EvolDir

November 1, 2009

Month in Review

Foreword

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

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

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

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Conferences

Amsterdam DiseaseEvolution Nov3-5

Dear Colleague,

I thought the following event would be of interest to you: 10th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID X). It will take place in Amsterdam, November, 3-5, 2010. The organizers are currently calling for abstracts for poster presentations with an abstract deadline of June 4, 2010. Selected submissions may be offered an oral presentation slot. For further information see http://www.meegidconference.com Best regards,

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.com/locate/meegid Official 2008 Impact Factor: 2.792 Laboratory of Genetics and Evolution of Infectious Diseases (GEMI) IRD Center BP 64501 34394 Montpellier Cedex 5 France E-mail : Michel.Tibayrenc@ird.fr Website : http://gemi.mpl.ird.fr Michel.Tibayrenc@ird.fr

Aspen PopulationsEvolutionAndPhysics Jan3-9

Dear Colleague,

We are organizing a conference on the topic of

Populations, Evolution, and Physics

at the Aspen Center for Physics, to be held January 3-9, 2010.

The aim of the conference is to bring together experimental biologists, population geneticists, and physicists, to discuss research on the dynamics of evolving populations. We hope that the combination of exciting science, diverse approaches, and Colorado skiing will lead to new scientific insights, and a rewarding exchange of ideas.

Speakers (partial list):

Tim Cooper (University of Houston) Michael Desai (Harvard University) Maitreya Dunham (University of

Washington) Daniel Fisher (Stanford University) Philip Gerrish (University of New Mexico) Alexander Grosberg (New York University) Calin Güet (Harvard University & IST Austria) Eugene Koonin (NCBI) Christopher Marx (Harvard University) Alan Moses (University of Toronto) Richard Neher (UC Santa Barbara) David Nelson (Harvard University) Luca Peliti (Università di Napoli "Federico II") Estelle Pitard (Université Montpellier) Eugene Shakhnovich (Harvard University) Daniel Weinreich (Brown University)

Organizers:

Edo Kussell (New York University) Michael Lässig (University of Cologne) Mark Siegal (New York University)

Several conference talks will be invited from submitted abstracts. Applications to attend are now being accepted, through October 31st, at www.aspenphys.org We encourage you to share this information with your students, post- docs, and colleagues.

mark.siegal@nyu.edu mark.siegal@nyu.edu

Dahlonega Georgia SEPEEG Oct16-18

Subject: 2009 SEPEEG Conference in Dahlonega, GA - three days to register!

Text: The 2009 SouthEastern Population Ecology and Evolutionary Genetics (SEPEEG) meeting will take place October 16th - 18th at the beautiful Wahsega 4H Center near Dahlonega, GA (http://www.georgia4h.org/public/ facilities/wahsega/default.htm). Mark your calendars! Keeping with the tradition of SEPEEG, the 2009 meeting will be informal and accommodations will be on the rustic side. Talk and poster submissions are encouraged from undergrads, grad students, post-docs, and faculty. The keynote speaker will be Les Real from the Emory University.

Early registration is now open through October 2nd on our official conference website: http://www.sepeeg.com/, and the low registration fee of $130 can be paid using PayPal.

The meeting organizers are Nicole Gerardo and Todd Schlenke, and the Emory University PBEE Program. Please contact any of us with questions at sepeeg2009@gmail.com. We hope to see you there! Todd

Todd Schlenke Department of Biology Emory University Atlanta, GA 30322 phone: 404-727-0817 fax: 404-727-2880

Todd Schlenke <tschlen@emory.edu>

GeorgiaTech Bioinformatics Nov12-14 2

Call for Paper Abstracts is extened

Dear Colleagues

The 7th Georgia Tech - ORNL Conference on Bioinformatics - In silico Biology: Genome Biology and Bioinformatics will be held in Atlanta, Georgia, November 12-14, 2009 http://www2.isye.gatech.edu/binf2009/ Georgia Tech continues the tradition of organizing biennial International Conference on Bioinformatics, bringing together leading researchers in genomics, bioinformatics and genome biology to present recent advances in the field and to discuss open problems.

Important Dates

Deadline for poster abstract subsmission: October 11, 2009 Notification of acceptance of abstracts: October 20, 2009 Deadline for early registration: October 23, 2009

We invite papers submissions in the following areas * genomics * transcriptomics * proteomics * reconstruction and modeling of gene networks * evolutionary biology

SPEAKERS

Margaret O. Dayhoff lecture:

David Lipman, NCBI/NIH, Bethesda, MD, USA

Plenary Speakers:

Vineet Bafna, University of California at San Diego, USA Gill Bejerano, Stanford University, Stanford, CA, USA Jeffrey Bennetzen, University of Georgia, Athens, GA, USA Mark Borodovsky, Georgia Tech and Emory University, Atlanta, GA, USA Nick Grishin, University of Texas, Dallas, TX, USA Curtis Huttenhower, Harvard University, Boston, MA, USA King Jordan, Georgia Tech, Atlanta, GA, USA Igor Jouline (Zhulin), University of Tennessee - ORNL, Oak Ridge, TN, USA Eugene Koonin, NCBI/NIH, Bethesda, MD, USA Nikos Kyrpides, DOE Joint Genome Institute, Walnut Creek, CA, USA Boris Lenhard, University of Bergen, Norway Jian Ma, University of Illinois at Urbana Champaign, Urbana, IL, USA Yael Mandel-Gutfreund, Technion, Israel Insitute of Technology, Haifa, Israel Joanna Masel, University of Arizona, Tucson, AZ, USA Andrey Mironov, Moscow State University, Russia Andrei Osterman, Burnham Institute for Medical Research, La Jolla, CA USA Karen Nelson, J. Craig Venter Institute, Rockville, MD, USA Natasa Przulj, Imperial College London, UK John Reinitz, State Uiversity of New York at Stony Brook, NY, USA Pierre Rouze, Gent University, Gent, Belgium

CONFERENCE CHAIRS Mark Borodovsky, Georgia Tech and Emory University Eva K. Lee, Georgia Tech and Emory University

PROGRAM COMMITTEE Nicholas Bergman, Georgia Tech Dmitrij Frishman, Technische Universitaet Muenchen, Germany Andrey Gorin, Oak Ridge National Laboratory Andrzej M. Kierzek, University of Surrey, UK. Eileen Kraemer, University of Georgia Jun Liu, Harvard University Hannah Margalit, Hebrew University Andrey Rzhetsky, University of Chicago Andre Rogatko, Samuel Oschin Comprehensive Cancer Institute Gary Stormo, Washington University Lance Waller, Emory University Ying Xu, University of Georgia and Oak Ridge National Laboratory Soojin Yi, Georgia Tech Igor Zhulin, Oak Ridge National Laboratory and University of Tennessee

ADMINISTRATION Harry Sharp, Georgia Tech

CONFERENCE LOCATION

The Georgia Tech Ferst Center for the Arts.

Georgia Tech Conference Announcement <conf@topaz.gatech.edu>

GeorgiaTech GenomeBiologyBioinformatics Nov12-14

Dear Colleagues,

The 7th Georgia Tech - ORNL Conference - "Genome Biology and Bioinformatics" to be held on November 12-14, 2009 is now less than a month away: http://www2.isye.gatech.edu/binf2009/ The program of the conference features talks of many leading experts in the field http://www2.isye.gatech.edu/binf2009/speakers_2009.php Thanks to financial support from a larger group of sponsors we are happy to announce that the registration fee is reduced to:

$20 student/postdoc $50 - academic $100 - industry

Deadline for poster abstract submission is extended to November 1

We hope to see you soon in the Georgia Tech Ferst Center for the Arts

Invited Speakers

Margaret O. Dayhoff Lecture David Lipman, NCBI/NIH, Bethesda, MD, USA Margaret Dayhoff and Molecular Evolution in the 21st Century

Vineet Bafna, University of California at San Diego, USA Proteogenomics

Gill Bejerano, Stanford University, Stanford, CA, USA Genomics and the Evolution of Human-Specific Traits

Jeffrey Bennetzen, University of Georgia, Athens, GA, USA The Hyperevolution of Artifacts and Realities in the Structure and Function of Higher Plant Genomes

Mark Borodovsky, Georgia Tech and Emory University, Atlanta, GA, USA Gene Finding in the Era of Next Generation Sequencing

Nick Grishin, Howard Hughes Medical Institute, University of Texas, Dallas, TX, USA Evolutionary Classification of Protein Structures

Curtis Huttenhower, Harvard University, Boston, MA, USA Large Scale Genomic Data Mining

King Jordan, Georgia Tech, Atlanta, GA, USA MIR Elements Provide Chromatin Boundaries to the Human Genome

Igor Jouline, University of Tennessee - Oak Ridge National Laboratory, Oak Ridge, TN, USA Molecular Evolution of a Complex Signal Transduction System in Prokaryotes

Eugene Koonin, NCBI/NIH, Bethesda, MD, USA Systems Biology and the Prospects of a Post-Modern Evolutionary Synthesis

Nikos Kyrpides, DOE Joint Genome Institute, Walnut Creek, CA, USA The Future of Microbial Genomics

Boris Lenhard, University of Bergen, Norway Long-, Short- and Mid-Range Gene Regulation: Lessons from Genome-Wide Patterns of Sequence Conservation and Transcription Factor Binding

Jian Ma, University of Illinois at Urbana Champaign, Urbana, IL, USA Unraveling the Ancestral Mammalian Genome Yields Insights into the Human Genome

Yael Mandel-Gutfreund, Technion, Israel Institute of

Technology, Haifa, Israel Deciphering the Role of Alternative Splicing in Modulating the Human Gene Regulatory Network

Joanna Masel, University of Arizona, Tucson, AZ, USA The Origin of New Coding Sequences

Andrey Mironov, Moscow State University, Russia Conserved Intronic RNA Secondary Structures

Karen Nelson, J. Craig Venter Institute, Rockville, MD, USA Studies of The Human Microbiome

Andrei Osterman, Burnham Institute for Medical Research, La Jolla, CA USA Integrated Genomic Reconstruction of Metabolic and Regulatory Networks in Bacteria

Natasa Przulj, Imperial College London, UK >From Network Topology to Biological Function and Disease

John Reinitz, State University of New York at Stony Brook, NY, USA When Two Plus Two Doesn't Equal Four: Modeling Non-Modular Enhancer Behavior in the Eve Promoter

Pierre Rouze, Gent University, Gent, Belgium >From Protists to Plants, Fungi and Animals: Eukaryote Genomes Are Not Born Equal

This email was sent to brian@helix.biology.mcmaster.ca. You can instantly unsubscribe from these emails by clicking the link below: http://institutebioengineeringbiosciences.createsend5.com/t/r/u/hjljv/jltkkljtd/ Megan McDevitt <mcdevitt@ibb.gatech.edu>

Ghent Belgium AlgalGenomics Apr7-9

The 3rd /Ectocarpus/ meeting â âA decade of algal genomicsâ will be held in Ghent (Belgium), **April 7-9, 2010.

The meeting marks the release of the assembled /Ectocarpus/ genome, the first genome of a complex multicellular alga and the publication of the accompanying paper(s). Previous meetings have served as a forum for researchers working on /Ectocarpus/ or by extension brown algae and diatoms to present their ongoing research. For the upcoming meeting we are broadening up the perspective by inviting leading scientists who have gone through the process of assembling and annotating genomes and are now in the phase of using these data to address specific research questions.

Sessions will include presentations providing an overview and update of - organism and cell biology of algal model organisms - environmental genomics - comparative genomics - systematics / phylogenomics

Confirmed speakers include: - Yves Van de Peer - Pierre RouzÃ© - Chris Bowler - Gareth Pearson

More information and a preliminary programme are available at http://www.phycology.ugent.be/ectocarpus/ Opening of the registration is scheduled for mid-November.

With kind regards,

Olivier De Clerck & Mark Cock

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/

Hinxton CelegansEvolution Jun5-8

Greetings!

In 2010 those working on evolutionary aspects of Caenorhabditis nematodes, and nematodes more broadly, will have their own topic meeting. It will happen at the Sanger Institute's Genome Campus in Hinxton (near Cambridge), UK, June 5-8.

Abstract submission deadline: Friday, April 2, 2010 Registration will begin on 7 December, 2009, and remain open until the meeting. For further details and links to registration (when available), visit this link:

https://registration.hinxton.wellcome.ac.uk/display_info.asp?id=171 Please note that only the first 100 or so applicants can be accommodated at the meeting site (others will stay in Cambridge proper).

See you Hinxton!

The Organizers:

Eric Haag (University of Maryland, College Park USA) Avril Coghlan (University College Cork, Ireland) Ralf Sommer (Max Plank Institute for Developmental Biology, Germany)

˜ ˜ ˜ ˜ ˜ ˜ ˜˜ ˜ ˜ Eric S. Haag, Ph.D. ˜ Associate Professor, Department of Biology ˜˜ ˜ Director, BEES Concentration Area, BISI Graduate Program ˜ 0256 Biology/Psychology Building ˜ ˜ University of Maryland ˜ ˜˜ ˜ College Park, MD 20742 ˜ ˜ ˜ ehaag@umd.edu ˜ ˜ ˜ phone: (301) 405-8534 fax: (301) 314-9358 http://www.life.umd.edu/-biology/faculty/haag/index.html "I'd rather be here now."

Eric Haag <ehaag@umd.edu>

KansasCity Genomics Nov13-15 4

ECOLOGICAL GENOMICS SYMPOSIUM, Kansas City, 11/13-15/2009

Deadline to Register at Early-Bird Rates: Tuesday, 10/13/09

Deadline to submit Poster Abstract for oral presentation consideration: Tuesday, 10/13/09

Deadline to reserve hotel room within room block: Friday, 10/23/09

REGISTRATION: After October 13, we will continue to welcome your registration to attend the 7th Annual "Genes in Ecology, Ecology in Genes" Symposium at a slightly higher cost.

POSTER ABSTRACTS: Please note that if you wish to have your poster abstract considered for an oral presentation, the deadline for submission is Tuesday, October 13. Abstract submission guidelines for submitting your poster abstract are available at:

www.ecogen.k-state.edu/symp2009 . Poster sessions will be held on Friday night and Saturday afternoon. Poster topics should be related to the field of Ecological Genomics. A limited number of submitted poster abstracts will be selected for oral presentations.

