applicant will examine the basis of environmental and genetic interactions that influence the effects of potentially adaptive mutations when they are introduced into a collection of natural isolates of Escherichia coli. This work will involve a combination of molecular genetic and genomic techniques. (Funded by the National Science Foundation.)

Applicants must have a Ph.D. in Biology or a related discipline and should have experience in molecular and/or evolutionary genetics. Microbiology experience would be an advantage. The initial term of the position will be for a period of two years with the possibility of a one year extension. Applications should be emailed to Tim Cooper (tfcooper@uh.edu). They will be reviewed from April 1 2010 until the position is filled. Applications should include a cover letter, CV and the names and addresses of two referees.

The University of Houston is situated in Houston, Texas. UH is a major metropolitan university with particular strengths in Biology and Mathematics. In addition Houston is the home of the Texas Medical Center, a collection of over 40 institutions, and several formal and informal opportunities exist for collaboration with members. In addition, Houston is a great place to live - a very green city with a lively arts scene and many good bars and restaurants.

tim.f.cooper@gmail.com

UIllinois KillifishAdaptation

A 3-year post-doc is available in the School of Integrative Biology at the University of Illinois. This NSF funded project is designed to study the role of environmental adaptation to salinity in generating reproductive isolation among populations of rainwater killifish. Specifically, this project involves comparing the extent to which extrinsic, intrinsic, and behavioral isolation evolves as a function of adaptation within and between 20 population pairs of the rainwater killifish that have been isolated for various amounts of time and that occur in either fresh or salt water. The responsibilities will include field sampling, performing fish crosses, raising offspring, analyzing EST libraries, developing SNP markers, using SNP markers to measure genetic distance among populations, and performing quantitative-genetic analyses. In addition, the post-doctoral associate will participate in an outreach project to develop resources for teaching evolution in the classroom as well as the general public.

The University of Illinois provides a vibrant atmosphere for studying evolution and speciation. The University hosts a number of integrative institutes including the Program in Ecology, Evolution, and Conservation, the Institute of Genomic Biology, the Neuroscience Program, and an across-campus consortium of fish biologists.

Qualified applicants will have a Ph.D. with expertise in some aspect of evolution, genetics, fish ecology or fish physiology. Starting salary is $34K (plus benefits) for candidates that hold a Ph.D. For candidates with Ph.D. pending, salary is $28K (plus benefits).

Please submit a CV, contact information for three references, and a cover letter summarizing your research interests via email to Becky Fuller at fuller@life.illinois.edu or mail to Becky Fuller, 104 Shelford Vivarium, 606 E. Healey, Urbana, IL 61801, USA. I prefer to fill this position by July 1, 2010, but the position will remain open until a suitable candidate is found.

Becky Fuller Department of Animal Biology University of Illinois 104 Shelford Vivarium 606 E. Healey St. Champaign, IL 61820 phone: 217 333 9065 e-mail: fuller@life.uiuc.edu

Becky Fuller <fuller@life.uiuc.edu>

UKansas EpigeneticsOfConflict

A postdoctoral position is available in the lab of Dr. Justin Blumenstiel to study function and evolution of epigenetic silencing by piRNA and endo-siRNA in Drosophila. The dominant focus of the lab is to determine how evolutionary conflict between transposable elements and their hosts shapes RNA silencing mechanisms in the germline. A second focus of the lab is to determine how these conflicts contribute as an evolutionary force in shaping the machinery of meiosis. The primary responsibility for this position is to determine how epigenetic inheritance of piRNA and endo-siRNA contributes to transposon regulation in populations but there will be significant opportunity to develop an independent research program related to this subject. Research will be highly integrative in nature and include small RNA sequencing, molecular evolution, cytology and population genetics. For more information contact: jblumens@ku.edu

See also the lab web page: http://www.people.ku.edu/~jblumens/ Justin Blumenstiel Assistant Professor

Department of Ecology and Evolutionary Biology University of Kansas 1200 Sunnyside Avenue Haworth Room 7026 Lawrence, KS 66045

jblumens@ku.edu 785-864-3915 http://www2.ku.edu/~eeb/faculty/blumenstiel.shtml jblumens@ku.edu jblumens@ku.edu

UManchester ProteinEvolution

Project title: Computational Identification of Protein-Protein Interactions Supervisors: Simon Whelan (PI) + Simon Lovell (CoI) Closing date: 17/03/2010 Salary: Â£28,983 - Â£35,646 p.a.

Brief project details – Working in the laboratory of Dr Simon Whelan you will work on a project for computational identification of protein-protein interactions. The aim of this project is to exploit our knowledge of how proteins change and adapt during evolution to produce more effective inferential tools. These tools will be applied to a yeast model system to generate experimentally testable hypotheses, which in turn will be tested through collaboration with wet-lab scientists. You will be an experienced and talented individual capable of developing tools numerical tools usable by computational biologists. You will hold (or expect to hold shortly) a PhD in a relevant scientific discipline or have gained equivalent experience in a research environment. You will also have a familiarity with at least a subset of the following techniques: the probabilistic models used in phylogenetics, systems biology, development of computational heuristics, and statistical inference. The position is available immediately for up to 36 months.

For full details see: http://www.ls.manchester.ac.uk/-about/jobs/job/index.asp?ref=3D169826 If you would like further details please contact me at <simon.whelan@manchester.ac.uk>.

I look forward to hearing from you.

Simon

– Simon Whelan | T: +44-(0)161-3068901 | F: +44-(0)161-2755586 Computational and Evolutionary Biology, University of Manchester Michael Smith Building, Oxford Road, Manchester, M13 9PT, UK http://www.ls.manchester.ac.uk/-people/profile/index.aspx?id=3D3678 simon.whelan@manchester.ac.uk

UMassAmherst DarwinFellow

DARWIN FELLOW

The Graduate Program in Organismic and Evolutionary Biology at University of Massachusetts Amherst announces a two-year* POSTDOCTORAL FELLOWSHIP/LECTURESHIP*. OEB draws together more than 80 faculty from the Five Colleges (University of Massachusetts Amherst and Smith, Hampshire, Mount Holyoke and Amherst Colleges), offering unique training and research opportunities in the fields of ecology, organismic and evolutionary biology. Our research/lecture position provides recent PhD's with an opportunity for independent research with an OEB faculty sponsor as well as experience developing and teaching a one-semester undergraduate biology course. Proven teaching skills are required./ / Position subject to availability of funds. 1st year salary: $35,000, 2nd year salary: $37,000.

To apply, send curriculum vitae, three letters of reference, statements of research and teaching interests, and arrange for a letter of support from your proposed OEB faculty sponsor. Electronic applications will be accepted (make sure your last name is on all documents). A list of faculty and additional information is available at* www.bio.umass.edu/oeb.* *OEB Darwin Fellowship* 319 Morrill Science Center 611 N. Pleasant Street University of Massachusetts Amherst Amherst, MA 01003 413-545-0928 darwin@bio.umass.edu Application review begins: 4/1/10 Start date: 8/15/10

/The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer./ /Women and members of minority groups are encouraged to apply./

caicedo@bio.umass.edu

UMontana SelfishChromosomeEvolution

Postdoctoral Position in Plant Evolutionary Genetics/Cytogenetics

A postdoctoral position is available in the lab of Lila Fishman at the University of Montana. We study the evolutionary genetics of speciation, adaptation, and within-population fitness variation in Mimulus (monkeyflowers): http://dbs.umt.edu/-research%5Flabs/fishmanlab/. The postdoc will focus on a project investigating the mechanisms and consequences of selfish chromosomal segregation (female meiotic drive) in yellow monkeyflowers (Fishman & Saunders 2008, Science 322:1559).

The project includes cytogenetic work to test whether female meiotic drive is centromeric in origin and mechanism, genetic mapping experiments to determine the causes of variation in the strength of drive, molecular population genetic analyses of the drive locus and centromeric proteins, and field and greenhouse experiments to characterize fitness costs of drive. The postdocs' primary responsibility will be conducting the molecular and cytogenetic components of this integrative project, but there are great opportunities for the development of an independent research program in a related area. The postdoc will also participate in outreach/training activities associated with the project, which is funded by an NSF CAREER grant.

The ideal candidate will have a PhD in a relevant field, excellent laboratory skills in molecular cytogenetics, genetics, and/or genomics, and excellent organizational and communication skills. Prior experience with DNA and/or antibody FISH to plant chromosomes is highly desirable, but not absolutely necessary for exceptional applicants willing to learn new techniques.

The position is based at the University of Montana, but will involve some work in collaborating labs elsewhere. Funding is available for two years, subject to review after the first year, with an annual salary range of $35,000-38,000 (plus benefits) depending on qualifications. The start date is flexible, but June-September

2010 is preferred.

For further information, please contact Lila Fishman (lila.fishman AT mso.umt.edu). To apply, send a letter of interest and CV (including names and contact info for 3 references) to lila.fishman AT mso.umt.edu. Review of applications will begin immediately and continue until the position is filled. –

Lila Fishman, Ph.D. Assistant Professor Division of Biological Sciences University of Montana Missoula, MT 59812

phone: (406) 243-5166 fax: (406) 243-4184

lila.fishman@mso.umt.edu

UNorthCarolina ChapelHill MateChoiceModels

Postdoctoral Position at the University of North Carolina, Chapel Hill

A position is available for a Postdoctoral Research Associate in the lab of Maria Servedio at the University of North Carolina, Chapel Hill, to work on theoretical models of male and mutual mate choice. The applicant will be expected to develop an independent research project in addition to collaborating with the PI on theoretical projects. Prior experience with theoretical modeling techniques, a strong mathematical background, and/or programming skills is preferred. A Ph.D. and a strong background in evolution is required.

Research in the Servedio lab concentrates developing mathematical models of speciation and mate choice. Please see http://www.bio.unc.edu/Faculty/Servedio/-Lab/Home.html for more information on projects ongoing in the lab.

The appointment is for 1-2 years starting preferably in the summer of 2010 (start date somewhat flexible). Send applications including a CV, description of research experience and interests, brief description of background in theory and related skills, and names and addresses of three references to Maria Servedio at servedio@email.unc.edu

Informal inquiries are welcome as well. Review of applications will begin on March 31 and continue until the position is filled.

servedio@email.unc.edu

UNottingham MobileDNAEvolution

Post-doctoral Research Fellow "Inference of the evolutionary histories of mobile DNAs", University of Nottingham, UK

Applications are invited for the above post to work on a project funded by the BBSRC on "Inference of evolutionary histories of mobile DNAs". The genomes of higher organisms contain very many active or now-inactive copies of mobile DNA elements, which can be accessed from genome project information. It is possible to apply population genetics theory to the analysis of these sequences, (as, for example, in Brookfield and Johnson (2006) Genetics 173: 1115). The new work will develop bioinformatic tools that will allow the inference of the evolutionary histories of mobile element families, based of population genetics theory and analysis.

The person appointed will join an active group of researchers in population and evolutionary genetics in the School. For additional information on Professor Brookfield's research see: http://www.nottingham.ac.uk/-biology/People/john.brookfield . Candidates must possess a PhD in bioinformatics, population or quantitative genetics (or an equivalent qualification in a related discipline). Experience of bioinformatic analysis of DNA sequences is essential, and experience in population genetics or with mobile DNA sequences is desirable.

Salary will be within the range £27,319 - £29,853 per annum, depending on qualifications and experience. This post is available from 1 July 2010 and will be offered on a fixed-term contract for a period of three years.

Informal enquiries may be addressed to Professor J Brookfield, tel: (44) 115 823 0392 or Email: John.Brookfield@Nottingham.ac.uk. Please note that applications sent directly to this Email addresses will not be accepted.

For more details and/or to apply on-line please access: http://jobs.nottingham.ac.uk/MED673. Please quote ref. MED/673. Closing date: 19 April 2010.

John Brookfield <John.Brookfield@nottingham.ac.uk>

UNovaDeLisboa DiseaseEvolution

Dear Evoldir Members

I ask you to please advertise this position. Thanks

H.Silveira hsilveira@ihmt.unl.pt IHMT Portugal

Post-Doc grant.

One year renewable up to 32 months.

Instituto de Higiene e Medicina Tropical (IHMT), Universidade Nova de Lisboa (UNL), Portugal

Salary: 1.495,00 /month

Please quote post reference: Imunostim/MAL/1/2010

Closing date for applications: 13th April 2010

Applications are invited for a Postdoctoral Research scientist to work on a project funded by the FCT (National Scientific Foundation), Portugal to investigate the role of immune stimulatory molecules on mosquito Anopheles gambiae response against the malaria parasite Plasmodium berghei (PTDC/SAU-MII/102596/2008). The project will identify immune stimulatory molecules capable of triggering protective responses in the mosquito and characterize the molecular mechanisms of resistance to infection.

We seek a highly motivated individual with experience in molecular biology, able to used murine malaria models and an interest in innate immune system and host parasite interactions. Prior experience in bioinformatics, mainly on microarray analysis, image analysis and parasite biology would be advantageous. Applicants must have a PhD or postdoctoral experience in a relevant subject.

The successful candidate will be based at IHMT-UNL, Lisbon, the proteomics part of the project will be performed at the INSA Ricardo Jorge, Lisboa. For further information regarding the post please contact Dr. Henrique Silveira (hsilveira@ihmt.unl.pt; +351 213652657)

Applicants should send to the above address or e-mail:

a) Letter of motivation

b) Curriculum vitae (maximum 10 pages)

c) Letters of recommendation

d) Copy of degree certificate

e) Copy of ID document

H. Silveira

e-mail: hsilveira@ihmt.unl.pt

Ref. Imunostim/MAL/1/2010

Instituto de Higiene e Medicina Tropical

Rua da Junqueira, 100

1349-008 Lisboa

Portugal

cbsilveira@netcabo.pt

UOulu Arabidopsis speciation

A post doctoral position (or possibly doctoral student) at the University of Oulu is available to work on genetics of speciation in Arabidopsis lyrata. (https://wiki.oulu.fi/display/PGG/-The+Plant+genetics+group). There is evidence of incipient reproductive isolation between highly diverged lineages of A. lyrata. One part of the research consists of a comparative study of genetics of the reproductive isolation. Another part deals with examining the consequences of the genetic and phenotypic divergence in an artificial hybrid zone of two diverged lineages. Other studies in the group deal with the genetics of adaptation of the different populations. The University of Oulu has good greenhouse, garden and laboratory facilities. The position is funded by the Biosciences and Environment Research council. The position is for two years, but can be extended.

It is also possible to work on aspects of this project as a doctoral student.

For further information, please get in touch with Outi.Savolainen@oulu.fi. Please send application as soon as possible, preferably by March 28, but applications are considered until position is filled.

Outi Savolainen Dept. Biology FIN-90014 University of Oulu +358-8-5531782 mobile 0358-40-5168900 outi.savolainen@oulu.fi

Outi Savolainen <Outi.Savolainen@oulu.fi>

UOxford GeneExpressionEvolution

A postdoctoral position is available, for two years, from 1 July 2010, to study the evolution of gene expression in birds. The post is funded as part of a BBSRC grant to Dr. Judith Mank (http://www.zoo.ox.ac.uk/staff/-academics/mank_je.htm). The post will be based in the Edward Grey Institute, Department of Zoology, University of Oxford. The main duties of the post-holder will involve the analysis of next-generation sequencing data at both gene expression and coding sequence level in order to study the genomic and transcriptomic basis of phenotypic evolution in avian systems. In addition, the post holder will be expected to play an important role in discussing and helping to plan the work of other post-docs and graduate students within the research group.

The successful candidate will have a PhD in evolutionary biology, genetics or a related subject, and skills in the handling of next-generation (Illumina, 454) sequencing data and in molecular evolutionary analysis. In addition, experience of supervision in a research context, and working as part of a research team are desirable. Previous experience and knowledge of avian biology are not vital.

The post is based in a dynamic and expanding research-active institute, of c. 40 people, fully integrated within the Department of Zoology. Further details about the institute available at: http://www.zoo.ox.ac.uk/egi/.

Informal inquiries (with CV) to Dr. Judith Mank (judith.mank@zoo.ox.ac.uk)

Start date 1 July 2010. The post is funded at salary grade 7 (£28,839-32,458 p.a.).

Further particulars and application forms can be downloaded from http://www.zoo.ox.ac.uk/jobs or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS (tel: 01865 271190); email: recruit@zoo.ox.ac.uk <mailto:recruit@zoo.ox.ac.uk> . Applications, together with CV and contact details of three referees, an electronic copy of three publications and a cover letter explaining how the candidate meets the selection criteria, as outlined in the further particulars, should be sent to the above address quoting reference number AT10010. The closing date for applications is 30 May 2010. Interviews will take place in June.