PLENARY SPEAKER:

Jonathan F. Wendel, Iowa State University, "Genes, jeans, and genomes: Exploring the mysteries of polyploidy in cotton"

FEATURED SPEAKERS:

+Andres Aguilar, University of California-Merced, "Genomic differentiation and adaptive divergence in rockfish (genus Sebastes)"

+May R. Berenbaum, University of Illinois at Urbana-Champaign, "Cytochrome P450 genes in plant-insect interactions: War and peace?"

+Jeffrey L. Feder, University of Notre Dame, "Sympatric speciation in Rhagoletis: Islands of speciation or genomic continents of divergence?"

+David C. Queller, Rice University, "The selfish gene at the genetic level: Cooperation and cheating in social amoebas"

+Matthew Rockman, New York University, "Causes of heritable variation in C. elegans"

+Erica Bree Rosenblum, University of Idaho, "The genetics of adaptation: Investigating the functional basis of phenotypic convergence"

+Jay F. Storz, University of Nebraska, "Genetics of high altitude adaptation in vertebrates"

+Chris Toomajian, Kansas State University, "Flowering-time genes as genomic targets of selection in Arabidopsis thaliana"

+Michael J. Wade, Indiana University, "The evolutionary genetics of spatially and temporally plastic phenotypes"

SYMPOSIUM SCHEDULE: The Ecological Genomics Symposium will convene in the historic Muehlebach/Marriott Hotel in downtown Kansas City Friday evening at 6:00 p.m. and conclude on Sunday at noon. For a complete schedule, please visit our Symposium website, http://ecogen.ksu.edu/symp2009.

DEADLINES:

10/13/09 Registration deadline at early bird rates.

10/13/09 Poster Abstracts are due for oral presentation consideration.

10/23/09 Hotel Rooms must be reserved to receive reduced group rate.

10/31/09 Poster Abstracts are due if NOT being considered for oral presentation.

SPONSORS:

Kansas State University Targeted Excellence

National Science Foundation

JMP Genomics

INFORMATION will be posted on our website, ecogen.ksu.edu/symp2009, as details are finalized.

We have an outstanding lineup of speakers for the 2009 Symposium and we encourage you to attend! Please share this announcement with colleagues and students. If you have questions, please contact us at (785) 532-3482 or dmerrill@ksu.edu.

Symposium Organizing Committee:

Michael Herman, Co-Chair, Biology

Loretta Johnson, Co-Chair, Biology

Ted Morgan, Biology

Tim Todd, Plant Pathology

Kun Yan Zhu, Entomology

Lindsey Fallis, Graduate Student Rep, Biology

Doris R. Merrill, dmerrill@k-state.edu

Program Coordinator, Kansas State University

ECOLOGICAL GENOMICS INSTITUTE

Kansas State University

Biology, 104 Ackert Hall

Manhattan, KS 66506-4901

(785) 532-3482, < http://www.ecogen.ksu.edu/ > ecogen.ksu.edu

Doris Merrill <dmerrill@ksu.edu>

KansasCity Genomics Nov13-15 CallAbstracts

ECOLOGICAL GENOMICS SYMPOSIUM, Kansas City, November 13 to 15, 2009

www.ecogen.ksu.edu/symp2009

Hotel Room Block Reservation Deadline is Friday, October 23.

Abstract Deadline for posters is Saturday, October 31.

It's not too late. You can still register to attend and submit a poster abstract for presentation at the:

7th ANNUAL ECOLOGICAL GENOMICS SYMPOSIUM

November 13 to 15, 2009

Kansas City, Downtown Marriott Hotel

www.ecogen.ksu.edu/symp2009

HOTEL RESERVATIONS: The Muehlebach/Marriott Hotel in downtown Kansas City has reserved a block of rooms for symposium participants at a discounted rate. Call 1-800-810-0850 on or before Friday, October 23, or book online at http://ecogen.ksu.edu/symp2009/-hotel.html .

POSTER ABSTRACTS: Abstract submission guidelines for submitting your poster abstract are available at:

http://ecogen.ksu.edu/downloads/-AbstractGuidelines.pdf. Poster sessions will be held on Friday night and Saturday afternoon. Poster topics should be related to the field of Ecological Genomics.

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Symposium Organizing Committee:

Michael Herman, Co-Chair, Biology Loretta Johnson, Co-Chair, Biology Ted Morgan, Biology Tim Todd, Plant Pathology Kun Yan Zhu, Entomology Lindsey Fallis, Graduate Student Rep, Biology

Doris R. Merrill, dmerrill@k-state.edu Program Coordinator ECOLOGICAL GENOMICS INSTITUTE Kansas State University Biology, 104 Ackert Hall Manhattan, KS 66506-4901 (785) 532-3482, www.ecogen.ksu.edu < http://www.ecogen.ksu.edu/ >

dmerrill@ksu.edu dmerrill@ksu.edu

Lyon SMBE Jul4-8 CallSymposia

SMBE 2010 - call for external symposia

The call for external symposia is now open. If you are interested in organising an external symposium for the SMBE 2010 conference, please e-mail a proposal before December 18th, 2009 to smbe2010symposia@biomserv.univ-lyon1.fr

The conference will be held in Lyon, France July 4-8, 2010. See http://smbe2010.univ-lyon1.fr for the latest information.

The proposal (1 page maximum) must include: Symposium title Organisers names Names of 2-3 invited speakers Abstract

We suggest you to pick a title making a trade off between reminding the latest hot questions and federating the sub-community that each symposium represents. Note that one of the organisers can be invited speaker. State in the proposal whether speakers are confirmed or not. Invited speakers will not pay registration fees and will be offered the gala dinner. Travel and accomodation expenses may be partly reimbursed depending on the meeting income. The abstract should be a brief description of the symposium, including a justification of your invited speakers.

The scientific committee will select about 14 external symposia. To avoid redundancy in the scientific program, we will favour those that complement the locally developed symposia listed below.

With best regards,

On behalf of the SMBE Scientific Committee,

Gabriel Marais and Manolo Gouy

Local symposia:

Recombination and genome evolution (L. Duret, M. Webster) Evolutionary genomics of prokaryotes (E. Rocha, E. Feil) Plant ecological genomics (S. Glemin, X. Vekemans) Mathematical and computational phylogenetics (O. Gascuel, S. Guindon) Integrative phylogenomics: from genes to organisms history (V. Daubin, B. Boussau) Patterns of gene and genome duplication in eukaryotic genomes (F. Brunet, M. Semon, A. McLysaght) Species life-history traits and molecular evolution (N. Galtier, A. Eyre-Walker) Evolution of molecular networks (M-F. Sagot, V. Lacroix, B. Teusink) Modular evolution of biological molecules and systems (D. Kahn, E. Bornberg-Bauer) Genome, evolution and development (V. Laudet, M. Robinson-Rechavi) Cooperation and conflict: a molecular perspective (S. Charlat, F. Jiggins) Phylogeny and evolution of prokaryotes (G. Perriere, C. Brochier) The impact of transposable elements on genome evolution (E. Lerat, C. Vieira) Next generation ancient DNA: genomic clues about the past (C. Hanni, L. Orlando, T. Gilbert)

http://smbe2010.univ-lyon1.fr mgouy@biomserv.univ-lyon1.fr mgouy@biomserv.univ-lyon1.fr

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Marseilles 14thEvolutionaryBiol 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, Marseilles, France.

The following subjects will be discussed:

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

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

Pierre Antoine Pontarotti

Directeur de Recherche CNRS

UMR 6632 Université de Aix Marseille/CNRS Equipe Evolution biologique et Modélisation case 19 3 place Victor Hugo 13331 Marseille Cedex 03 France Tel: 33491106489

we are organizing the 14th Evolutionary Biology Meeting at Marseilles http://sites.univ-provence.fr/evol-cgr/ Egee@univ-provence.fr

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MexicoCity BarcodeOfLife Nov7-12 CorrectedDates

Dear Colleagues:

Two important dates were incorrect in the update newsletter we sent yesterday (highlighted in red below). Please note that online registration for the barcode conference closes next Friday, 30 OCTOBER, and reservations for multi-day excursions must be made two weeks prior to the tour. The deadline for the first multi-day excursion is Friday, 23 OCTOBER.

My apologies for these errors.

[cid:image001.jpg@01CA5265.7815CE70]< http://dnabarcodes2009.org/ >

Third International Barcode of Life Conference Updates Newsletter 5 (22 October 2009)

Conference Website: http://dnabarcodes2009.org Registration Deadline Approaching

Online registration for the Third International Barcode of Life Conference will close at midnight CST on Friday, 30 October. If you have not registered by then, you will have to register on-site, either at UNAM during the pre-conference workshops or at the conference at the Mexican Academy of Sciences. Information about on-site registration will be posted at the conference website.< http://dnabarcodes2009.org > The conference fee for onsite registration will be: * US$300 for delegates, * US$175 for delegates from developing countries, and * US$100 for students

The registration fee entitles you to: * Admission to all the pre-conference workshops and conference sessions; * Lunches and coffee breaks during the pre-conference workshops and conference meetings * Bus transportation between the two conference hotels and the pre-conference and conference venues; * Admission to the opening reception on Monday evening, 9 November 2009; * Admission to the closing banquet on Wednesday evening, 11 November 2009; * Bus transportation to the opening reception and closing banquet with return to the two conference hotels; and * Copies of the conference documents.

We need your input!

Have you ever arrived at a workshop or seminar and found that the organizers picked a room that was too small, and there was no room for you (or that you had to stand through the whole thing)? We want to be sure that this doesn't happen to any of you at the barcode conference.

Please take a few minutes to complete an online survey<http://www.surveymonkey.com/s.aspx?sm=SH_2fe00BQpYhMD_2bQ2_2f88qFw_3d_3d> that will help us make sure that everyone will have room in the sessions they want to attend. It's also a great way to organize your plan for participating in the conference! You'll be asked to look through the agenda for the pre- conference workshops and the afternoon technical sessions during the conference, and mark the ones you plan to attend.

Thanks in advance for helping us make sure that there will be room for you in the sessions you want to attend.

Sign up for Tours

The conference organizers have assembled information on half- and full- day tours in and around Mexico City, and multi-day excursions in Mexico (see Tour Information< http://dnabarcodes2009.org/sidetours.html >). If you are interested in one of the multi-day excursions, you must sign up two weeks in advance!

The first of these tours begins on Friday, 6 November so you must sign up by Friday, 23 OCTOBER. Don't miss these opportunities to see some of Mexico beyond the hotel and conference venues!

[cid:image002.jpg@01CA5265.7815CE70]

The opening reception will be housed at the beautiful Ex Hacienda de Tlalpan. Be sure to keep an eye out for their exotic white peacocks.

Opening Reception

The official start of the Third International Barcode of Life Conference will be an opening reception on Monday, 9 November 2009 at 7:30pm. Buses will take conference registrants from the pre-conference workshops at UNAM and from the two conference hotels to the Ex Hacienda de Tlalpan< http://www.antiguahaciendatlalpan.com.mx/Ingles.aspx >, a historic country estate on the southern outskirts of Mexico City. Bus schedules will be posted on the conference website< http://dnabarcodes2009.org > and in the Conference Program which will be released online on 2 November 2009.

Conference Website: http://dnabarcodes2009.org schindeld@si.edu

MexicoCity BarcodeOfLife Nov7-12 LastDay

Last Day for Conference Registration

The online system for advance registration (https://secure37.softcomca.com/servimed_com_mx/bol09/registration.htm) to the Third International Barcode of Life Conference (www.dnabarcodes2009.org) will close at midnight CST on Friday, 30 October 2009. After that, people wishing to attend the conference will have to register on-site. The conference fee for onsite registration will be:

* US$300 for delegates, * US$175 for delegates from developing countries, and * US$100 for students

The registration fee entitles you to:

* Admission to all the pre-conference workshops and conference sessions; * Lunches and coffee breaks during the pre-conference workshops and conference meetings * Bus transportation between the two conference hotels and the pre-conference and conference venues; * Admission to the opening reception on Monday evening, 9 November 2009; * Admission to the closing banquet on Wednesday evening, 11 November 2009; * Bus transportation to the opening reception and closing banquet with return to the two conference hotels; and * Copies of the conference documents.

Final Travel Information

All conference registrants will be receiving an information packet by e-mail during the week of 2-6 November. This will include information on how to get from the airport to the hotel and from the hotel to the meeting venues. This information will also be posted on the conference website (www.dnabarcodes2009.org).

Accompanying Persons

Registrants are welcome to bring traveling companions to the conference's opening reception (Monday evening, 9 November) and closing banquet (Wednesday evening, 11 November) for a fee of US$100. Tickets can be purchased at the registration desk during the pre-conference workshops and the conference.

David E. Schindel, Executive Secretary

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

Office and overnight delivery address:

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

Postal mailing address:

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

"Schindel, David" <schindeld@si.edu>

Montpellier Evolution of dispersal Jun13-18

Dear all,

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

We propose a symposium entitled "Evolution of dispersal". Dispersal is a ubiquitous trait in living organisms. In plants, adaptations to dispersal are highly diversified, from passive dispersal of seeds to active seed dispersal involving highly complex chemical or visual signals designed to attract dispersing agents. Despite the great diversity of adaptations, only a few selection pressures favor the evolution of dispersal. The cost of dispersal structures or the increased mortality risk that organisms face during the dispersal phase select against dispersal. In contrast, competition between relatives or temporal variability of the environment generally favors dispersal. Since the recent development of tools in population biology (molecular markers, methods for analyzing demographic data, etc), it is now possible to better characterize the features of dispersal and to infer the drivers of its evolution. Variations in selective pressures arising from global changes, such as habitat fragmentation or the spread of a new species in a new geographic area provide exciting opportunities for studying the evolution of dispersal in a context where ecological and evolutionary drivers are more easily identified. Our symposium aims at presenting the state of the art in this topic in order to discuss emergent research themes based on both theoretical and experimental studies.