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

+44 (1865) 281 312

judith.mank@zoo.ox.ac.uk

UPierreMarieCurie NeuralPhylogenetics

Postdoc position available at the Department of Systematics, Adaptation, Evolution (UMR 7138), University Pierre & Marie Curie (Paris 6).

A postdoctoral research position in evo-devo, funded by the French “Agence Nationale de la Recherche”, is available at the Department of Systematics, Adaptation, Evolution at Pierre & Marie Curie University in Paris. This postdoc will be in the research group of Pr. Michael Manuel and will explore the evolutionary origin of neuro-sensory cells by phylogenetic analyses of neural gene families, expression analyses and functional study of candidate genes, and/or comparative transcriptomics, in the hydrozoan cnidarian Clytia hemisphaerica and the ctenophore Pleurobrachia pileus.

Our research group investigates the origin and early evolution of animal cell types and developmental regulatory mechanisms, taking advantage of the unique experimental possibilities offered by our two model organisms Clytia hemisphaerica (complete genome sequencing under progress) and Pleurobrachia pileus (36000 available ESTs, and 454 transcriptome sequencing under progress). The range of available experimental tools includes in situ hybridisation with embryonic and adult stages, immunofluorescence, morpholino-mediated gene inactivation, and gene over-expression using synthetic mRNA. Complementary to the candidate gene approach, we are currently undertaking a transcriptome profiling approach to the systematic identification of transcripts that are over-expressed in neuro-sensory tissues.

The post-doc project can be developed after the interest of the applicant, but should preferably combine experimental approaches (gene expression and function studies) and bioinformatics (comparative transcriptomics).

Our lab is situated in the campus of University Pierre & Marie Curie, on the Left Bank (Rive Gauche) of the river Seine, at the heart of one of the most famous districts of the city centre, the lively Quartier Latin (Latin Quarter). It is where the first great Parisian university, the Sorbonne, was founded, and the area has both a significant student presence and a very intense cultural life. Our Department is an exciting arena for multidisciplinary research in evolutionary biology, with research groups working on systematics, phylogeny, evolutionary genetics, genomics and bioinformatics, developmental biology.

Required qualifications for the applicants are (i) a PhD in developmental biology, genetics, evolutionary biology or related fields, (ii) demonstrated scientific experience in one or several of the following areas: developmental biology, phylogenetics, bioinformatics, genomics, transcriptome analysis, (iii) good communication skills in English.

The position is for two years and will imply full salary. Start date ASAP. Review of applications will begin immediately and continue until the position is filled.

To apply, send your CV, including contact information for two references, and a cover letter stating your research interest to: Pr. Michael Manuel, Michael.Manuel@snv.jussieu.fr

Michael MANUEL <michael.manuel@snv.jussieu.fr>

UPittsburgh PlantEvolutionaryGenet

POSTDOCTORAL FELLOW in PLANT EVOLUTIONARY GENETICS A postdoctoral fellow is sought to participate in work furthering the understanding the evolution of sex chromosomes in strawberry (Fragaria species) (see Spigler et al 2008 Heredity 101:507; Moore 2009 Heredity 102: 211). The project will include, but is not limited to, recombination mapping, comparative genomics and analysis of trait-fitness relationships and the role of ecological context.

The ideal candidate will be an independent thinker but be able to work creatively on a team, have a PhD in quantitative, population or molecular genetics, evolution, or related field, and have experience using molecular markers (SNPs, SSR) and/or analysis of DNA sequences, and either experience with programs for statistical analysis and mapping of genetic data or willingness to learn. Exceptional organizational and communication skills strongly desired.

The start date is flexible, but June-August 2010 is preferred, and the position is renewable annually. Applicants should email (tia1@pitt.edu) a letter of interest, CV and the names/contact information for three references. Review of applications will begin immediately and continue until the position is filled.

Tia-Lynn Ashman Professor Department of Biological Sciences 4249 Fifth Ave. & Ruskin University of Pittsburgh Pittsburgh, PA 15260-3929 phone: 412-624-0984 fax: 412-624-4759 web: http://www.pitt.edu/~biohome/Dept/Frame/Faculty/ashman.htm "Ashman, Tia-Lynn" <tia1@pitt.edu>

UVienna SystematicBotany

Postdoc: Structural botany/systematic botany, University of Vienna

A 6-year postdoctoral position is available at the Department of Structural and Functional Botany, Faculty Centre of Biodiversity, University of Vienna.

Identification number of advertisement: 1060

Expected starting date: June 2010 or according to agreement

Research at the department is focused on structure, function, and evolution of flowers and the main task of the successful candidate will be to explore and develop new applications for Micro X-ray Computed Tomography (MicroCT) in plant structural research. Candidates are also required to engage in the department's teaching activities. Qualified applicants will have a PhD degree in botany (preferably with focus on floral structure and evolution and/or flowering plant systematics), a flair for technical matters, the readiness to acquaint oneself with new methods and techniques, as well as good communication skills in English (both oral and written).

We are looking forward to receive your application (including CV, publication list, short summary of research interests, and a letter of support); preferably via the website of the Job Center at the University of Vienna (http://jobcenter.univie.ac.at); no later than April 20, 2010 and labeled with the above reference no.

For further information please contact Schönenberger, Jürg +43-1-4277-54080, juerg.schoenenberger@univie.ac.at

Jürg Schönenberger Professor, Head of Department Department of Structural and Functional Botany University of Vienna Rennweg 14 A-1030 Wien

t ..43 1 4277 54080 f ..43 1 4277 9541

juerg.schoenenberger@univie.ac.at

UWisconsinMadison GeneFlow

The following postdoctoral position is available in the laboratoryof Dr. Johanne Brunet in the Department of Entomology at the University of Wisconsin-Madison. This is a USDA-AgriculturalResearch Service postdoc that is available now until filled. For more information contact Dr. Brunet via e-mail or phone (608) 265-3587. Details of the position are presented below and can also be found at the USA jobs website under Postdoctoral Associate and Madison, WI. If interested in this position, make sure to send withthe listed of required items a cover letter explaining how your background fulfills the job qualifications listed below, a current CV with lists of publications and the names and addresses ofÂthree references.

Job Title: Research Biologist/Ecologist (Pollination Biologist) (Postdoctoral Research Associate)

Department: Department Of Agriculture

Agency: Agricultural Research Service

Sub Agency: Vegetable Crops Research Unit

Job Announcement Number: RA-10-060- L

SalaryRange: 57,408.00 - 74,628.00 USD /year

Series & Grade: GS-0408 0401-11

Open Period: Wednesday, March 03, 2010 to Friday, December 31, 2010

Position Information: Full-Time ÂTemporary position not to exceedÂ2 years with a possible extension up to 2 years

Duty Locations: 1 vacancy - Madison, WI

Who May Be Considered: Applications will be accepted from both US Citizens andÂNon-Citizens as allowed by appropriations and statute.Â For more information on citizenship restrictions log onto: http://www.afm.ars.usda.gov/hrd/jobs/VISA/Countries.htm
Job Summary:

The Agricultural Research Service (ARS) is the United States Department of Agriculture's chief scientific research agency and one of the world's premiere scientific organization.Â ARS Postdoctoral Research Associates are hired to supplement a leadÂscientist'sÂresearch onÂagricultural problems of high national priorityÂeffecting American agriculture.ÂÂ

ANNOUNCEMENT IS OPENED UNTIL FILLED OR DECEMBER 31, 2010

Major Duties:

The assignment is part of a long-range research program to study gene flow in agricultural systems, with particular emphasis on the potential risk of transgene escape.Â The current research assignment goal is to examine the impact of landscape features on gene flow for different groups of pollinators using alfalfa as a model system.Â The incumbent will set up experiments in the field and the greenhouse to examine the impact of landscape features such as plant density, population size, and degree of aggregation on gene flow for distinct groups of pollinators.Â The incumbent will determine the role of native pollinators on seed set and potential for gene escape.Â

Qualifications:

This position requires aÂPh.DÂin BiologyÂor a related field of study that has equipped the applicant with the necessary knowledge, skills and abilities to perform the duties and responsibilities of the position.Â

Requires knowledge of pollination biology.Â Skill in designing and setting up field experiments is a must.Â Skill in the use ofÂmolecular markers is preferred.Â Ability to conduct independent research and write manuscripts is necessary.

Applicants must meet basicÂOffice of Personnel Management (OPM) Qualification Standard's requirements of theÂscientific discipline necessary to perform the duties and responsibilities of the position.Â

This position has a positive education requirement.Â You must submit a copy of your academic transcripts OR a list of college courses with credit hours, dates completed, and grades received to verify education when applying for this position.Â If this information is not provided, your education may not be appropriately evaluated and you may lose consideration for this position.Â If you are selected for this position, you will have to provide an official copy of your transcripts prior to entering on duty.Â Application materials will not be returned.

Education completed in foreign colleges or universities may be used to meet the above requirements if you can show that the foreign education is comparable to that received in an accredited educational institution in the United States.Â It is your responsibility to provide such evidence when applying.Â Please visit the Office of Personnel Management's website at http://www.opm.gov/qualifications/SEC-II/s22-e4.htm#e4a for additional information on this topic.

How You Will Be Evaluated:

Your application will be evaluated to determine if you meet eligibility and minimum qualification requirements, and on the extent to which your application shows that you possess the knowledge, skills, and abilities (KSAs) associated with the position as defined above under "Qualifications".

Benefits:

— / —

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

UZurich ExperimentalEvolution

Postdoctoral fellowship in experimental evolution

A postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The Wagner lab studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects involve laboratory evolution of yeast, E. coli and fruit-flies, as well as in vitro evolution of ribozymes. A sample of the laboratory's research can be found at http://www.bioc.uzh.ch/wagner/.* *Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles. **

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will develop. The labs work is concept-driven instead of system-driven, and projects are not restricted to the model organisms mentioned above. A successful candidate will have substantial research experience with molecular biological techniques, acquired in research with an evolutionary orientation. State of the art experimental technology is available through the Functional Genomics Center Zurich, which provides platforms for ultra-high throughput sequencing, transcriptomics, proteomics, and metabolomics. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further. The position offers a highly competitive salary of up to three years on annually renewable contracts.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch <mailto:jobs_aw@bioc.uzh.ch>: CV including publication list, a statement of research interests not exceeding three pages, including a sketch of an experimental evolution project, as well as three academic references. Please include the word "EXPEVOL10" in the subject line. The application deadline is May 1, 2010. The position is available immediately.

Prof. A. Wagner

–

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

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

Tel. 0041 (0)44 635 61 42 (secretariat Prof. Wagner) Fax 0041 (0)44 635 61 44 (secretariat Prof. Wagner)

Christiane Gujan <gujan@bioc.uzh.ch>

Vienna SexualSelection

POST-DOCTORAL POSITION: Behavioral Ecology Konrad Lorenz Institute for Ethology Austrian Academy of Sciences, Vienna, Austria

We seek a highly motivated scientist to collaborate on research on sexual selection, kin recognition, and/or host-pathogen interactions in wild house mice with the institutes director, Dustin Penn. Specific research topics will be determined based on the interests and strengths of the successful candidate. Applicants must have a strong background in behavioral ecology or evolutionary biology and preferably with experience with molecular and population genetics. The position is initially for one year with the possibility of extension, and the salary depends upon experience. Review of applications begins immediately and the dead line is April

15, 2010.

The Konrad Lorenz Institute for Ethology is located in the Vienna Woods, on the outskirts of Vienna. It has large seminatural enclosures for studying a variety of species and a state-of-the art molecular genetics laboratory (see http://www.oeaw.ac.at/klivv/). The institute operates bilingually, and English is widely spoken in Vienna. To apply, please send pdfs of the following: (1) CV, (2) selected publications, (3) a brief statement of research interests, and (4) letters of recommendation or references who can be contacted to the following address: Office@klivv.oeaw.ac.at

Dustin Penn, PhD Director and Senior Scientist Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna Austria

Secretary Tel: +43 1 51581 2700 Fax: +43 1 51581 2800

D.Penn@klivv.oeaw.ac.at

http://www.oeaw.ac.at/klivv/ Dustin Penn <D.Penn@klivv.oeaw.ac.at>

YaleU BacteriaEvolution

A one-year postdoctoral position is available immediately under the co-supervision of Paul Turner and David Post in the Department of Ecology and Evolutionary Biology at Yale University. The project concerns empirical tests of theory on niche invasion and eco-evolutionary feedbacks, using bacteria as a model system. The project will be conducted using high-throughput, especially automated measures of evolving bacterial phenotypes and culturing of populations using liquid-handling robotics. Experience with high-throughput technology and with a bacterial system such as E. coli is preferred, but all strong candidates will be considered. Please direct inquiries to paul.turner@yale.edu

paul.turner@yale.edu

WorkshopsCourses

Arizona Lepidoptera Aug7-14

The Lep course, Chirichahua Mountains, SE Arizona

A Comprehensive Introduction to Lepidoptera Identification and Classification

URL: www.lepcourse.org DATES 7-14 August 2010.

APPLICATION INFORMATION Applications due by 7 June 2010. Limited to 16 students. Application form on website. Tuition for the course is $900 for students and $1000 for non-students

OVERVIEW: With over 15,000 North American species, Lepidoptera are an ideal indicator group for biodiversity studies and are widely used in ecology and evolutionary studies. Held at the SouthWest Research Station (SWRS) in the Chirichahua Mountains in SE Arizona (a 2 1/2 hour drive from Tucson), the focus of the lep course is to train graduate students, post-docs, faculty, and serious citizen-scientists in the classification and identification of adult lepidoptera and their larvae.

Topics to be covered include an extensive introduction into adult and larval morphology with a focus on taxonomically-important traits, extensive field work on both adults and larvae, collecting and curatoral techniques, genitalic dissection and preparation, larval classification, use (and abuse) of DNA bar coding, and general issues in lepidoptera systematics, ecology, and evolution.

THE LOCATION:

With its extensive series of Sky-Island mountain ranges, SE Arizona has the highest lepidoptera diversity in the US. With low desert scrub, oak and mixed oak-pine woodland, lush riparian, juniper, Douglas fir, and mountain meadow habitats all within a 40 minute drive from the station, the SWRS is an ideal location from which to sample this diversity (of both habitats and species).

INSTRUCTORS

* Jim Brock, Tucson (Internationally known butterfly expert) * Dr. John Brown, USDA and the Smithsonian Museum * P. D. Hulce, SW Research Station * Dr. Jim Miller, American Museum of Natural History * Professor Ray Nagle, University of Arizona * Dr. Chris Schmidt, Canadian National Collection * Professor Bruce Walsh, University of Arizona * Professor Ian Watkinson, Arizona Western College/Northern Arizona University

jbwalsh@email.arizona.edu

BamfieldCentre EvolutionaryModeling Aug16-Sep3

Announcing a university-level course in evolutionary modelling at the Bamfield Marine Sciences Centre (Vancouver Island, British Columbia, Canada), Aug 16 V Sep 3.

MODELS IN EVOLUTION

Models help evolutionary biologists understand concepts and processes that are fundamental to their science. For example models help answer questions like is fitness? or kind of adaptation can be promoted by selection? Models can also help set research priorities by guiding experimental design. In particular, models can answer questions like X really affect Y? in advance of costly and time-consuming experiments.

Whether you are inclined or inclined, then, you have something to gain from adopting a modellers perspective. This course will focus on modelling techniques used in evolutionary ecology. As a student, you will be introduced to the mathematics applied in evolutionary game theory, population genetics, and combinations thereof (i.e. kin selection or inclusive fitness modelling). You will learn how to formulate and analyse mathematical models of evolution at a level that will allow you to understand (and hopefully contribute to) the current literature.

Concepts will be reinforced with small assignments (set by instructor) and one larger research project (topic to be decided upon by the student).

Students may take the course for university credit, but places are available to those wishing to audit. To apply, visit

http://www.bms.bc.ca/university/courses2010/-summer10.html Pre-requisites: one full-year university-level course in calculus, or one half-year university-level course in calculus with one half-year university-level course in linear algebra.

Geoff Wild <gwild@uwo.ca>

Chioggia Italy MarineConsGenetics Jul26-30

“Summer School in Conservation Genetics of Marine organisms” 25 ’ 31 July 2010, Chioggia (VE), Italy

Organisers: Maria Berica Rasotto, Giorgio Bertorelle, Leonardo Congiu, Marti Pujolar, Lorenzo Zane

Selected PhD students and advanced undergraduates will initially learn the basics of conservation genetics, and will then follow a series of lectures on more recent advances in this field, including applications to marine environments. Practical activities will include collection and handling of samples for genetic analyses, genetic typing, and software sessions for data analysis.