Further information is available at http://www.fsd2010.org and by contacting the organizers (Pierre-Olivier Cheptou (CNRS-CEFE) : pierre-olivier.cheptou@cefe.cnrs.fr, Hélène Fréville (MNHN, CNRS-CEFE) : helene.freville@cefe.cnrs.fr, Isabelle Olivieri (ISEM) : Isabelle.Olivieri@univ-montp2.fr)

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

freville@mnhn.fr

NHM London AncientDNAandEvolution Oct14

CEE Symposium

Ancient DNA and Evolution

14 October 2009 10:30am - 5:30pm Venue: Flett Lecture Theatre, Natural History Museum, London

Organisers: Ian Barnes (RHUL) & Adrian Lister (NHM)

All welcome. No booking required

For further information, email ian.barnes@rhul.ac.uk

Symposium poster Abstracts How to get to the Flett Theatre

Invited speakers

Robin Allaby (University of Warwick) Cia Anderung (Natural History Museum, London) Mim Bower (University of Cambridge) Matthew Collins (University of York) Love Dalén (Naturhistoriska riksmuseet, Stockholm) Tom Gilbert (Statens Naturhistoriskemuseum, Copenhagen) Michael Hofreiter (University of York) Greger Larsen (University of Durham) Adam Powell (University College London)

Programme details and talk abstracts to follow.

Sponsored by the CEE, the Natural History Museum and Synthesys

Last updated on 30 September 2009

Dr Amber Teacher School of Biological Sciences Royal Holloway, University of London Egham, TW20 0EX Tel: +44 (0)1784 443769 Email: amber.teacher@rhul.ac.uk Web: http://personal.rhul.ac.uk/utba/323 Amber Teacher <amber.teacher@rhul.ac.uk>

QueenMaryU DarwinianRenaissance Nov13

Please find below details of a one-day symposium titled "The Darwinian Renaissance in the Humanities and Social Sciences", which will be held at Queen Mary University of London on Friday 13th November 2009 (9.30am - 5pm followed by wine reception).

Speakers and talk titles: Alex Bentley (University of Durham): "Social influence and drift in collective behaviour"

Mhairi Gibson (University of Bristol): "Applying Darwin to contemporary world issues"

Dominic Johnson (University of Edinburgh): "Darwinian Security: Evolutionary Lessons for the 21st Century"

Stephen Lycett (University of Kent at Canterbury): "Most beautiful and most wonderful": those endless stone tool forms

Alex Mesoudi (Queen Mary University of London): "Towards a unified science of cultural evolution"

Daniel Nettle (Newcastle University): "Darwin, Tinbergen and behavioural science: The enduring value of the evolutionary perspective"

Ian Penton-Voak (University of Bristol): TBA

Rebecca Sear (London School of Economics and Political Science): "Darwin and Malthus reunited: the growth of biological thought in demography"

We would be grateful if you could forward these details to potentially interested colleagues/postgraduates.

https://eshop.qmul.ac.uk/events/-eventdetails.asp?eventidS The website is available for registration (special reduced rates for EHBEA and Galton Institute members).

Please book soon as the symposium is limited to 100 participants.

Best regards,

Qazi Rahman

Tom Dickins

Dr Qazi Rahman, Lecturer [Assistant Professor] in Cognitive Biology, Director of Psychology Programmes (Natural Sciences),

Biological & Experimental Psychology Group, School of Biological and Chemical Sciences, Queen Mary University of London, Mile End Road, London E1 4NS. United Kingdom.

Alan McElligott <amcellig1@yahoo.ie>

QueenMaryU LanguageEvolution Feb26

Symposium "Integrating Genetic and Cultural Approaches to Language" at Queen Mary University of London. Date: Friday, 26th February 2010

Description: This symposium will ask how the diverse and complex languages of today evolved from a non-linguistic ancestral state, encompassing both genetic evolution (of the language faculty) and cultural evolution (of languages themselves). Topics to be addressed include comparative studies of vocal communication in birds, ungulates and primates, the genetic and neurobiological basis of human speech and language, cognitive influences on language evolution, and phylogenetic analyses of language history.

http://sites.google.com/site/cee2010symposium/ The website is now online for registration and/or poster abstract submission and/or hotel accomodation booking in nearby Stratford (special reduced rate).

The symposium has generated a lot of interest so we strongly advise early booking - the symposium is limited to 100 participants.

Best regards,

Alan McElligott Alex Mesoudi

School of Biological and Chemical Sciences Queen Mary University of London

CEE 2010 Symposium - Integrating Genetic and Cultural Approaches to Language

Date: Friday, 26th February 2010 (9am-5pm)

Location: The Octagon, Queen Mary University of London

Speakers and talk titles:

Tecumseh Fitch, University of Vienna - Language Evolution: Testing the Hypotheses with Comparative and Genetic Data

Simon Fisher, University of Oxford - Molecular windows into speech and language

Chris Petkov, University of Newcastle - Communication and the primate brain: Insights from comparing the neuroimaging evidence in humans, chimpanzees and macaques

Gabriel Beckers, Max Planck Institute for Ornithology - Mechanisms of bird vocal production, perception and learning: a comparison to speech and language.

Katie Slocombe, University of York - Primate vocal communication: links to human language?

Mark Pagel, Reading University - Language as a Culturally Transmitted Replicator

Kenny Smith, Northumbria University - Language evolution in the lab

Fiona Jordan, Max Planck Institute for Psycholinguistics - Kinship terminology and the evolution of semantic systems

Nick Chater, University College London - Cultural Evolution and Language Acquisition

Dan Dediu, Max Planck Institute for Psycholinguistics - Are languages really independent from genes? If not, what would a genetic bias affecting language diversity look like?

http://sites.google.com/site/cee2010symposium/ Symposium support: The Centre for Ecology and Evolution The Galton Institute The Genetics Society School of Biological and Chemical Sciences, QMUL Department of Linguistics, QMUL

Send instant messages to your online friends http://uk.messenger.yahoo.com Alan McElligott <amcellig1@yahoo.ie>

Trondheim SustainableConservation

The conference Sustainable Conservation: Bridging the gap between disciplines is arranged by Centre for Conservation Biology (CCB) at the Norwegian University for Science and Technology (NTNU) and is part of the 250th Anniversary of the Royal Norwegian Society of Sciences and Letters.

The aim of the conference will be to present and discuss the scientific basis for a sustainable conservation of natural resources, in particular focusing on the process of extinction. A central goal for the conference will be to identify common principles for a sustainable management that also can ensure conservation.

Organizers: Prof. Bernt-Erik Saether and prof. Gunilla Rosenqvist, CCB, NTNU

Speakers: S. R. Beissinger, H. Caswell, K. Danell, J. M. Drake, S.P. Ellner, S. Engen, W. F. Fagan, J.M Fryxell, I. Hanski, S.P. Hubbell, P. Kareiva, R. Lande, G. Mace, S Pimm, H. Possingham, J. Reid, W.J. Sutherland, D. Tilman, H. Weimerskirch

Submissions of contributed talk are welcomed. For further information and registration see: http://www.biodivconf.ccb2010.no/ – Professor Gunilla Rosenqvist

Department of Biology Norwegian University of Science and Technology N-7491 Trondheim Phone: +47 73596296 Norway FAX: +47 73596100 Mobil: +47 91897147 e-mail: gunilla.rosenqvist@bio.ntnu.no

Gunilla Rosenqvist <gunilla.rosenqvist@bio.ntnu.no>

UCaliforniaBerkeley WesternEvolBiol Dec5

I'd like to announce a regional meeting, the 3rd annual WEB (Western Evolutionary Biologists) Meeting. This year it will be held at UC-Berkeley on Saturday Dec. 5. The UC organization NERE funds the meeting. Each UC campus has some travel funds available for NERE members, for more information contact the NERE Associate Director at your UC campus (see website below for details).

If you'd like to give a (15-20 min) talk or poster, note the deadline for abstract submission is not too long from now (Oct 16). The registration deadline is Oct. 29.

The WEB web site and registration is here: http://www.lifesci.ucsb.edu/nere-web/ -

Todd H. Oakley Professor Ecology Evolution and Marine Biology University of California-Santa Barbara Santa Barbara, CA 93106 (805) 893-4715 http://www.lifesci.ucsb.edu/eemb/labs/oakley/ oakley@lifesci.ucsb.edu oakley@lifesci.ucsb.edu

UCaliforniaIrvine DarwinColloquium Dec10-12

December 10-12, 2009 In the Light of Evolution IV: The Human Condition Organizers: John C. Avise and Francisco J. Ayala Beckman Center of the National Academies, Irvine, CA

The year of Darwinian celebration will close with a Sackler Colloquium devoted expressly to human evolution. Darwin addressed the topic at length in “The Descent of Man and Selection in Relation to Sex” (1871). Much has been learned since then, not least from the evidence of paleontology, comparative vertebrate biology, and comparative genomics. This Sackler Colloquium will bring together leading biologists with special expertise about human evolution, both biological and cultural. A preliminary program can be viewed at http://www.nasonline.org/SACKLER_Human_Condition $300 EARLY REGISTRATION BY NOVEMBER 15, 2009 Attendance at the Colloquium is limited to 230 registered individuals. Registrations will be accepted only when the registration fee is included and in the order in which they are received. The EARLY registration fee ($300) includes the cost of meals, reception, and banquet.

$150 STUDENT / POST DOC REGISTRATION BY NOVEMBER 15, 2009 - TRAVEL/HOTEL AWARDS AVAILABLE A reduced all-inclusive (meals, reception, and banquet) registration fee of $150 is offered to Graduate Students and Postdocs who register by November 15, 2009. The NAS has provided funds to supplement the expenses of participating graduate students and postdocs up to $125 for hotel costs and up to $150 for air travel (see award qualification details on the registration page). Awards will be approved on a first come basis when accompanied by the registration fee. Reimbursements will be paid after the Colloquium, upon documentation of qualifying expenses.

After November 15, 2009 - All Registrations are $350

Register at http://www.nasonline.org/SACKLER_Human_Condition "Francisco J. Ayala" <fjayala@uci.edu>

UEdinburgh PathogenEvolution Dec8

The following one-day symposium may be of interest to evoldir subscribers. Registration is free, but we do ask that people register so we have an idea of numbers (see: http://ciie.bio.ed.ac.uk/). Lunch will be provided.

What limits pathogen host range?

Tuesday, December 8th, 2009 University of Edinburgh Ashworth Laboratories, Lecture Theatre III Kings Buildings West Mains Road, Edinburgh

Hosted by the Centre for Immunity, Infection, and Evolution (http://ciie.bio.ed.ac.uk/)

Organisers: Amy Pedersen (amy.pedersen@ed.ac.uk) & Tom Little (tom.little@ed.ac.uk)

This is a one-day symposium of The Centre for Immunity, Infection and Evolution (CIIE), a Wellcome Trust-funded initiative designed to connect Evolutionary Biology to Immunology and Infection research and gain an interdisciplinary perspective on challenges to global health.

The central question what limits host range? i.e. what are the molecular and ecological constraints that determine why some pathogens are specific to a single host, while others can infect many hosts, is a key concern as host shifts and disease emergence threaten human and wildlife health. In this symposium, we have a broad programme of speakers, ranging from molecular epidemiologists to disease ecologists, and working on systems such as avian flu to fungal pathogens of plants.

Confirmed Speakers Debbie Smith (York University) Amy Pedersen (University of Edinburgh) Michael Hood (Amherst College, USA) Dan Haydon (University of Glasgow) Mike Brockhurst (University of Liverpool) Roman Biek (University of Glasgow) James Cook (University of Reading) Heather Ferguson (University of Glasgow) Paul Sharp (University of Edinburgh)

Registration at: http://ciie.bio.ed.ac.uk/ 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/littlelab – The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

tom little <tom.little@ed.ac.uk>

ULausanne EvolutionMedicine Nov5-6

Dear Colleagues,

let me bring your your attention a symposium on the implications of evolutionary biology for medicine and public health issues ("Evolution & Medicine"), which takes place in Lausanne (Switzerland) on November 5-6, 2009. The speakers include Randolph Nesse, Steve Stearns, Ruth Mace, Dieter Ebert, Andrew Read, Paul Sharp, Rudi Westendorp, Francois Taddei, Wayne Potts and Carlo Maley, and the topics range from reproduction to aging, from infectious disease to cancer.

For the program and registration, go to www.unil.ch/evolmed2009/page67844.html There is no registration fee, but please do register until October 25 so that we know how many participants to expect.

Sincerely, Tad Kawecki

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lausanne, Switzerland

tadeusz.kawecki@unil.ch

ULeuven DaphniaGenomics Mar26-30

First announcement of the Daphnia Genomics Consortium (DGC) Meeting 2010

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

http://bio.kuleuven.be/DGCmeeting2010.html . Dear colleagues and friends,

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

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

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

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

The meeting will have plenary lectures from keynote speakers in several research fields related to Daphnia and other organisms, and will offer young investigators the chance to discuss their research with more experienced senior researchers in a relaxed atmosphere.

Our meeting is organized as a series of symposia touching on several research topics:

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

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

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

Registration begins on November 15, 2009 Abstracts for poster and platform presentations are due by January 15, 2010.

Details for registration will be sent with the second announcement and at the following web-page:

http://bio.kuleuven.be/DGCmeeting2010.html . We look forward to welcoming you in Leuven

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

Luisa Orsini <Luisa.Orsini@bio.kuleuven.be>

ULiverpool PopulationGenetics Jan5-8

The next (43rd) Population Genetics Group meeting to be held at the University of Liverpool, 5-8 January 2010. Further information on the programme and on how to register is available at http://sites.google.com/site/popgroup2010/Home . The deadline for submitting titles and abstracts for oral and poster presentations is 30th November (a £10 surcharge will be levied for all registrations after this date). You are encouraged to book accommodation early as the discounted rates that have been negotiated are guaranteed only till 5th December.

Thanks Ilik

DR ILIK J. SACCHERI School of Biological Sciences University of Liverpool The Biosciences Building Crown Street Liverpool L69 7ZB UK

Tel. 44 (0)151 795 4522 Fax. 44 (0)151 795 4408 email saccheri@liv.ac.uk

“Saccheri, Ilik” <I.J.Saccheri@liverpool.ac.uk>

UMichigan ExperimentalEvol Apr17 Call for nominations

CALL FOR NOMINATIONS

SIXTH ANNUAL UNIVERSITY OF MICHIGAN EARLY CAREER SCIENTISTS SYMPOSIUM:

EXPERIMENTAL EVOLUTION

The Department of Ecology and Evolutionary Biology at the University of Michigan invites nominations of outstanding scientists early in their careers to take part in a symposium on experimental evolution. This symposium will be held in Ann Arbor, Michigan on Saturday, April 17, 2010. Eight scientists will be selected to present their work. All research involving observation of long-term changes in controlled populations, investigating response of natural populations to experimental manipulation, or performing evolution in silico, will be favorably considered.

Early career scientists are defined as senior graduate students (who will receive their Ph.D. within one year) or postdoctoral researchers. Potential speakers can be nominated by their advisor or a senior colleague.

Nominations must include a brief letter of recommendation addressing the nominee's scientific and communication skills, a copy of the nominee's curriculum vitae, and a brief abstract of the proposed presentation (< 200 words, written by the nominee). Nominations can be sent electronically (in a single file if possible) to kuhnlein@umich.edu with the subject line: "Nominee for ECSS." More information is available at http://sitemaker.umich.edu/ecss2010 . All nominations must be received by December 15, 2009. Selected participants will be contacted by January 15, 2010.

For more information, contact Gail Kuhnlein (kuhnlein@umich.edu).

2010 ECSS organizing committee: Alex Kondrashov kondrash@umich.edu, Timothy James tyjames@umich.edu, Amanda Izzo mizzo@umich.edu, Zhi Wang zcwang@umich.edu

EEB Web site: http://www.eeb.lsa.umich.edu tyjames@umich.edu tyjames@umich.edu

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Uruguay VertebrateEvolution Jul26-31

Dear Evolutionary Biologists,

We are pleased to announce that, following the request made by some colleagues, we have extended the deadline for early registration to the 9^th International Congress of Vertebrate Morphology until November 1^st . This is a golden chance to enjoy the great pleasures of morphology in Punta del Este, Uruguay, from 26^th to 31^st July 2010, taking advantage of our really low registration fee, one of the lowest, we proudly claim, if compared with similarly sized and reputable events, at: only USD 220 for regular attendees and USD 100 for students

After that date the prices will be still quite affordable: USD 300 for regular attendees and USD 150 for students.

At the same time, we have already said that we are committed to turn this event into something unforgettable, and for that well need your kind help. Please register as soon as possible, using our web page (http://icvm-9.edu.uy/) or directly in that of Jetmar, our dependable travel agency (http://www.jetmar.com.uy/icvm2010/), and let them help you about accommodation and other details. If you have any difficulties or concerns, please write to us at once and well do our best to overcome them (send an e-mail to: fari~a@fcien.edu.uy). __

The final deadline for registration and abstract submission is February 10^th , 2010. After this date, only posters will be accepted. Once you have registered (and paid), youll be able to submit your abstract. The web page will soon be available for this.

We are pleased to inform you that the following scholars have agreed to give plenary lectures at the congress:

- Arkhat Abzhanov (Harvard University, USA)

- Melina Hale (University of Chicago, USA)

- Peter Wainwright (University of California at Davis, USA)

- Gabriel Marroig (Universidade de São Paulo, Brazil) and

- Eugenia del Pino (Pontificia Universidad Católica, Ecuador).

Please, feel free to distribute this second circular among colleagues and students.

passer@fcien.edu.uy

GradStudentPositions

Buffalo CoralAlgalOntogeny

A PhD position is available in the laboratory of Dr. Mary Alice Coffroth

Description: The PhD student will contribute to an NSF-funded project that focuses on the ontogenic change in cnidarian-algal symbioses from a genomic and ecologic perspective. The overall aim of this project is to identify the mechanisms and selective processes that lead to the final assemblage of symbionts harbored by adult hosts. Specifically, the student will participate in studies to determine (1) if different /Symbiodinium /strains differentially affect fitness of corals as the adult settles into a mature symbiosis (2) if competition among symbionts or environmental conditions contribute to the final host-symbiont pairing and (3) how host/symbiont transcriptomes varying as the symbiont community within a host is winnowed to the final assemblage found in the adult host.

The student would begin her/his studies in September

2010, but will be encouraged to join the lab over the summer and participate in coral spawning in August 2010

Candidate Experience: Candidates for this position should have a strong interest in symbiotic relationships, ecology and evolution. Qualifications specifically sought are students with a background in photophysiology and/or experience in molecular methods including knowledge of bioinformatics and microarray analysis. SCUBA certification is beneficial but not required. Periodic field trips to our study sites in Florida and/or Mexico will occur throughout the year, thus a passport is necessary.

For consideration, please send a cover letter, curriculum vitae, and a statement of research experience that explains your background and specific interests in the project to Coffroth@buffalo.edu <mailto:Coffroth@buffalo.edu>

NOTE: The selected student is expected to enroll in the Graduate Program in Evolution, Ecology and Behavior at the University at Buffalo for Fall 2010. Additional information about policies and entrance requirements pertaining to university admission are found at: http://evolutionecologybehavior.buffalo.edu/

– PLEASE NOTE NEW PHONE NUMBERS Mary Alice Coffroth, PhD Professor 447 Hochstetter Hall Department of Geology Graduate Program in Evolution, Ecology and Behavior State University of New York at Buffalo Buffalo NY 14260

Phone: 716-645-4871 716-645- 4874 Fax: 716-645-3999 Email: Coffroth@buffalo.edu Web page: http://www.nsm.buffalo.edu/Bio/burr/ Mary Alice Coffroth <coffroth@buffalo.edu>

CNRS France MolecularAdaptation

PhD position available at the LEGS (Laboratoire Evolution, genomes et spéciation), CNRS, 91198 Gif sur Yvette cedex, France.

Contact: Dr Jean-Luc Da Lage (jldl@legs.cnrs-gif.fr)

Subject: Adaptation at the molecular level: role of alpha-amylases in the adaptation of insects to their environment

Keywords: selection, adaptation, nutrition, digestion, alpha-amylase inhibitors

Duration: 3 years

The PhD position is funded by the Agence Nationale de la Recherche (ANR), and is part of the project "Adaptanthrop". The project stems from the observation that anthropization affects ecosystems by decreasing biodiversity, by changing landscapes, and also by polluting the environment with xenobiotics. When populations are confronted by environmental change, they can compensate for a decrease in their fitness in three ways: through plasticity, migration, or genetic evolution (i.e. by adapting themselves). One of the goals of the project is to investigate genes and regulation mechanisms involved in adaptive processes at the population or species level, as a response to a change in food resources. With this aim in view, we have chosen two animal models of agronomic importance currently confronted by rapid environmental changes: the stem borers Busseola in Africa; and the potato moth Tecia solanivora in the Andes (indeed, a change of host-plant is a risk for phytophagous insects). We have also chosen two models of medical importance: Triatoma and Rhodnius, both vectors of Chagas' disease in South America. In addition, we will also use populations of Drosophila melanogaster and D. simulans, which are excellent models for investigating scenarios in evolutionary genetics.

Within the framework of this thesis, we intend to study the alpha-amylase gene family. These enzymes should respond rapidly to natural selection as dictated by the environmental constraints, in order to maintain optimal performance. Alpha-amylases are ubiquitous digestive enzymes, which are responsible for the hydrolysis of starch and related polysaccharides, into maltose. They are directly linked to the external environment as they are required to act readily upon food. Furthermore, their function is simple and has been well characterized. Therefore, alpha-amylases are good models in adaptive molecular evolution, as modifications of the enzymes may be rather easily correlated to modifications of the environment. One may expect adaptation to the food substrate itself, since a variety of starches exist. Various physical and chemical parameters, related to the host plant or its environment may also exert selective pressure: pH, local temperature, etc. The possible presence of alpha-amylase inhibitors may also be a major problem, and could be a good example of coevolution. Indeed, plants often produce alpha-amylase inhibitors as a defense mechanism, preventing the development of larval pests. Insects must evolve their own amylases to circumvent this.

The PhD student will endeavour to identify evidence for the rapid evolution of alpha-amylases in insects subjected to anthropization of their environment (e.g. endemic forest vs. cultured field, or replacement of traditional crops by “exogenous” ones), likely to trigger host change or alternate manifestations of adaptation.

Two approaches will be used: i) detecting positive selection by analysis of DNA polymorphism at the Amy loci, or variations of expression level (indirect approach); and complementary to this, ii) constructs in expression vectors will be made in order to mimic the variations observed in nature, the resulting enzymes produced in vitro will be analyzed enzymologically to test the functional consequences of the variations assumed to play an adaptive role in nature (direct approach).

Skills required: Throughout the PhD, the candidate will need to develop knowledge in population genetics, and enzymology, and will use contemporary tools of molecular biology, and techniques in biochemistry. A keen interest in evolution is mandatory, as well as an enthusiasm for experimental work and analysis. Knowledge in ecology and zoology (particularly entomology) would be of a distinct advantage.

Send a detailed CV to Dr Jean-Luc Da Lage (jldl@legs.cnrs-gif.fr)

– Jean-Luc Da Lage

UPR 9034 Laboratoire Evolution, Genomes et Speciation (LEGS) Centre National de la Recherche Scientifique 91198 Gif sur Yvette Cedex France Tel: +33 1 69 82 37 27 Fax: +33 1 69 82 37 01

http://www.legs.cnrs-gif.fr/ Jean-Luc Da Lage <Jean-Luc.Da-Lage@legs.cnrs-gif.fr>

ColoradoStateU EvolutionaryGenomicsPhylogenetics

Graduate Student Position Available:

Genome Evolution and Phylogenetic Systematics Department of Biology, Colorado State University

We are seeking a creative and motivated graduate student (M.S. or Ph.D.) to join the laboratory of Rachel L. Mueller in the Fall of 2010. Our lab is currently working on projects that span three main avenues of research: mitochondrial genome evolution, nuclear genome evolution, and phylogenetic methodology. Our labs approach combines large-scale genomic sequence data, simulations, natural history collections, and fieldwork.

The majority of our current work is focused on plethodontid salamanders because they have two unusual genomes; both their nuclear and mitochondrial DNA is remarkable and illustrative of some fundamental processes governing genome evolution. However, work in the lab is not taxon-limited. Possibilities exist for graduate students to pursue degrees working on, or related to, the following projects (For more detailed information, please visit the lab website at http://rydberg.biology.colostate.edu/-muellerlab/MuellerLab/Home.html):

Nuclear genome evolution in plethodontid salamanders Among vertebrates, many of the largest genomes are found within the Plethodontidae, the most speciose family of salamanders. Five-fold variation in genome size exists among plethodontid species, from 14.5 Gb to 74.5 Gb. These values are larger than all bird, mammal, frog, and reptile genomes, as well as most fish genomes. This size variation reflects different levels of repetitive DNA, as in most eukaryotes; however, such repeat elements remain almost completely uncharacterized. We are combining next-generation sequence data and phylogeny-based modeling analyses to understand how mutational processes and selection have translated into extreme genomic expansion through time.

Mitochondrial genome evolution in plethodontid salamanders Plethodontid salamanders also have some of the largest mitochondrial genomes among vertebrates; these genomes contain novel gene orders, pseudogenes, and both tandem and non-tandem repeat elements, all of which are extremely rare among vertebrates. We are studying the evolutionary history of mitochondrial genomes in five plethodontid clades, each of which experienced an independent duplication event resulting in genomic reorganization. More generally, we are using these pseudogene sequences as a model system to understand the dynamics of neutral mutation in the mitochondrial genome. Our analyses of deletions may model the process through which an ancestral bacterial genome was streamlined into the present-day mitochondrial genome.

Phylogenetics and systematics Phylogenies for the same taxa estimated using different genes (even those that share the same history) are often incongruent, indicating that genes vary in their ability to yield accurate estimates of relationships. Therefore, choosing appropriate molecular markers is critical to the success of phylogenetic analyses and to any research that builds on these results. The characteristics of genes likely contribute to their phylogenetic utility; however, no formal method exists for selecting loci based on such characteristics. We are using a combination of empirical data and large-scale simulations to test the effects of different gene characteristics on phylogenetic performance. We are also focusing on branch length and the characteristics of datasets and analyses that minimize error in branch length estimation.

The Department of Biology at Colorado State University is an interdisciplinary group with a strong crew of evolutionary biologists. Fort Collins is a beautiful city of 120,000 people located at the base of the Rocky Mountains. We enjoy easy access to world-class outdoor recreation and 300+ days of sunshine each year.

Please contact Rachel Mueller (rlm@colostate.edu) for information.

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Rachel Lockridge Mueller Assistant Professor Department of Biology Colorado State University Fort Collins, CO 80523-1878 (970) 491-6717

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DeepFin FishSystematics

http://www.deepfin.org/studenExchange.php FISH SYSTEMATICS Student Exchange Program 2009-2010 This program is designed to facilitate communication between traditionally isolated research groups and to foster broader educational opportunities to students. Undergraduate and graduate students with research activities under the supervision of DeepFin participants (see www.deepfin.org) will be able to experience new research environments, not available to them at their home institutions. For example, a student working in a molecular systematics lab could acquire hands-on experience in morphological analysis of living or fossil fishes (and vice versa). The goal is to help lower existing barriers between traditionally isolated disciplines by raising a new generation of scientists with broad academic training experiences.

CALL FOR APPLICATIONS Proposal Deadline: Applications should be received by 15 NOVEMBER 2009; pre-application inquiries are welcome.

Stipends of up to $4,000 will be given to participating students to cover travel and room and board.

Eligibility: participants have to be affiliated to an accredited United States institution of research and/or education.

To apply for the student exchange program please provide the following information via email to Terry Grande attgrande@luc.edu or Guillermo Orti guilleorti@gmail.com (or both). Electronic submissions are required either as a single .pdf or a .doc file containing the following sections.

1.Cover sheet with your name, education (undergrad, grad, postdoc), institutional affiliation and research supervisor, the proposed host laboratory and hosting advisor, dates of proposed exchange, title of the project, and a summary (100 word maximum) describing the goals of the exchange experience, the type of training that you will gain via the laboratory exchange, and why this is important to your research project.