The summer school will be held at Palazzo Grassi, Chioggia. Chioggia is a coastal town of the province of Venice in the Veneto region of northern Italy, situated on a small island at the southern entrance to the Lagoon of Venice about 25 km south of Venice (http://en.wikipedia.org/wiki/Chioggia).

The course will include five full days of teaching (26-30 July), with arrival and departure dates scheduled for July 25 and 31, respectively. The number of students will be limited to 25.

Confirmed speakers are: M. Abbiati, V. Almada, G. Bertorelle, M. Bruford, M. Casiraghi, L. Congiu, O. Gaggiotti, J.C. Garza, L. Hauser, Rus Hoelzel, E.E. Nielsen, C. vanOosterhout, T. Patarnello, G. Procaccini, E. Randi, M.B. Rasotto, C.A. Stockwell, F. Tinti, E. Valsecchi, C. Vernesi and L. Zane.

Deadline for application is May 15 Full details on the program, applications and registration fee are available at: http://chioggia.scienze.unipd.it/ITA/ScuoladiGenetica_2010.html Lorenzo Zane Dipartimento di Biologia University of Padova

lorenz@bio.unipd.it lorenz@bio.unipd.it

EMBL-EBI Hinxton

Title: Small Molecule Bioactivity Resources At The EBI Date: 14-18 February 2011 Venue: EMBL-EBI, Hinxton, Nr Cambridge, CB10 1SD, UK Organisers: John Overington, Anne Hersey, Vicky Schneider Admin Support: Alison Barker, Holly Foster, Frank O’Donnell Registration Opens: 14th August 2010 Registration Deadline: 14th January 2011

http://www.ebi.ac.uk/training/handson/course_110214_smallbioactives.html

Title: In silico systems biology for complex diseases: network reconstruction, analysis and network based modelling Date: 23-27 May 2011 Venue: EMBL-EBI, Hinxton, Nr Cambridge, CB10 1SD, UK Organisers: Vicky Schneider, Nicolas Le Novère Admin Support: Alison Barker, Holly Foster, Frank O’Donnell Registration Opens: 1st October 2010 Registration Deadline: 23rd March 2011

http://www.ebi.ac.uk/training/handson/course_110523_sysbiol.html

Title: Summer school in bioinformatics Date: 20-24 June 2011 Venue: EMBL-EBI, Hinxton, Nr Cambridge, CB10 1SD, UK Organisers: Vicky Schneider, James Watson Admin Support: Alison Barker, Holly Foster, Frank O’Donnell Registration Opens: 5th January 2011 Registration Deadline: 20th May 2011

http://www.ebi.ac.uk/training/handson/course_110620_summerschool.html

Title: Proteomics Bioinformatics workshop Date: 15-20 July 2011 Venue: EMBL-EBI, Hinxton, Nr Cambridge, CB10 1SD, UK Organisers: Vicky Schneider, James Watson Admin Support: Alison Barker, Holly Foster, Frank O’Donnell Registration Opens: 15th February 2011 Registration Deadline: 15 June 2011

http://www.ebi.ac.uk/training/handson/course_110715_proteomics.html

Title: Data resources and tools for structural biologists Date: 12-16 September 2011 Venue: EMBL-EBI, Hinxton, Nr Cambridge, CB10 1SD, UK Organisers: Gerard Klewegt, James Watson, Rosemary Wilson Admin Support: Alison Barker, Holly Foster, Frank O’Donnell Registration Opens: 12th March 2011 Registration Deadline: 12th August 2011

http://www.ebi.ac.uk/training/handson/course_110912_structures.html

Title: Advanced analysis and informatics for microarray data Date: 24-29 October 2011 Venue: EMBL-EBI, Hinxton, Nr Cambridge, CB10 1SD, UK Organisers: Gabriella Rustici Admin Support: Alison Barker, Holly Foster, Frank O’Donnell Registration Opens: 1st June 2011 Registration Deadline: 1st September 2011

http://www.ebi.ac.uk/training/handson/-

course_111023_microarray.html

Many thanks

Holly Foster

Workshops and Exhibitions Organiser

European Bioinformatics Institute, Hinxton, Cambridge, CB10 1SD, UK

Tel: +44 (0) 1223 492650

Fax: +44 (0) 1223 492621

Email: Holly@ebi.ac.uk

http://www.ebi.ac.uk/training/

Upcoming hands on training courses:

17-18 May 2010 - Joint EBI-Industry Workshop: Cheminformatics in R

14-18 Jun 2010: Joint EBI-Wellcome Trust Bioinformatics Summer School

6-10 September 2010 - EMBO Practical Course Computational aspects of protein structure determination and analysis: from data to structure to function

18-23 October 2010 - EMBO Practical Course: Advanced analysis and informatics of microarray data

12-18 December 2010 - Joint EBI-Wellcome Trust Proteomics workshop

Please subscribe at www.embl.de/events/newsletter for our newsletter Follow us on www.twitter.com/-embl_events

Holly Foster <holly@ebi.ac.uk>

Finland MathematicalEvolution Aug22-29

Summer school (repost): Mathematical ecology and evolution, Finland, 22-29 August 2010

The Helsinki Summer School on Mathematical Ecology and Evolution 2010 invites applications from students and young researchers with appropriate background in mathematics to attend the one-week intense program of five topics at the research frontier:

Evolutionary game theory (Karl Sigmund) Bifurcation analysis (Yuri Kuznetsov) Stochastic differential equations (Carlos Braumann) Population genetics (Reinhard Bürger) Stochastic models for epidemics (Tom Britton)

The school will be held between 22 and 29 August 2010 in Turku, Finland, organised by the Biomathematics Group of the University of Helsinki and endorsed by EMS and ESMTB.

The deadline for applications is **** 15 April 2010 ****. There is no registration fee.

For more details and application, see http://-wiki.helsinki.fi/display/huippu/mathbio2010 . Welcome, Eva Kisdi and Petr Ondracek

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Frauenchiemsee Germany GenomeEvolution Sep5-11

Summer School on "Genome Evolution"

5th until 11th of September 2010, Frauenchiemsee, Germany

Faculty: William Cresko (University of Oregon) Jan Korbel (EMBL Heidelberg) Claudia Acquisti (Arizona State University) Kai Müller (WWU Münster) Alexandros Stamatakis (TU Munich) John Parsch (LMU Munich) Erich Bornberg-Bauer (WWU Münster)

Target participants: early PhD students, advanced master students

During our summer school 18 participants will enjoy lectures, seminars and hands on practical training. Lecturers will give insights into current topics of genome evolution and demonstrate recent genomic approaches. Participants are asked to bring their laptop along for our practical sessions. In addition the participants will get the chance to present and discuss their own projects and obtain advice on their project design and analysis setup.

The costs of participation (board and lodging at Frauenchiemsee < http://www.frauenwoerth.de/->http://www.frauenwoerth.de/) will be covered by the VW foundation. The summer school is jointly organised be the WWU Münster and the LMU Munich.

To apply, send a single file (pdf) containing a short motivation letter, a cv and an abstract of your project to p.feulner@uni-muenster.de

Deadline for application: July 15th, 2010

Dr Philine Feulner Westfälische Wilhelms University Institute for Evolution and Biodiversity Evolutionary

Bioinformatics Group Hüfferstrasse 1 48149 Münster Germany Tel: +49 (0) 251 83 21636 Fax: +49 (0) 251 83 24668

p.feulner@uni-muenster.de

Germany EvolutionDiversity ArthropodSymbiosis Jun30-Jul3

In the frame of the COST Action FA0701

≪ Arthropod Symbioses: from fundamental studies to pest and disease management ≫

We are pleased to announce the workshop entitled:

Evolution and Diversity of Symbioses of Arthropods

The workshop will be held from the 30th of June to the 3rd of July 2010 in Bad Bevensen, Germany.

Symbioses with bacteria and other microorganisms have contributed greatly to the ecological and evolutionary success of arthropods, either by providing essential nutrients or digestive functions, or more unusual functions such as bioluminescence or contributing to healthcare of their hosts. Other endosymbionts engage in more parasitic interactions with their hosts by distorting their hosts sex ration to ensure their own transmission. This stunning diversity of symbioses already became evident early in the 20th century, e.g. by the wide range of associations included in Paul Buchners seminal book “Endosymbiose der Tiere emit Pflanzlichen Mikroorganismen” published in 1953.