2. A brief description (1 page maximum) of your research project, its goals, and an indication of where you are in your research time line. Include information to make it clear how the project will contribute to our knowledge of the tree of life for fishes. Please provide some details of the type of training that you already have experience with (e.g., morphological, paleontology, molecular) and how the new training sought will enrich your education.

3. A curriculum vitae no longer than 2 pages listing educational background, work experience, publications, and presentations.

Additionally, two letter of recommendation are required from the academic advisors, one from the current advisor and one from the hosting advisor. These should be sent directly by the advisors to Terry or Carol via email. The letters should include statements concerning the following:

- The competence of the applicant - The significance of the new training sought for the applicant's education and the project goal's - The need for the funds being requested by the applicant and the availability of matching funds for the project that could supplement DeepFin stipends and extend the duration of the training period. Proposal Deadline: Applications should be received by 15 NOVEMBER 2009; pre-application inquiries are welcomed.

To ensure that applications are not lost in electronic transfer, confirmation e-mail will be sent to the applicants. If you do not receive this confirmation within three days of your submission, please re-contact Terry Grande or Guillermo Orti (guilleorti@gmail.com).Funding decisions will be made within 30 days of the deadline.

Reporting Requirement: Recipients will be expected to provide a report to DeepFin (1 page) describing the accomplishments and value of the exchange experience, and any product (such as publication or thesis that might result from this work) within three months of the end of their exchange. This report should be sent via email to Terry Grande (tgrande@luc.edu). Recipients might also be invited to contribute Tree of Life pages (http://tolweb.org/tree/phylogeny.html) with the phylogeny for the focal group of their project.

guilleorti@gmail.com

EastCarolinaU EvolutionaryBiol

GRADUATE STUDIES IN EVOLUTION AND ECOLOGY AT EAST CAROLINA UNIVERSITY

The Department of Biology at East Carolina University, the third largest campus in the North Carolina System, invites inquiries and applications from prospective graduate students for Fall 2010. We have an active and well-supported group of faculty in Evolution and Ecology and will guarantee accepted PhD students (in IDPBS, the Interdisciplinary Doctoral Program in Biological Sciences) at least two years of support with no teaching obligations and at least five years of support total, at a very competitive level. We also offer two MS programs (TA-ships readily available) and have students in ECU's Coastal Resources Management PhD program. Graduate students will be encouraged to participate in the newly formed North Carolina Center for Biodiversity (NCCB) at East Carolina University. Goals of the NCCB include training graduate students in biodiversity research and providing them opportunities to participate in related outreach.

Situated in the attractive and affordable community of Greenville, we are in easy reach of North Carolina's Research Triangle (including the National Evolutionary Synthesis Center), several marine institutes and laboratories, and the diverse natural communities of the Coastal Plain and Outer Banks. Thus excellent opportunities exist for collaboration and to work in terrestrial, aquatic, wetland and marine systems. A readily available 454 sequencer at ECU's Brody School of Medicine facilitates genomic research. Travel is convenient through either Pitt-Greenville or Raleigh-Durham International Airport and our faculty members are engaged in research on every continent but Antarctica.

Please visit http://www.ecu.edu/biology/ to find out more about our department. Information on our graduate programs is available here: http://www.ecu.edu/-biology/graduate.cfm Our Evolution and Ecology faculty (http://www.ecu.edu/biology/faculty.cfm) include:

Jason Bond: Arthropod systematics. Mark Brinson: Wetland restoration ecology, ecosystem ecology. David Chalcraft: Population and community ecology; ecological aspects of biodiversity. Robert Christian: Systems and network theory; ecology of coastal ecosystems. Lisa Clough: Marine benthic ecology (Arctic and Atlantic). Carol Goodwillie: Plant mating system evolution. Jinling Huang: Evolutionary genomics, bioinformatics; horizontal gene transfer. Claudia Jolls: Plant evolutionary ecology and conservation. Dave Kimmel: Plankton ecology. Trip Lamb: Systematics and phylogeography. Joe Luczkovich: Food web ecology and fish bioacoustics. Jeff McKinnon: Sexual selection, speciation, mainly in fish. Sue McRae: Behavioral ecology and social evolution in birds. Anthony Overton: Larval fish ecology, fisheries biology. Enrique Reyes: Landscape ecology, ecological modeling, coastal management. Roger Rulifson: Fish ecology and fisheries. Jean-Luc Scemama: Post-duplication gene evolution. Matt Schrenk: Microbial ecology, geo-microbiology. Ed Stellwag: Vertebrate evo-devo and cis-regulatory network evolution. John Stiller: Molecular evolution and comparative genomics. Kyle Summers: Evolution of color, behavior in poison frogs; evolutionary medicine. Heather Vance-Chalcraft: Predation and community ecology. Terry West: Human impacts on coastal ecosystems. Baohong Zhang: MicroRNA evolution, comparative genomics, and molecular genetics.

In addition to visiting the websites, please contact prospective mentors directly for more information, or graduate studies director Terry West: westt@ecu.edu

Jeffrey S. McKinnon, Chair Dep. of Biology, N108 Howell Science Complex East Carolina University Greenville, NC 27858-4353 Phone 252-328-5258; mckinnonj@ecu.edu http://personal.ecu.edu/mckinnonj/ "McKinnon, Jeffrey" <MCKINNONJ@ecu.edu>

ETH Zurich Bioinformatics

PhD position in Bioinformatics/ Molecular Evolution

Three-year Ph.D. studentship is available at the Computational Biochemistry Research Group (CBRG), department of Computer Science at the Swiss Federal Institute of Technology (ETH Zurich), highly reputable internationally. CBRG is a member of the Swiss Bioinformatics Institute (SIB) and benefits from SIB training courses and networking.

The research focus will be to study selective pressures and other patterns in proteins with tandem repeats (which often play role as receptors, implicated in human disease, and more). The project will involve modeling the evolutionary process at the codon level and developing/adapting machine-learning techniques to recognize patterns in complex multi-facet data. Planned collaborations with structural biologists (CNRS, Montpellier) promise an exciting case for motivated young scientists.

Successful candidates will have a strong background in bioinformatics, computer science, statistics, and/or computational biology. Fluency in a major scripting language, and experience in software development is a must. Some background in biology is desirable, but interest in biology and bioinformatics is required. Candidates should be highly motivated and have the ability to work independently. As the research will involve a mix of disciplines, candidates with experience in several fields will be preferred (bioinformatics, genetics, protein structure, computational science, mathematics, physics, statistics).

ETH Zurich boasts excellent facilities for studying and recreation. The working language in the laboratory is English, which is also widely used in Switzerland. Zurich is located less than one hour from the Alps, and is a small but vibrant city offering one of the best living standards in the world. Zurich is well connected to major European cities, and has a large international community.

The successful applicant will be supervised by Dr Maria Anisimova, whose interests include a variety of topics in Molecular Evolution and Bioinformatics.

To apply, please send a single PDF file to maria.anisimova@inf.ethz.ch containing:

* CV (with publication list if applicable)

* a scanned academic transcript (list of grades in university courses)

* a short statement of research interests, mentioning research topics of master/diploma theses (not exceeding two pages)

* three references

Please mention “PhD position” in the subject of your e-mail.

The position is open until filled (but quick response is recommended).

maria.anisimova@inf.ethz.ch
maria.anisimova@inf.ethz.ch

GeorgeMasonU PlantSystematics

Graduate Research Assistantship in Systematic Botany

Description: A graduate research assistantship (MS or Ph.D.) is available in the Department of Environmental Science and Policy at George Mason University to study the systematic biology of tropical trees. The successful candidate will conduct research associated with the NSF- funded project, $B!H(BPhylogeny, Diversification and Evolutionary Trajectories in the $B!F(BTerebinthaceae$B!G(B (Anacardiaceae and Burseraceae).$B!I(B Specifically, the student will assist the phylogenetic reconstruction of the myrrh genus, Commiphora, using DNA sequence data and the analysis of wood anatomy in Commiphora species endemic to Madagascar.

Candidates should have strong academic standing, excellent communication skills, the ability to work independently and a genuine passion for systematic botany. The two-year position is offered starting August 2010 and includes a salary of $18,349 plus health insurance and in-state tuition.

George Mason University is a large state university located in Northern Virginia and is connected to Washington, DC by metrorail. The University maintains an excellent research library and regional herbarium, offers a diverse range of graduate coursework, and has long-term collaborations with nearby governmental and non- governmental organizations. The ESP department houses an active graduate student association and comprises faculty and students with research interests in ecology, evolutionary biology, conservation biology and environmental policy.

Applications: Applicants should submit 1) a letter outlining personal research interests, experience and career goals, 2) a CV, 3) academic transcripts and GRE scores, 4) and the names of three professional references. Inquiries and all application materials should be directed to the principal investigator, Dr. Andrea Weeks (aweeks3@gmu.edu). Students from groups under-represented in the field of science are especially encouraged to apply. The deadline for application is 12/15/2009. The selected candidate will then be invited to submit a formal application to the university (http:// admissions.gmu.edu/grad/).

Andrea Weeks <aweeks3@gmu.edu>

GeorgetownU QuantBiol

The departments of Biology and Mathematics at Georgetown University have an ongoing collaboration involving several research projects that span a wide spectrum of applications in population genetics, ecology, immunology, and molecular evolution. The projects are unified through their focus on modeling, analyzing and exploiting genetic data to understand the interaction of complex systems. Ongoing projects include the development and application of coalescent models that better suit fish populations in order to infer biological mechanisms acting on genetic polymorphism, and the development of novel quantitative models to analyze the evolution of HIV within an infected individual.

We are seeking an outstanding student who is interested in working at the interface of biology and mathematics. The terminal degree will be a PhD in biology and the course of study will include classes in biology, mathematics and computer science, with the goal of providing the student with a firm background in population genetics, ecology, statistics, probability, and computation. The specific topic of research is flexible and can favor theory or a particular application depending on the interest of individual students. The ideal student should possess a BS degree in biology or mathematics (with some course work and experience in the alternate field) with some experience in computation. Most importantly, an ideal student will have a strong desire to engage in interdisciplinary research in quantitative biology.

Interested students should contact Dr. Sivan Leviyang via e-mail:

sr286@georgetown.edu

GeorgetownU QuantBiol 2

The departments of Biology and Mathematics at Georgetown University have an ongoing collaboration involving several research projects that span a wide spectrum of applications in population genetics, ecology, immunology, and molecular evolution. The projects are unified through their focus on modeling, analyzing and exploiting genetic data to understand the interaction of complex systems. Ongoing projects include the development and application of coalescent models that better suit fish populations in order to infer biological mechanisms acting on genetic polymorphism, and the development of novel quantitative models to analyze the evolution of HIV within an infected individual.

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Interested students should contact Dr. Sivan Leviyang via e-mail:

sr286@georgetown.edu

IowaStateU SexualSelection

PhD Research in Sexual selection

A 5-year funded PhD position is available under the supervision of Dr. Clint Kelly at Iowa State University (http://web.mac.com/clintkelly1/Site/Home.html) beginning August 2010. I am seeking a motivated student to study sexual selection including, but not limited to, 1) sperm competition and ejaculate expenditure in fish or insects; or 2) the physiological and reproductive trade-offs of investment in immunity. My lab uses an empirical approach in the field and laboratory to examine a broad set of topics in behavioural and evolutionary ecology and we employ a variety of techniques and procedures to address research questions, including: molecular genotyping, immunological assays, phylogenetic comparative studies, geometric morphometrics and meta-analysis. The Kelly research group belongs to the large, research-active Department of Ecology, Evolution & Organismal Biology at ISU (http://www.eeob.iastate.edu/). If interested in pursuing a graduate degree in my lab please send a brief description of your research interests and a CV (pdf) to cdkelly@iastate.edu .

cdkelly@iastate.edu

KansasStateU GrassAdaptation

PhD Assistantship Available: Ecological Genomics of Drought Stress in Prairie Grasses

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

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

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

Review of applicants will begin Dec 15, and continue until the successful applicant is identified. The starting date is summer 2010.The position offers competitive salary of $25,000 and benefits.

Applications should include a cover letter with a statement of research interests and timing of availability, a CV, and names and contact information for three professional references. Please send your application through e-mail to Loretta Johnson (Johnson@ksu.edu). To ensure that your application is received, please include the following in the subject of your e-mail: Application for Ecological Genomics Assistantship.

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

Dr. Loretta C. Johnson Associate Professor Division of Biology Ackert Hall Rm 232 Kansas State University Manhattan, KS 66506 USA email: johnson@ksu.edu phone: 785-532-6921 FAX: 785-532-6653 http://www.ksu.edu/johnsonlab/ Learn about our new Ecological Genomics research initiative and student and post-doctoral training opportunities by visiting our web page at http://ecogen.ksu.edu Loretta Johnson <johnson@ksu.edu>

KansasStateU PlantEvolution

I am actually looking for a developmental biologist who is taking different angles to answer biological questions - including evolutionary studies. We also plan to look at the occurrence of steryl glucosides across species, although I don't mention it in the ad.

Kathrin

Ph.D. position in Plant Molecular Biology

The Schrick lab is seeking candidates to fill a Ph.D. studentship in the Division of Biology at Kansas State University to begin in the Fall of 2010. We are studying the role of plant sterols in growth and development with an emphasis on metabolic regulatory networks. Our research is divided into two areas using Arabidopsis and Pisum sativum as model systems. One involves the study of candidate lipid/sterol-binding domains that are found in homeodomain transcription factors. Their occurrence as a plant-specific domain arrangement corresponds with the evolution of the land plants, and this work includes comparative analysis of genome data from diverse species. The other focus area is on the role of steryl glucosides in cellulose synthesis. Work in our laboratory is interdisciplinary, and will involve close interactions with the Kansas Lipidomics Research Center as well as with the Biotechnology/Proteomics Core Lab, Bioinformatics Center, Integrated Genomics Facility, and Ecological Genomics Institute at Kansas State University. For more information on the Schrick lab see http://www.k-state.edu/biology/faculty_pages/schrick.html. Additional information on the Ph.D. program in Biology at Kansas State University can be found at http://www.k-state.edu/biology/graduate.html. Qualified applicants should submit an email message (with $B!H(BPh.D. position$B!I(B in the subject line) containing a cover letter, academic transcript from relevant undergraduate degree, and CV, including contact information for three academic references, to kschrick@ksu.edu by November 30, 2009.

Kathrin Schrick Assistant Professor Plant Genomics & Molecular Biology Division of Biology 116 Ackert Hall Kansas State University Manhattan, KS 66506-4901

Tel (office): +1-785-532-6360 Tel (lab): +1-785-532-7322 Fax: +1-785-532-6653 Email: kschrick@ksu.edu http://www.k-state.edu/biology/faculty_pages/-schrick.html Kathrin Schrick <kschrick@ksu.edu>

LouisianStateU AvianSpeciationGenetics

PhD Position Available in Speciation Genetics of Streamer-tailed Hummingbirds in Jamaica We are seeking an outstanding doctoral student to pursue a PhD at the Museum of Natural Science and Department of Biological Sciences at Louisiana State University. The student would be co-advised by Robb Brumfield (Louisiana State University) and Gary Graves (Smithsonian Institution). The student's doctoral dissertation would use genomics tools and behavioral experiments to elucidate the mechanisms maintaining reproductive isolation between two species of Streamer- tailed Hummingbirds that are endemic to Jamaica. The student would receive support to conduct their research as well as a teaching assistantship, research assistantship, or curatorial assistantship. The ideal candidate would have a M.S., with research experience in molecular ecology, population genetics, and/or behavioral ecology, as well as field experience working with birds. Extensive fieldwork in Jamaica will be required for this position. The selected student is expected to enroll in the Department of Biological Sciences at LSU for the Fall 2010 semester. Application materials will be accepted until December 31, 2009 or until a suitable candidate is found.

Please contact Robb Brumfield (brumfld@lsu.edu) for information

Robb Brumfield, PhD Museum of Natural Science & Department of Biological Sciences 119 Foster Hall Louisiana State University Baton Rouge, LA 70803

Robb Brumfield <brumfld@lsu.edu>

ManchesterU EvolutionaryBiol

PhD studentship in evolutionary biology / behavioural ecology starting October 2010

Title: The effects of genetic variation in the social environment on behavioural and life history

The social environment provided by family or group members has been shown to be highly influential for adult phenotypes and variation in individual fitness, particularly in early development. Recent research has highlighted that the social environment is determined by the genotypes of interacting individuals and can thus respond to selection and evolve, yet, the significance of this is poorly understood. The aim of the project is to investigate how important genetic variation in the social environment is in determining phenotypic variation in both behavioural and life history traits. What is the nature and the genetic basis of social interactions, how do these interactions affect complex traits such as parental behaviour or sexually selected traits and how do they differ across taxa and why? The project will address these unresolved issues using experimental work in model (mice) and non-model organisms (insects e.g. cockroaches and earwigs) combining behavioural, genetical and statistical analyses. There is the opportunity to develop own research projects in conjunction with ongoing research in the tropics and to contribute to teaching on field courses.

Further Information This studentship is open to all nationalities although no funding is available to cover the higher tuition fees for non-EU applicants and EU applicants from outside in the UK must have been resident in the UK for purposes other than education for 3 or more years to qualify for the living expenses stipend. Applicants should have an excellent undergraduate record and ideally some research experience. Further information can be obtained by contacting Reinmar Hager reinmar.hager@manchester.ac.uk

How to Apply Applications must be submitted online and accompanied by a number of supporting documents by 7 December 2009: http://www.ls.manchester.ac.uk/postgraduate/ukoreu/research/apply/ AND send an email to openday.lifesciences@manchester.ac.uk expressing your interest in attending the external admissions day on 7 January 2010.

Reinmar Hager <reinmar.hager@cantab.net>

MaxPlanckInst Jena InsectBacteriaSymbioses

Open PhD Positions in the Insect Symbiosis Research Group at the Max Planck Institute for Chemical Ecology in Jena, Germany

The Insect Symbiosis Research Group at the Max Planck Institute for Chemical Ecology in Jena, Germany (http://www.ice.mpg.de/snwg/home/home_en.htm), will be established by the end of this year to study the evolution and chemical ecology of insect-bacteria symbioses. Two PhD positions are available from January 2010 for an initial period of two years with a prospective third year extension.

PhD Studentship - Molecular ecology of a defensive insect-bacteria symbiosis Solitary digger wasps of the genus Philanthus cultivate Streptomyces bacteria that protect the wasp offspring against pathogen infestation by producing antibiotics. One PhD position is available to study the dynamics of antibiotic production and to identify the genes involved. We are seeking a highly motivated candidate with strong communication and excellent organizational skills who can operate in an interdisciplinary research environment. The successful candidate should have a strong background in evolutionary biology, genetics and/or molecular biology. Experience with basic molecular techniques (PCR, cloning, analysis of sequence data) is required, more advanced techniques (FISH, qPCR, rt-PCR, rt-qPCR) and basic programming skills (Perl) are advantageous. Applicants should have an excellent Diploma degree or M.Sc. in evolutionary biology, biochemistry or molecular biology.

PhD Studentship - Nutritional interactions between insects and actinomycete bacteria Many insects require symbiotic bacteria for their nutrition. Most of these symbionts belong to the gamma-proteobacteria. The red soldier bug (Pyrrhocoris apterus, Hemiptera, Pyrrhocoridae) represents one of the few cases in which an actinobacterium is found as a symbiont in the midgut of an insect. A PhD position is available to study the molecular basis and the specificity of the symbiosis. The successful candidate should have a strong background in biochemistry, entomology and/or molecular biology in addition to a strong motivation and interest for research projects in the evolution and ecology of insect-bacteria interactions. Experience with molecular techniques (PCR, FISH, sequencing) is a plus. Applicants should have an excellent Diploma degree or M.Sc. in biochemistry, molecular biology or entomology.

The Max Planck Institute is an equal-opportunity employer and especially encourages women to apply. Applications from handicapped persons will be favored when all other qualifications are equal.

Please send your applications (including cover letter with statement of purpose and previous research experience, CV, and contact information for 2 referees) until October 31, 2009 to:

Dr. Martin Kaltenpoth Zoological Institute University of Regensburg Universitätsstr. 31 93053 Regensburg Germany Email: martin.kaltenpoth@biologie.uni-regensburg.de

Dr. Martin Kaltenpoth University of Regensburg Department of Zoology 93040 Regensburg Germany phone: +49-941-943-3057 fax: +49-941-943-3325 email: martin.kaltenpoth@biologie.uni-regensburg.de http://www.biologie.uni-regensburg.de/Zoologie/Strohm/martin_kaltenpoth Martin Kaltenpoth <Martin.Kaltenpoth@biologie.uni-regensburg.de>

MichiganStateU EvolGeneticsDevel

Four PhD Studentships in Evolutionary Genetics and Integrative Developmental Biology, Michigan State University, USA.

Four graduate positions in evolutionary genetics/developmental biology are available in the laboratories of Dr. Alex Shingleton and Dr. Ian Dworkin in the Department of Zoology and Program in Ecology, Evolutionary Biology and Behavior at Michigan State University. The positions are funded as part of three NSF grants working at the interface of evolution, development and genetics. The Shingleton and Dworkin laboratories work closely together and employ molecular, genetic, genomic, physiological and behavioral methods to address their research questions, using Drosophila as a model organism. More details on the research being conducted in the laboratories are available at www.msu.ed/˜shingle9 and www.msu.edu/˜idworkin. Students will be immersed in an integrative and collaborative research environment within the diverse and dynamic life-science community at Michigan State University.

Potential projects for graduate students include:

1) Uncovering the molecular and developmental regulation of morphological scaling relationships. Previous research in the Shingleton lab has identified the insulin-signaling pathway as being differently regulated in organs that differ in their scaling relationship with body size. The goal of the project is to elucidate the molecular basis for this differential regulation.

2) Exploring the evolution of wing-body scaling in Drosophila populations. This project involves applying artificial selection on scaling relationships in Drosophila and elucidating the genetic and developmental basis for the selection response.

3) Examining the role of conditional and pleiotropic genetic effects in the evolutionary process, and mapping genetic modifiers that contribute to these effects. Previous work (Dworkin et al. 2009) demonstrated that a genetic modifier of the allelic effects of a mutant results in profound difference in phenotypes. The student will fine map the genetic modifier and examine its potential pleiotropic contributions in natural populations.

4) Explore the effects of different genetic backgrounds on gene interactions and ordering of allelic series for mutations that affect wing development and shape. This work will examine the effects of a series of mutations in different "wild-type" genetic backgrounds, across several rearing environments (manipulations of diet and temperature).

The projects will suit students with an interest in evolutionary genetics and/or integrative developmental biology. The ideal candidate should have good general laboratory skills, with a firm grasp of basic statistical methods.

Michigan State University is a large land-grant institution with an outstanding faculty and inter-disciplinary programs at the departmental and university levels. Interested applicants are encouraged to review additional background on faculty and graduate programs in Zoology (http://www.zoology.msu.edu), and in the Ecology, Evolutionary Biology and Behavior (EEBB) program (https://www.msu.edu/˜eebb).

Applicants should submit a statement of interest, a CV, GRE scores and their cumulative GPA along with names and contact information of three references (everything as one PDF document) to shingle9@msu.edu. Applications will be accepted until the positions are filled. The start date is September 2010, although applicants who wish to start sooner should also apply.

shingle9@msu.edu shingle9@msu.edu

MichiganStateU GeneExpressionEvolution

PhD assistantships - Experimental design and statistical analysis of transcriptional profiling experiments.

Statistical Genomics Laboratory, Departments of Animal Science and Fisheries and Wildlife, Michigan State University.

We are looking for students to join our group and work towards a doctoral degree while collaborating with an interdisciplinary group that includes Statisticians, Immunologists, Molecular Biologists, Physiologists and Animal Breeders.

Empirical data from gene expression experiments will be available for such studies, including oligonucleotide microarray and high throughput quantitative PCR studies. The students' work will consist of development and adaptation of statistical methods to answer current questions in functional genomics and genetical genomics of livestock and wildlife species.

Qualifications: Candidates should be highly motivated and have an interest in molecular and statistical genetics/genomics. Ability to effectively communicate in English is essential. A MSc degree or equivalent in Statistics, Biostatistics, Animal Breeding or similar field is strongly preferred. Exceptional candidates without a MSc degree, but who have completed substantial coursework in calculus, algebra and statistics will be considered as well. Experience with programming in R, C++ and/or Fortran, a plus.

Tentative dissertation topics: 1) Adaptation and application of conditionally heteroskedastic hierarchical linear models to the analysis of gene expression data. 2) Development of computationally efficient tools based on statistically powerful models for high-throughput analysis of gene expression. 3) Designs and models exploiting selective phenotyping in transcriptional profiling studies.

Available projects/datasets: 1) Differential expression of genes and pathways in response to Porcine Reproductive and Respiratory Syndrome Virus infection. 2) Differential gene expression in Sea Lamprey throughout its complex life history and in response to pheromone stimulation. 3) eQTL mapping in crosses of outbred pig populations.

Contact: Dr. Juan P. Steibel, steibel

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Juan Pedro Steibel

Assistant Professor Statistical Genetics and Genomics

Department of Animal Science & Department of Fisheries and Wildlife

Michigan State University 1205-I Anthony Hall East Lansing, MI 48824 USA

Phone: 1-517-353-5102 E-mail: steibelj@msu.edu

Juan Pedro Steibel <steibelj@msu.edu>

NorthCarolinaStateU EvolutionaryEcology

Available Graduate Positions in Evolutionary Ecology

The Langerhans Lab at North Carolina State University is looking for exceptional and enthusiastic Ph.D. students, and anticipates accepting approximately two new students starting fall 2010. While the lab primarily accepts Ph.D. students, exceptional students wishing to pursue a M.S. will also be considered. Additional information for prospective students can be found here: http://faculty-staff.ou.edu/L/Randall.B.Langerhans-1/labopps.html . Research in the Langerhans Lab investigates a wide range of questions in evolutionary ecology, with empirical work focusing on aquatic systems (e.g., fishes, amphibians) and lizards. Due to this breadth of interests, graduate students can pursue a variety of research trajectories. Examples of ongoing research interests in the lab include: evolutionary consequences of anthropogenic impacts, ecological speciation, morphological and locomotor evolution, predictability of phenotypic evolution, functional morphology of locomotion, predator-prey coevolution, genital evolution in livebearing fishes, phylogeography, phenotypic plasticity, adaptive constraints of gene flow, sensory bias, evolution of sexual dimorphism, and links between locomotor, feeding, and life history evolution.

North Carolina State University is located in Raleigh, North Carolina's state capital. The campus is home to a vibrant research community, and immersed within a thriving area for ecology and evolutionary biology research (e.g., within a 30-minute drive of Duke University, UNC Chapel Hill, the National Evolutionary Synthesis Center). The city is further conveniently located approximately 2 hours from both the ocean and the mountains.

If you are interested in joining the lab, please contact Dr. Brian Langerhans (langerhans@ncsu.edu) and provide a short description of your research interests and accomplishments, CV (including GPA and GRE scores), and contact information for three references. For those subsequently encouraged to apply, information on the application process can be found here: http://harvest.cals.ncsu.edu/biology/index.cfm?pageID=951 . More information on research in the lab can be found at: http://faculty-staff.ou.edu/L/Randall.B.Langerhans-1/ More information on the Department of Biology at NCSU can be found at: http://harvest.cals.ncsu.edu/biology/ langerhans@ncsu.edu langerhans@ncsu.edu

OklahomaStateUniversity PlantSystematics

PhD position: Plant Systematics, Department of Botany, Oklahoma State University

A PhD position is available to apply genomic approaches to plant systematics in the laboratory of Dr. Mark Fishbein at Oklahoma State University. This is an NSF-funded collaborative project with Dr. Aaron Liston and Dr. Richard Cronn at Oregon State University. The position involves sequencing the complete genome of Asclepias syriaca (milkweed) and chloroplast genomes from ca. 150 species of Asclepias and relatives. Research will involve field collecting plant samples, laboratory preparation of sequencing templates for the Illumina platform, and phylogenetic analysis. Opportunities exist for participation in genome assembly and annotation, and the development of an independent project in the area of genome analysis. A B.S. degree in Botany, Biology, Bioinformatics, or Computer Science is required; a M.S. degree with specialization in phylogenetics, plant taxonomy, or bioinformatics is desirable.