Since then numerous symbiotic associations have been characterized in great detail, with microbial partners being identified, genomes of endosymbionts being sequenced and functions of the symbionts uncovered. The use of culture independent techniques has led to a great leap forward in uncovering the diversity present in arthropod hosts as well as their specificity. Recent work on a broad range of arthropod symbioses will be presented, with a wide range of microorganisms involved that are located in a variety of organs such has antennal glands, gut, malphigian tubules or reproductive tissue.

Whereas biologists recently became aware of the importance of mechanisms of host-symbiont interactions and the involvement of the immune system as an interface between the two, we are only beginning to understand how the crosstalk between different endosymbionts can alter the outcome of symbiotic associations when hosts harbour endosymbiont consortia and how diverse some of these consortia can be. In addition more and more players in symbiotic interactions are uncovered as well as new functions. Are such endosymbiont consortia stable in composition? Does competition among different endosymbionts for host resources harm the host as certain functions are provided in a lesser manner? How easily can such endosymbiont consortia including gut microflora be invaded by other microorganisms?

In this workshop, we welcome talks on different kinds of symbiotic interactions from mutualistic to parasitisic and comprising either single endosymbionts or endosymbiont consortia. The very beginning of endosymbiosis will be discussed. How are free living organisms incorporated into other organisms to become endosymbionts?

Tentative list of invited speakers:

James Lake (UCLA, USA)

William Martin (University Düsseldorf, Germany)

Andreas Brune (Max-Planck Institute Marburg, Germany)

Molly Hunter (University of Arizona, USA)

Edouard Jurkevitch (University Jerusalem, Israel)

Martin Kaltenpoth (Max-Planck Insitute Jena, Germany)

Eva Novakova (University South Bohemia, Czech Republic)

Ameur Cherif (University Tunis, Tunisia)

Daniele Daffonchio (University Milano, Italy)

Fabrice Vavre (University Lyon, France)

Alison Dunn (University Leeds, UK)

Massimo Marzorati (University Gent, Belgium)

Jan Engelstädter (ETH Zürich, Switzerland)

Cara Gibson (National Ecological Observatory Network (NEON), Boulder, USA)

Einat Zchori-Fein (Newe Ya'ar Research Center, Israel)

Peter Neumann (Swiss Bee Research Centre Agroscope, Switzerland)

Alexandre Aebi (Forschungsanstalt Agroscope, Switzerland)

Richard Cordaux (University Poitiers, France)

Julien Varaldi (University Lyon, France)

Matthias Horn (University Wien, Austria)

Outline of the program

June 30: arrival day, welcome reception.

July 1st: Oral communications, Evening poster session.

July 2nd: Oral communications, Evening poster session.

July 3rd: departure Day

Communications and Poster session

Communications will be on invitation. However, a poster session will be organized and there will be time for discussions. Participants willing to present a poster should send a title and an abstract to Heike Feldhaar (feldhaar@biologie.uni-osnabrueck.de) before March 30th, 2010. In case that there is still time for oral contributions we will contact registered participants.

Location and access

The workshop will be held in the Gustav-Stresemann Institute in Bad Bevensen, Germany. Bad Bevensen can be reached easily by train either from Hamburg or Hannover. Both towns have an international Airport (alternatively from Frankfurt Airport via Hannover by train).

Bad Bevensen is a small town in Northern Germany, close to the Luneburg

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

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Jyvaskyla Finlad BioDiversity May31-Jun2

"Integrating Ecology and Evolution in Diversity Research" A workshop funded by the EU Marie Curie Initial Training Network SPECIATION

31 May 2 June 2010, Jyväskylä, Finland

Organisers: Anneli Hoikkala, Emily Knott, Maaria Kankare, Venera Tyukmaeva, Elzemiek Gueverink, and Jackson Jennings on behalf of the Marie Curie ITN

The fourth workshop organized by the EU Marie Curie ITN SPECIATION will focus on integrative topics. Particular focus will be on the genetics of adaptation and on using phylogenetic methods for studying divergence and diversification. Confirmed speakers: Rodolfo Costa (University of Padova), David Dolozel (Biology Centre ASCR), Lacey Knowles (University of Michigan), Albert Phillimore (Imperial College London), and Johanna Mappes (University of Jyväskylä)

The workshop will be held at the Konnevesi Research Station, near the University of Jyväskylä in idyllic central Finland (see https://www.jyu.fi/bioenv/en/konnevesi). The workshop will comprise lectures, computer-based practicals and a workshop on complementary skills. Participants should plan to arrive in Jyväskylä on Sunday, May 30 and the workshop will end mid-day on June 2. For more information go to http://speciation.group.shef.ac.uk/?page_id@ There is space and funding available for 15 external participants who are at an early stage of their research careers. There is no registration fee and accommodation as well as catering will be provided free, but participants will have to pay for their own travel costs. There are no nationality restrictions.

Applications should include a CV and a brief letter of motivation explaining why you are interested in attending the workshop. Please send applications to Emily Knott (emily.knott@bytl.jyu.fi) by April 8.

Jackson H. Jennings

Centre of Excellence in Evolutionary Research, Department of Biological and Environmental Science, P.O. Box 35, 40014 University of Jyväskylä, Finland

Tel: +358 14 260 4253 Room: YAC421.1

https://www.jyu.fi/bioenv/en/divisions/eko/coeevolution http://speciation.group.shef.ac.uk/ "Science is the great antidote to the poison of enthusiasm and superstition."

- Adam Smith (The Wealth of Nations, 1776)

"Jackson H. Jennings" <jackson.h.jennings@jyu.fi>

LakeheadU AncientDNA May10-28

The Paleo-DNA Laboratory at Lakehead University in Thunder Bay, Ontario, Canada is offering the opportunity to participate in our annual Ancient DNA Training Program. This year we are delivering the course from May 10th to 28th, 2010.

During this hands-on laboratory and lecture program, participants are taught various extraction, purification, and amplification methodologies applied to ancient, degraded or damaged DNA. They will also be provided instruction in data analysis. They will analyse their own blood, buccal, and hair samples and generate their own nuclear DNA profile, determine their own mitochondrial haplotype, and learn sex identification and DNA sequencing. The methodology will include Polymerase Chain Reaction (PCR), PCR-RFLP (Restriction Fragment Length Polymorphism), multiplex PCR, sequencing, and gel and capillary electrophoresis. Students will practice preparing samples from a number of different tissue types such as bone, teeth, hair, blood residues and mummified tissue.

Students will learn to recognize the use of genetic analysis and its potential in evolutionary biology, archaeozoology, palaeopathology, archaeology, forensic science, palaeobotany and palaeontology. Lectures by experts in the fields of archaeology, genetics, ancient DNA, forensic science, palaeopathology and more are integrated with the laboratory sessions.

If you would like registration forms or further information, please visit our website at www.ancientdna.com or feel free to contact me direct at cjaspers@lakeheadu.ca or toll free at 1-866-DNA-LABS.

Cheryl Jaspers

Administrative Coordinator

2010 Ancient DNA Training Program

Carney Matheson <cmatheso@lakeheadu.ca>

LakeheadU PaleoDNA May10-28

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Cheryl Jaspers Administrative Coordinator 2010 Ancient DNA Training Program

Carney Matheson <cmatheso@lakeheadu.ca>

OregonStateU TreeGenomics Jun21-25

Shortcourse: Genomics in Tree Breeding and Forest Ecosystems A shortcourse on genomics-based strategies for plant breeding and gene resource management, with examples from forest trees, food crops, livestock, and humans.

The CTGN is committed to providing an annual shortcourse on genomics-based breeding in forest trees (given sufficiently enrollment). “Genomics in Tree Breeding and Forest Ecosystems” is an intensive five-day shortcourse that provides a detailed overview of several topical disciplines leading up to and including genomics-based breeding strategies in forestry.

When: June 21-25, 2010 Where: Oregon State University, Corvallis, Oregon Application Deadline: April 1, 2010 Registration Fee: $250 Participation in the shortcourse will be guided by a two-step process: application and registration.

Interested individuals may apply here: http://dendrome.ucdavis.edu/ctgn/educationextension/registration.php The application collects basic contact information and also requires the submission of two documents (pdf format): CV/resume and a 1-2 page essay.

Accepted applicants will be asked to register at a second link, to be provided at a later date. A registration fee of $250.00 US will be levied to offset facilities rental, refreshments, dorm rooms and meal tickets and sundry costs.