The position can be filled as early as January 2010 and is funded by a combination of research and teaching assistantships. The Oklahoma State University Botany Department (http://botany.okstate.edu) has a core strength in plant systematics and evolution coupled with active collaborations in the areas of systematics and molecular biology across many departments, including Zoology, Plant and Soil Sciences, Biochemistry and Molecular Biology, and Microbiology and Molecular Genetics, among others. Research is supported by state-of-art core facilities in the areas of Recombinant DNA/Protein Resources and Bioinformatics, among many others.

To apply for this position, please email a cover letter, curriculum vitae, unofficial course transcript, and contact information for two references to mark.fishbein@okstate.edu

Mark Fishbein Oklahoma State University Department of Botany 104 Life Sciences East Stillwater, OK 74074 USA

ph: +1-405-744-4757 fax: +1-405-744-7074

http://fishbein.okstate.edu mark.fishbein@okstate.edu mark.fishbein@okstate.edu

RutgersU TrichopteraPhylogenetics

Graduate Assistantship in Trichoptera Phylogenetics Karl Kjer has a graduate assistantship (G.A.) position available at Rutgers University, associated with an NSF-funded project on Trichoptera phylogenetics. Position includes health insurance and a stipend of approximately $25,000/year, funded for two years as a G.A. on the grant, and then as a T.A. afterward. Rutgers is a large research university in New Jersey, between New York City, and Philadelphia. Please E-mail me for details. kjer@aesop.rutgers.edu. I will send you a copy of the grant and we can discuss possible projects. Applications to Rutgers should be completed by February, 2010, but prior contact by E-mail is highly recommended. Rutgers requires competitive GRE scores (if you are unfamiliar with the GRE exam, please ask about it in your E-mail). I am looking for talent, drive and initiative, but all these qualities can come from a variety of disciplines. For example, experience with Trichoptera is an asset; I can teach you the molecular part. Or experience with molecular systematics is an asset; I can teach you about Trichoptera. Bioinformatics, Mathematics, programming skills are all relevant. In other words, I am not looking for any ONE set of skills, but I AM looking for skills. The successful applicant must be able to demonstrate some prior interest in systematics or evolutionary studies, broadly defined. My website is at http://www.mosquito.rutgers.edu/-kjer.htm kjer@AESOP.Rutgers.edu

StockholmU AncientDNA

STOCKHOLM UNIVERSITY announces a PhD position in Systematics and Evolution (ancient DNA) at the Department of Zoology, Stockholm University (placed at the Molecular Systematics Laboratory, the Swedish Museum of Natural History).

Project title: Population turnover and range dynamics during the last Ice Age

Final date for applications: November 20, 2009

Project description: The aim of this PhD project is to investigate the degree of population turnover and range fluctuation during the Late Pleistocene, and to evaluate to what extent these processes are related to the environmental changes that occurred during this dynamic period. This will be done through genetic analyses on fossils up to 50 000 years old. The resulting genetic data will be integrated with information on past distributions and climate through back-casted species distribution models. In addition, molecular analyses on faeces as well as permafrost sediments will be used to assess changes in diet through time and across space. Potential model species for the project include collared lemming, reindeer and arctic fox. Specific topics that will be examined in the project comprise i) the timing of extinctions and demographic change in relation to past environmental change, ii) to what extent local populations tracked changes in habitat availability when faced with climate change, and iii) how changes in plant diversity affected herbivore diet through time. The long-term aim of the project is to provide increased knowledge on how habitat change drives the speciation and extinction processes and, on a more practical level, to increase the accuracy of models used to forecast the impact of future climate change on biodiversity. The project will be done within the ancient DNA research group at the Molecular Systematics Laboratory (MSL) in the Swedish Museum of Natural History. A part of the research carried out by the PhD student will be done within the cross-disciplinary research network CLIMIGRATE, funded by the European Union's FP7 ERA-NET program BiodivERsA. The PhD degree will be awarded in Systematics and Evolution at the Department of Zoology. Dr. Love Dalén at the Swedish Museum of Natural History (MSL) will be the main supervisor.

Qualifications: To be qualified for research studies the applicant must have completed a research degree (e.g. Master's), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level ("examensarbete") within systematics and evolution, ecology, population genetics or a similar subject. Applicants who have in principle acquired the corresponding competence in Sweden or abroad, are also qualified.

Criteria for selection: Among qualified applicants, selection is made according to the ability to profit from the studies. The criteria to be used are the applicant's documented knowledge in subjects of relevance for the research area, ability to master language (including both spoken and written English), analytical ability, creativity, initiative, independence and ability to cooperate. The basis for judgement of how well the applicant fulfils these criteria is: the relevance of earlier studies for the research area, grades on courses at the university level, the quality of the independent project (master thesis or "examensarbete"), references, interviews and the applicant's letter of intent. Previous experience in practical genetic analyses is highly desirable, and knowledge in ecology, population genetics, past climates and environments, and ecological modelling are considered as additional qualifications.

To be included in the application: Maximum one A4-page of personal presentation and your reasons for applying (letter of intent). Curriculum vitae. Copy of independent project report (master thesis or "examensarbete"). Copy of degree certificates and transcripts of academic records (all attested). Also provide a list of two persons who may act as references (with phone numbers and e-mail addresses). Provide two copies of all documents and the thesis. To be considered, the application labelled "PhD ref.no. 02/09 LDII" must have arrived at the address below by November 20, 2009.

Address to which the application should be sent: Stockholms universitet Prefekten Zoologiska institutionen 106 91 Stockholm Sweden

Terms of employment: The research education comprises 48 months at full time. The position is financed by a fellowship ("utbildningsbidrag") for the first years, and then continues with PhD-employment until the end of the PhD-program. Up to 20% of teaching may be included in the position. (If teaching is included, the position will be extended).

Union representatives: Bo Ekengren SACO Lisbeth Häggberg ST Gunnar Stenberg SEKO. Phone: + 46 (0)8 16 20 00. PhD student representative e-mail: do@sus.su.se

For further information about the project, contact:

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StockholmU InsectHostPlantPreference

STOCKHOLM UNIVERSITY announces a PhD POSITION IN ANIMAL ECOLOGY at the Department of Zoology, Stockholm University.

Project title: Evolutionary and mechanistic aspects of insect host plant preference.

Final date for applications: November 20, 2009

Project description: The aim of this PhD project is to investigate the evolutionary and mechanistic causes of insect host plant preference. Host preference in insects is a complex behavioural process where several sensory modalities interact to produce a series of decisions that ultimately decides whether a particular plant should be accepted as a host or not. The project will initially focus on the butterfly Polygonia c-album, which has been the subject of a long series of host plant-related studies from the butterfly lab at the Department of Zoology. These studies - ranging from genetics to phylogenetics - offer a rich context of background knowledge for the present doctoral project.

In butterflies and many other plant-feeding insects the choice of oviposition site largely determines the feeding site of the offspring, since the ability of the newly hatched larva to move to another host is very limited. This means that this choice is also to a large extent determining the actual host range (host specificity) of the insect - a feature that has been shown to influence both host shifts and speciation rates in butterflies.

In spite of the paramount importance of host plant preference, we know disturbingly little about the actual mechanisms behind host plant choice, and this project is intended to elucidate how different behavioural sequences and sensory modalities interact at different levels of resolution to produce the final choice.

Most of the project will be carried out in the butterfly lab of the Department of Zoology, or at the Tovetorp Research Station and will mainly consist of behavioural essays of adult and larval responses to different plant-related cues.

The PhD degree will be awarded in Animal Ecology at the Department of Zoology. Dr. Niklas Janz at the Department of Zoology will be the main supervisor.

Qualifications: To be qualified for research studies the applicant must have completed a research degree (e.g. Master's), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level ("examensarbete") within ecology or ethology. Applicants who have in principle acquired the corresponding competence in Sweden or abroad, are also qualified.

Criteria for selection: Among qualified applicants, selection is made according to the ability to profit from the studies. The criteria to be used are the applicant's documented knowledge in subjects of relevance for the research area, ability to master language (including both spoken and written English), analytical ability, creativity, initiative, independence and ability to cooperate. The basis for judgementof how well the applicant fulfils these criteria is: the relevance of earlier studies for the research area, grades on courses at the university level, the quality of the independent project (master thesis or "examensarbete"), references, interviews and the applicant's letter of intent. Previous experience in experimental behavioural ecology or ethology is highly desirable.

To be included in the application: Maximum one A4-page of personal presentation and your reasons for applying (letter of intent). Curriculum vitae. Copy of independent project report (master thesis or "examensarbete"). Copy of degree certificates and transcripts of academic records (all attested). Also provide a list of two persons who may act as references (with phone numbers and e-mail addresses). Provide two copies of all documents and the thesis. To be considered, the application labelled "PhD ref.no. 02/09 NJ" must have arrived at the address below by November 20, 2009.

Address to which the application should be sent: Stockholms universitet Prefekten Zoologiska institutionen 106 91 Stockholm Sweden

Terms of employment: The research education comprises 48 months at full time. The position is financed by a fellowship ("utbildningsbidrag") for the first years, and then continues with PhD- employment until the end of the PhD- program. Up to 20% of teaching may be included in the position. (If teaching is included, the position will be extended).

Union representatives: Bo Ekengren SACO, Lisbeth Häggberg ST, and Gunnar Stenberg SEKO. Phone: + 46 (0)8 16 20 00. PhD student representative e-mail: do@sus.su.se

For further information about the project, contact: Assistant professor Niklas Janz + 46 (0)8 16 4048 e-mail: niklas.janz@zoologi.su.se

Further information on the web: Stockholm University: www.su.se Lab home page: www.zoologi.su.se/research/ihp/

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UAdelaide Biodiversity

Postgraduate Opportunities In Environmental Genomics, Adelaide, Australia

Projects in Forensics, Water, Health, Conservation Biology, Antarctic biodiversity.

Six PhD projects are available in the field of Environmental Genomics, at the University of Adelaide starting in early 2010, working on an ARC LINKAGE funded project at the Australian Centre for Ancient DNA (http://www.adelaide.edu.au/acad/). Each project focuses on the application of targeted metagenomic assays to perform rapid biodiversity and taxonomy assessment on complex biological samples in the following fields;

Project 1) Forensics: Using the genetic content of soil samples to predict crime scene/source areas. Focusing on invertebrate, plant and animal signals. Project partners - Australian Federal Police

Project 2) Water Quality: Analysing the biodiversity of standard, desalinated and recycled/re-used water systems, focusing on the detection and identification of novel pathogens. Project partners - SA Water

Project 3) Mining/Conservation biology: Using environmental genomic methods to rapidly analyse plant, animal and invertebrate taxonomic biodiversity in soil samples from survey sites across South Australia. Project partner - Primary Industries Research South Australia, and Department of Environment and Heritage, SA

Project 4) Health: Developing metagenomic methods to detect and monitor known and novel pathogens in medical systems, focusing on point of care. Project partner - SA Pathology Project 5) Antarctic biodiversity: Using environmental genomic approaches to analyse the biodiversity of Antarctic invertebrates using existing and field collected samples. Project partner: South Australian Museum

Project 6) Bioinformatics: Designing, programming and implementing software plug-ins for GENEIOUS, to allow the interface between environmental metagenomic data and end-users, including conservation, water and health managers. Project partners - Biomatters, NZ (producers of GENEIOUS)

The PhD projects are available to Australian and NZ citizens/permanent residents with a 1st class Honours degree. Applicants will also be encouraged to apply for Australian postgraduate awards (due Oct 31st) where applicable, refer to this website for the application process http://www.adelaide.edu.au/graduatecentre/-scholarships/postgrad/pgresearch/apa.html. International students are also invited to apply, although international course fees are likely to be applicable. Other PhD projects are also available at ACAD - http://www.adelaide.edu.au/acad/ .Please contact Maria Lekis (maria.lekis@adelaide.edu.au) or Prof. Alan Cooper (alan.cooper@adelaide.edu.au) for further details.

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Prof. Alan Cooper, Federation Fellow

Darling Blg (DP 418), Rm 209b University of Adelaide North Terrace Campus South Australia 5005 Australia

Email: alan.cooper@adelaide.edu.au Ph: 61-8 -8303-5950/3952 Fax: 61-8-8303 4364

http://www.ees.adelaide.edu.au/acad/
alan.cooper@adelaide.edu.au

UAdelaide EvolutionaryBiol

Subject line: Ph D scholarships in Evolutionary Biology - Adelaide, Australia

PH.D Scholarships in Evolutionary Biology - University of Adelaide

$20 427 per annum tax-free: closing date 31 October.

Australian Postgraduate Awards (APA's) are available to Australian residents with a First Class Honours result or equivalent (e.g. publications), to support their study towards a Higher Degree by Research. Value: approximately $20,427 per annum (2009 rate), tax free for up to 3 years (indexed annually), possible extension for up to six months. The awards are allocated as part of the Major Round of applications.

There are also Divisional Scholarships as well as the APA's: if an applicant is eligible to enrol, and has a project and agreed supervisor, a Divisional Scholarship is likely to be awarded.

See this site for information on how to apply and the application forms

http://www.adelaide.edu.au/graduatecentre/-scholarships/postgrad/pgresearch/apa.html See these sites for information on some potential supervisors: http://www.adelaide.edu.au/environment/acebb/-projects/evomol.html http://www.adelaide.edu.au/-environment/acebb/projects/vertebrates.html Regards,

Michael Lee

Michael Lee <michael.s.lee@adelaide.edu.au>

UArizona EvolutionaryBiol

PhD Studentships in Evolutionary Biology, University of Arizona

Two NSF-funded graduate positions are available in the laboratory of Dr Alex Badyaev http://-www.u.arizona.edu/ ˜ abadyaev in the Department of Ecology and Evolutionary Biology at the University of Arizona.