Course Topics Basic principles in population and quantitative genetics Introduction to conventional tree breeding Genetic markers, measuring, and interpreting marker variation Molecular population genomics Genetic maps and QTL mapping Association testing and mapping MAS in tree improvement - concepts and experimental results Implementation strategies and economics of MAS in tree improvement Genomic applications in genetic resource management: cross disciplinary studies On-line tools and resources

A detailed syllabus and more information on the course can be found on the CTGN website: http://dendrome.ucdavis.edu/ctgn/educationextension/shortcourse.php For more information on the course content, you can contact Nick Wheeler (nickwheeler@scattercreek.com)

Jill L. Wegrzyn Bioinformaticist Department of Plant Sciences University of California at Davis One Shields Avenue, MS 4 Davis, California 95616

http://dendrome.ucdavis.edu E-mail: jlwegrzyn@ucdavis.edu phone: 619-316-8548 fax: 530-754-9366

jillylee@gmail.com

Roscoff France MarineEvolutionaryGenomics May24-Jun4

Summer Course on Marine Evolutionary & Ecological Genomics

May 24th â June 4th, 2010

Station Biologique de Roscoff, France

LAST CALL

Aims: to introduce genetic and genomic approaches for the analysis of biological diversity,evolution and adaptation at the species and population level in the ocean

Target group:

PhD students (at least in their second year) and post docs with a solid knowledge in phylogenetics and/or population genetics.

Topics:

The course will consist of lectures, tutorials and computer based exercises in the following subjects.

* Phylogeny & tree of life- sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies

* Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies

* Population genetics â structure, connectivity and gene flow, assignment, effective size and population dynamics, case studies

* Functional genomics â database searching, genome structure, molecular evolution at the functional level

* Comparative genomics - whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, transposable elements in marine species, co-evolution

* Environmental and functional genomics - methods for detecting adaptive variation; detecting diversity; EST libraries: why and how; case studies.

Confirmed teachers

Sandie Baldauf, U. Uppsala, SE Jonas CollÃ©n, U Paris 6, FR Simon Creer, U Bangor, UK Yves Desdevises, CNRS Banyuls, FR Michael Hansen, U Aarhus, DK Galice Hoarau, U Bodo, NO Jeanine Olsen, Univ Groningen, NL FrÃ©dÃ©ric Partensky, SB-Roscoff, FR Heroen Verbruggen, U Gent, BE FrÃ©dÃ©rique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE Mathias Wegner, ETH Zurich, SW

Organizing committee

Claudie Perron, SB-Roscoff, FR Jeanine Olsen, Univ Groningen, NL Jonas CollÃ©n, SB-Roscoff, FR FrÃ©dÃ©rique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

Costs, course, accommodation and meals:

* The course fee is paid by the MGE Network and includes a welcome reception, excursion (incl. lunch) and farewell dinner.

* On site accommodation at the SBR guesthouse is included.

* All participants pay their own travel and board (self catering is possible)

The guesthouse offers lunch and supper at 5.50 â¬$per person and meal.$

Application and contact:

To apply please fill in the application form at http://www.marine-genomics- europe.org/Documents/meeg/

and send to Jonas CollÃ©n (collen@sb- roscoff.fr) together with a 2-page CV

before March 26th 2010.

16 participants will be selected on the following criteria:

1. Relevance of the course for their PhD or post-doc project

2. Background and experience of applicant

3. We will aim at mixing people with different research backgrounds; probably not more than one person per institute will be considered. We will also aim at an equal gender distribution.

The selected persons will be notified at the end of April and have to confirm within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Contacts:

Jonas CollÃ©n (collen@sb-roscoff.fr) FrÃ©dÃ©rique Viard (viard@sb-roscoff.fr) Station Biologique de Roscoff BP 74, 29680 ROSCOFF CEDEX France Phone: (33)2 98 29 23 23 Fax: (33)2 98 29 23 24

Organised by the EU Network of Excellence Marine Genomics Europe

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Seattle WomenEvolving Oct24-27

Dear Colleagues,

WEBS (Women Evolving Biological Sciences) is an annual three-day symposium aimed at addressing the retention of female scientists and issues related to the transition of women from early career stages to tenure track positions and leadership roles in academic and research settings. The 2007 and 2008 WEBS symposia were huge successes. Early career participants as well as our senior scientist panelists reported feeling inspired and equipped with new connections and tools that they expect will help them in their career in the years to come. We are now accepting applications online (http://www.webs.washington.edu < http://www.webs.washington.edu/ >) for participation in the 2010 symposium.

WEBS will target early career women in the Biological Sciences with an emphasis on ecology and evolutionary biology. In particular, it will focus on women who have earned their doctoral degrees within the past two to eight years and who do not have tenure in order to address the critical transition period from graduate studies and post-doctoral positions to permanent research and teaching positions. The symposia will provide a forum for professional development, including awareness and improvement of academic leadership skills; opportunities to establish mentoring relationships; and resources for developing professional networks. The 2010 symposium will be held at the Pack Forest Conference center near Seattle, WA from October 24-27, 2010.

Please visit our website (http://-www.webs.washington.edu < http://-www.webs.washington.edu/ >) for details and application materials. Applications are due April 15, 2010. Feel free to contact us with any questions you might have (webs@u.washington.edu).

Sincerely,

Samantha Forde, Ph.D. Claire Horner-Devine, Ph.D. Joyce Yen, Ph.D. University of California Santa Cruz University of Washington University of Washington

forde@biology.ucsc.edu

Trento Italy ForestGenomics Aug23-26

The INTERNATIONAL WORKSHOP -Landscape Genomics of Forest Trees and Applications to Climate Change' will be held at the Centro di Ecologia Alpina (CEA; http: www.cealp.it), Fondazione Edmund Mach, on Monte Bondone, near Trento, Italy, August 23-26, 2010. This workshop will be hosted by CEA, in collaboration with the University of California, Department of Plant Sciences, Davis, USA .

The goal for this workshop is to teach graduate students, postdocs and researchers contemporary methods in landscape genomics with examples from and applications to forest tree populations. The curriculum will be delivered over three full days. Morning sessions will consist of lectures given by course instructors on the underlying theory and methodology of landscape genomics. Late morning sessions will be dedicated to students presentations. Afternoon sessions will consist of hands-on computer exercises using population genomics and landscape genomics software applications with real forest tree datasets. A late afternoon session will be devoted to seminar presentations by invited speakers Aitken and St.Clair on their respective research programs that focus on genomics of adaptation and forest tree response to climate change.

Web site: http://conferences.cealp.eu/conferenceDisplay.py?confId=3D4 Organizers: David Neale (Dept. of Plant Sciences, UC Davis) Cristiano Vernesi (Centro di Ecologia Alpina, Research and Innovation Centre, Fondazione Edmund Mach)

Claudio Varotto (IASMA Research and Innovation Centre, Fondazione Edmund Mach)

Course Instructors: David Neale (UC Davis, USA) , Jill Wegrzyn (UC Davis, USA), Andrew Eckert (UC Davis, USA)

Invited speakers: Sally Aitken (University of British Columbia, Canada) and Brad St. Clair (USDA Forest Service, Corvallis, Oregon, USA)

Local committee: Cristiano Vernesi and Floriana Marin (secretary), Fondazione Edmund Mach.

Dates: August 23-26, 2010. Place: Centro di Ecologia Alpina, Viote del Monte Bondone, 38040 Trento, Italy.

Registration: Enrollment is limited to 20 participants. Potential participants are kindly requested to register through the web site. Deadline for registration is May 1, 2010. Applicants will be advised of acceptance by May 15, 2010.

Fee: 250 includes lunches and dinners (from August 24) and the course manual.

Contacts: Floriana Marin, Research and Innovation Centre, Fondazione Edmund Mach, (events@iasma.it), phone: +39 0461 615543 - Fax + 39 0461 615183

Cristiano Vernesi Centro di Ecologia Alpina Centro Ricerca e Innovazione - Fondazione Edmund Mach postal address: Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skypename: cvernesi

Please, consider your environmental responsibility before printing this email

vernesi@cealp.it

Trento Italy ForestGenomics Aug23-26 correction

dear all, in the previous advertisement of the workshop, there was an error about the web site address. I apologize for the inconvenience.

Please, find the correct link below: http://conferences.cealp.eu/conferenceDisplay.py?confId=3D4 Cristiano Vernesi Centro di Ecologia Alpina Centro Ricerca e Innovazione - Fondazione Edmund Mach postal address: Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skypename: cvernesi

Please, consider your environmental responsibility before printing this email

vernesi@cealp.it

UArizona TropicalButterfly Diversity May14-28

*** OPEN ENROLLMENT spaces still available***

Tropical Butterfly Ecology

This 2-week course is for advanced graduate students interested in conducting tropical field studies on butterflies. The course will focus on the Costa Rican Atlantic rainforest fauna, and include work at the La Selva Biological Station and the Tirimbina Biological Reserve both sites share a diverse assemblage of Neotropical butterflies, including many species that extend well into South America.

The major thrust of this course will be natural history and identification of butterfly adults and early stages. We will focus on behavior, diversity, ecological and evolutionary patterns, symbiotic associations, ecophysiology, quantitative sampling techniques, experimental design, and as well, the pleasures of conducting research on tropical insects.

The course combines lectures, hands-on field exploration, and major efforts on the part of students to understand and apply quantitative observational and sampling procedures in the field. The course will stress developing rigorous natural history questions from field observations.

Faculty: Dr. Phil DeVries, University of New Orleans

Dr. Bruce Walsh, University of Arizona

Guest faculty:

Isidro Chacon, Costa Rica National Museum and National Biodiversity Institute (INBIO)

Dates: May 14-28, 2010 Application Deadline: February 16, 2010 for priority admission followed by open enrollment until filled. Tuition: OTS consortium applicants - $2,000; non-member applicants $2,500

Partial need-based scholarships are available; priority given to OTS consortium and Latin American applicants.

Students: graduate students, postdoctoral fellows and other interested professionals For More information: consult the OTS website at www.ots.duke.edu or contact barbara.lewis@ots.ac.cr

jbwalsh@email.arizona.edu

UGeorgia China Genetics

DEADLINE APRIL 15, 2010

Unique (and Low-Cost) Opportunity for Ten Undergraduates 2011 Evolutionary Genetics Field Study Abroad in China

Learn Chinese and Evolutionary Genetics at the University of Georgia

With funding from NSF's Partnerships for International Research and Education (PIRE) program, we are offering 10 undergraduates (U.S. citizens or permanent residents only) the opportunity to participate in a unique study abroad opportunity in China during the spring and summer of 2011. This will be the 4th year of the program and students have found it to be enormously rewarding.

The research focus of our PIRE grant is a forensic phylogeographic study of species that are native to China and invasive in the southeastern U.S. as well as a growing number of species native to the southeastern U.S. and invasive in China.

Each summer, we run an 8 week field course where we visit biological communities throughout China. Students can elect to continue in short-term research internships in our partner labs in China.

Students will need to be prepared to take full advantage of this experience. Therefore, during the spring semester, students must enroll at the University of Georgia (UGA) and take 3 courses; two in intensive elementary Mandarin Chinese and a laboratory course in genetics. No prior experience with Chinese language is required, although students should have had at least a course in introductory biology and preferably courses in ecology and evolutionary biology.

The cost to the student of the summer program is minimal: the grant covers travel to and within China, lodging and most meals. The student is responsible for health insurance, visa costs and personal expenses. Students are also responsible for the costs of enrolling at the University of Georgia for all required courses (12 credit hours) (all students are charged in-state tuition rate plus fees).

Applications for the 2011 program are available on our website: http://www.genetics.uga.edu/pire/-undergrad.html. We encourage any interested students to contact Dr. Mauricio for more information (mauricio@uga.edu).

Rodney Mauricio Program Director, UGA-China PIRE

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Rodney Mauricio, Ph.D. Department of Genetics Phone: (706) 542-1417 University of Georgia FAX: (706) 542-3910 Athens, GA 30602-7223 e-mail: mauricio@uga.edu

Lab Web Page: http://www.genetics.uga.edu/-mauriciolab PIRE Grant Web Page: http://-www.genetics.uga.edu/pire Evolution at UGA: http://www.genetics.uga.edu/evolution mauricio@uga.edu

UMichigan EvolutionaryEpidemiology Jul12-16

*One Week Graduate Summer Course in Evolutionary Epidemiology at the School of Public Health, The University of Michigan *

*EPID 788 Evolutionary Epidemiology (1 credit hour) Randolph Nesse *New applications of evolutionary theory to medicine are growing and helping to explain apparent paradoxes, such as rapidly increasing rates of breast cancer, increased asthma vulnerability in certain populations and the metabolic syndrome (For details see The Evolution Network at http://evolutionandmedicine.org). Epidemiologists have begun to apply these principles and ask new questions, such as do genes that vary by latitude explain hypertension, and how might public health interventions for infectious disease be 'evolution-proofed' (see discussion of the American College of Epidemiology 2008 meeting: Dawn of Evolutionary Epidemiology (http://acepidemiology.org/meetings/-

2008Tuscon/08AMSpeakerHandouts.asp). This course will explore how epidemiologists and other public health workers can make use of these advances in their own work. Applying evolutionary theory can sharpen research questions, raise new possible explanations for observed phenomena and identify new types of exposure and outcome measures. Pre-requisite: No prior training in evolutionary biology is assumed.

http://www.sph.umich.edu/epid/GSS/courses/-1week.html#788 Afternoons, July 12-16, 2010, School of Public Health, The University of Michigan

http://www.sph.umich.edu/epid/GSS/index.html Randolph Nesse, M.D. The University of Michigan http://nesse.us nesse@umich.edu

UWashington StatisticalGenetics

In Spring quarter 2010 (March 29 -June 11)

University of Washington Online Learning is again offering the Stat 550B (DL) course Statistical Genetics I; Discrete Mendelian traits with instructor Elizabeth Thompson (eathomp@u.washington.edu) (http://www.stat.washington.edu/thompson/)

Interested participants should contact UW Online Learning http://www.outreach.washington.edu/ol/ for registration and administrative details, but are very welcome to contact Elizabeth Thompson (eathomp@u.washington.edu) for more information about course content or requirements.

Some information about the 2009 offering of this DL class is available at http://www.stat.washington.edu/-thompson/Stat550/Online_2009/ The 2010 class is expected to follow a very similar schedule.

eathomp@u.washington.edu

UWashington StatisticalGenetics Mar29-Jun11

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– Bruce S. Weir Professor and Chair, Department of Biostatistics University of Washington Seattle, WA 98195-7232 Phone (206) 221-7947. Fax (206) 543-3286.

Bruce Weir <bsweir@u.washington.edu>

Valencia Spain MolEvolution Jun14-18 2

SECOND ANNOUNCE

DEADLINE FOR APPLICATIONS: May 3th 2010

Dear mailing list member,

Registration is now open for:

MEPPA10 - Molecular Evolution, Phylogenetics, Phylogenomics and Adaptation

Please visit the Course website for details:

http://bioinfo.cipf.es/courses/mol_evol_phylo_5ed/ This course is likely to be very competitive for seats. Our maximum capacity is 25 seats. Early application is recommended!

Instructors: Hernan Dopazo, Toni Gabaldon, François Serra, Jaime Huerta-Cepas and Leonardo Arbiza Invited Instructors: David Posada, University of Vigo (Spain) and Rafael Zardoya, MNCN-CSIC (Madrid, Spain) Duration: 5 days. June 14-18, 2010 Course Fee: Eur 330, include meals. A limited number of grants will be available. Place: Centro de Investigacion Principe Felipe. Valencia. Spain

Course description:

Currently, the simplest Bioinformatics analysis uses species comparisons in order to hypothesise the function of a novel biological sequence. Moreover, in most

Molecular Biology labs, evolutionary and phylogenetic concepts are constantly being used with more or less formality: homology, similarity, evolutionary rates, long branch attraction, rooted and unrooted trees, monophyletic group, molecular clock, adaptation, lineage effects, neutralism, cladograms, phylograms, etc. The course aims to provide the necessary background to understand the basic concepts from comparative and evolutionary biology that are frequently used in molecular biology and bioinformatics analyses.

The course consists in five full-day sessions with an adequate balance between theory and computer practice, oriented to solve frequent problems and hypothesis testing. The program covers the basic and advanced analysis of Phylogenetic reconstruction, Phylogenomic analysis of genomes and Maximum likelihood tests for molecular adaptation. The software resources that will be used in the practical sessions include: Phyml, Phylip, MEGA, TreePuzzle, MrBayes, PAML, Modeltest-Protest, Jmodeltest and the Phylemon web server.

Please feel free to pass this information to colleagues in your community.

Co-ordinators: Hernan Dopazo and François Serra

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

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.