The first project addresses the developmental and genetic basis of convergence in local adaptations across recently established bird populations along northern Continental Divide of North America. The project combines landscape ecology, population genetics and molecular biology approaches and requires extensive and prolonged fieldwork in some of the most remote (and most beautiful) places in the northwest.

The second project addresses evolution and diversification of biochemical pathways for synthesis of diet-derived pigmentation in animals and requires interest in either microbiology or biochemistry, and a good grasp of basic statistical methods.

Students are expected to design their own doctoral projects under these general umbrellas. For more information and to apply, please contact Dr Alex Badyaev (abadyaev@email.arizona.edu) by 25 November 2009. Both positions start in August 2010, but an earlier start for field and lab work is available.

abadyaev@email.arizona.edu
abadyaev@email.arizona.edu

UBergen 2 SystematicBotany

2 PhD fellowships in systematic Botany available at University of Bergen - Museum of Natural History. See web page for full instructions on how to apply: http://www.jobbnorge.no/job.aspx?jobid=61843 http://www.jobbnorge.no/job.aspx?jobid=61844 1. PhD fellowship in Lichenology (Systematic Botany)

Apply: http://www.jobbnorge.no/job.aspx?jobid=61843 Closing date for application: 31.10.2009 Reference number: 09/11885

Applicants must hold a master-/cand. scient.-degree or equivalent in botanical systematics/taxonomy, preferably in the field of lichenology. The master's degree must be completed by the application deadline. Candidates with experience with morphological and molecular systematics will be preferred. The research fellow must take part in the University's approved PhD program leading to the degree within a time limit of 3 years. Hence, applicants must meet the formal admission requirements for the PhD program. A description of the proposed research project and a progress plan for the doctoral studies will be elaborated with the scientific group. The principal supervisor for the project must be a scientist with a permanent position at Museum of Natural History. In total, the fellowship period is 4 years. For positions with 4-year duration, 25 % of the period will consist of duties at Museum of Natural History. The length of the fellowship period may be reduced if the successful applicant has held previous research fellow employments.

Starting salaries at salary level 45 (code 1017) on the government salary scale (corresponding to NOK 355.600 per year), following ordinary meriting regulations (wage levels 45-51).

Additional information on the position is obtainable from Professor Tor Tønsberg, phone +47 55 58 33 33, e-mail: tor.tonsberg@bm.uib.no.

2. PhD fellowship in Systematic Botany

Apply: http://www.jobbnorge.no/job.aspx?jobid=61844 Closing date for application: 31.10.2009 Reference number: 09/11888

Applicants must hold a master-/cand.scient.-degree in botanical systematics/taxonomy, or equivalent. The master's degree must be completed by the application deadline. Candidates with experience with morphological and molecular systematics will be preferred. The Arboretum and Botanical garden at Milde has large living collections of plants that are aimed for research. Research on the systematics of the Rose family is one of the main focuses at the Arboretum, and the research fellow will take part in this research. A main aim will be to resolve the evolutionary relationship of the genus Sorbus.

The research fellows must take part in the University's approved PhD program leading to the degree within a time limit of 3 years. Hence, applicants must meet the formal admission requirements for the PhD program. A description of the proposed research project and a progress plan for the doctoral studies will be elaborated with the scientific group. The principal supervisor for the project must be a scientist with a permanent position at Museum of Natural History. In total, the fellowship period is 4 years. For positions with 4-year duration, 25 pct of the period will consist of duties at the Arboretum and Botanical garden. The length of the fellowship period may be reduced if the successful applicant has held previous employment as a research fellow.

Starting salaries at salary level 45 (code 1017) on the government salary scale (corresponding to NOK 355.600 per year, following ordinary meriting regulations (wage levels 45-51).

Additional information on the position is obtainable from associate professor Heidi Lie Andersen, phone +47 55 58 33 20/+47 55 98 72 57, e-mail: Heidi.Andersen@bm.uib.no.

Bjarte Henry Jordal <Bjarte.Jordal@zmb.uib.no>

UBern BeetleEvolution

Other: Master Thesis Project for the Study of Sociality and Mutualism in Ambrosia Beetles

We search for highly motivated students to join a study on haplodiploid Ambrosia beetles showing cooperative breeding and fungus gardening. Depending on interest, there are several potential projects to choose from in order to study the ecology, behaviour and microbial interactions of ambrosia beetles. Experiments will be performed in the field and laboratory, and questions to be studied include “The functional significance of different cooperative behaviours performed by larvae and adult female helpers”, “The conditions influencing dispersal”, “Interactions among beetles, fungi and bacteria within their galleries”, and “Male outbreeding tactics”, among others. The study will be located at the University of Bern, Switzerland, and involve collaborations with different laboratories in Europe and North America.

Competitive funding is available by the University Bern for excellent international students See application: http://www.int.unibe.ch/content/incoming/-master_grant/index_eng.html For details about potential projects and a description of the species see our homepage http://behav.zoology.unibe.ch/-index.php?pp=55&pF Master projects can start any time but the application deadline for the University of Bern Master grants for 2010/11 is 18 December 2009.

Interested? Please contact:

Peter Biedermann, MSc peterbiederm@students.unibe.ch <mailto:peterbiederm@students.unibe.ch>

Michael Taborsky, Prof michael.taborsky@iee.unibe.ch <mailto:michael.taborsky@iee.unibe.ch>

Peter Biedermann <peterbiederm@students.unibe.ch>

UBern PopulationGenomics

PhD position in Population Genomics

The CMPG lab (http://cmpg.iee.unibe.ch) is looking for a highly motivated student to work with Laurent Excoffier and Matthieu Foll on the joint estimation of selective and demographic processes having occurred in the recent history of populations.

These investigations will be done by a combination of theoretical and computational approaches. It will involve the simulation of selective processes in a spatially explicit and heterogeneous environment. These simulations should be integrated into an inferential framework (e.g. Approximate Bayesian Computations) with the aim of detecting loci responsible for adaptations to specific environments and measuring selective pressures from genomic data, including next generation sequencing data in humans and voles.

The successful applicant should have a Masters in Biology, Bioinformatics, or Statistics, and some previous experience in population genetics, statistics and programming (e.g. in C/C++, Java, or R).

Post-graduate teaching and seminars are held in English in the Institute of Ecology and Evolution, and it is also the working language in the CMPG lab. Notions of German or French could be helpful but not absolutely necessary for daily life. The CMPG lab is well equipped with computational tools including a 64 node Linux cluster, and access to the much larger Ubelix cluster of the University (1000+ CPUs). Our lab is also affiliated to the doctoral program in Ecology and Evolution (http://www.unil.ch/ee), the Swiss NSF ProDoc program in Population Genomics, and the Swiss Institute of Bioinformatics (http://www.isb-sib.ch), which all provide access to stimulating and helpful doctoral training and courses (held in English).

The position is open until filled, and could start, for a minimum of 3 years, earliest on 1st January 2010. Gross salary follows the UniBE scale and is around 40,000 CHF (about 25,000) per year.

Applicants should send (before December 1st 2009) within a single pdf file, a motivation letter with names and emails of two referees, a CV, and a publication list to laurent.excoffier@iee.unibe.ch

The city of Bern is listed among those offering the best quality of life in the world, and it is listed as a UNESCO world heritage site. The Swiss capital has a broad range of cultural activities, and is well connected to major Swiss and European cities. It is conveniently located near the Swiss Alps, offering a wide range of outdoor activities. Rents remain very affordable and there is a vast choice of accommodation. More information is available on http://www.berninfo.com/en . Relevant CMPG publications on this topic include:

Currat M, Excoffier L, Maddison W, et al. (2006) Comment on “Ongoing adaptive evolution of ASPM, a brain size determinant in Homo sapiens” and “Microcephalin, a gene regulating brain size, continues to evolve adaptively in humans”. Science 313, 172. Fagundes NJ, Ray N, Beaumont M, et al. (2007) Statistical evaluation of alternative models of human evolution. Proc Natl Acad Sci U S A 104, 17614-17619. Excoffier L, Foll M, Petit RJ (2009) Genetic Consequences of Range Expansions. Annual Review in Ecology, Evolution, and Systematics 40.481-501 Excoffier L, Hofer T, Foll M (2009) Detecting loci under selection in a hierarchically structured population. Heredity.

Deadline for application is December 1st 2009

– Laurent Excoffier

Computational and Molecular Population Genetics (CMPG) Institute of Ecology and Evolution, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email (NEW): laurent.excoffier@iee.unibe.ch http://cmpg.unibe.ch/people/excoffier.htm Computational Population Genetics Swiss Institute of Bioinformatics (SIB) http://www.isb-sib.ch/groups/-Computational_Population_Genetics.htm Laurent Excoffier <laurent.excoffier@iee.unibe.ch>

UBuffalo AngiospermGenomeEvolution

Graduate Research Assistantship - Basal Angiosperms

Research Assistantship, *pending funding*, 2 years, to study genome evolution in basal angiosperms. Good molecular biology background required, and hands-on experience with advanced microscopy, FISH (Fluorescence In Situ Hybridization) or other in situ methods *strongly* preferred. Interested persons should contact Prof. Victor A. Albert (vaalbertbuffalo.edu; http://biology.buffalo.edu/Faculty/Albert/albert.html). Include CV and list of 3 references. Target start date is the beginning of Spring semester, 2010, at the University at Buffalo. GREs (TOEFL, if necessary) and application will be required very soon to be considered.

– Victor A. Albert Empire Innovation Professor of Biological Sciences University at Buffalo (SUNY) http://biology.buffalo.edu/Faculty/Albert/albert.html “Victor A. Albert” <vaalbert@buffalo.edu>

UEastAnglia Warbler MHC Diversity

Evolutionary and Conservation Genetics in the Seychelles Warbler : MHC Diversity

The vertebrate Major histocompatability complex (MHC) locus, with its central function in detecting pathogen antigens and triggering the acquired immune response, plays an important role in individual fitness and, potentially, the long term viability of populations. The amazingly high polymorphism usually seen at the MHC appears to be maintained by pathogen mediated selection and/or sexual selection. The aim of this study is to measure the impact of individual MHC variation on fitness in a system where we have complete information on individual survival and fecundity. We have studied the Seychelles warblers on Cousin Island intensively since 1997; almost all nests and individuals are monitored and parentage is identified by DNA profiling. The project will use modern molecular techniques to identify the MHC characteristics of every individual within the population, and analyse how these, along with life-history traits and pathogen infection, effect individual survival. The data obtained will, therefore, allow us to investigate the role of pathogen mediated selection on the maintenance of variation at the MHC. Importantly the study will also investigate MHC variation in historical populations (sampled through museum specimens) and new populations which have been established as part of the ongoing conservation programme for this species. This assessment of historical, founder and new populations will allow us to investigate the impact of demographic changes (including those resulting from conservation measures) on levels of MHC variation, and test if MHC diversity in the new populations is adequate for their future long-term survival. The issue of how (and what type of) genetic variation is maintained in small bottlenecked populations of endangered species is an important question in contemporary conservation, hence the involvement of Birdlife International in this project. Training will be provided in molecular methods, evolutionary theory, statistical modelling and ornithological fieldwork.

SUPERVISOR(S) David S Richardson UEA, in conjunction with Prof . T Burke (Sheffield University) and Dr Nigel Collar (Birdlife International)

Application Deadline: Please apply as soon as possible to maximize options - but final deadline - December 4th 2009

Please contact David S Richardson (david.richardson@uea.ac.uk) with questions, but apply via the forms on the UEA web page

http://www.uea.ac.uk/mac/admissions/courses/-PG#pgr David S Richardson Centre for Ecology, Evolution and Conservation School of Biological Sciences University of East Anglia e-mail: david.richardson@uea.ac.uk<b.emerson@uea.ac.uk> Norwich NR4 7TJ ph: (44) 01603 591496 ENGLAND fax: (44) 01603 592250

http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=325 "Richardson David Dr (BIO)" <David.Richardson@uea.ac.uk>

UFlorida HostParasite Coevolution

A PhD position is available in the laboratory of Dr. David L. Reed, University of Florida, Florida Museum of Natural History.

Description: The PhD student will contribute to an NSF-funded project that infers patterns of human evolutionary history from a host- specific human parasite (lice). This person will split their time working on the objectives of the funded proposal as well as developing their own dissertation research. These parasitic lice have been cospeciating with their primate hosts for over 25 million years, which provides a great opportunity for phylogenetic and population level research topics. Because there is a sequenced and annotated genome for the human body louse, dissertation projects that utilize genome- level approaches to address population-level questions are encouraged. Work underway in my lab uses coalescent simulation and other tools of population genetics to determine the extent to which human lice can serve as markers of human evolutionary history. Dissertation questions could relate to the process of the Peopling of the Americas, interactions between modern and archaic humans, genes related to the louse's capacity as a vector of disease (only some types of lice carry disease), genetic or epigenetic change that induces ecophenotypic plasticity, or patterns of migration and gene flow among host and parasite populations.

Candidate Experience: Candidates for this position should have a strong interest in host/parasite relationships, evolution, and the use of molecular tools to study populations and species. Ideal qualifications include a background in population genetics, genomics, and/or experience in molecular methods including knowledge of bioinformatics and genome screening techniques. Extensive travel is expected to work with colleagues in clinics worldwide who are collecting parasites for this project. Therefore, a valid passport and an eagerness to travel are required.

For consideration, please send a cover letter, curriculum vitae, and a statement of research experience that explains your background and specific interests in the project to David Reed (dlreed@ufl.edu) The Reed Lab studies wide ranging projects on mammals and their parasites. Our lab is highly collaborative and collegial. You can find links to PDFs of publications, public press coverage of our work, photos, and project descriptions at the Reed Lab website at http://www.flmnh.ufl.edu/-mammals/ NOTE: The selected student is expected to enroll in the Graduate Program in the Department of Biology at UF for Fall 2010. Applications are due to the Dept. by Dec. 15th; additional information about admission requirements can be found at: http://www.biology.ufl.edu The Department of Biology guarantees funding for 5-6 years through Fellowships, Research Assistantships, or Teaching Assistantships.

best wishes, David Reed

David L. Reed, Ph.D. Associate Curator of Mammals Florida Museum of Natural History University of Florida Dickinson Hall, Museum Rd & Newell Dr. Gainesville, FL 32611 (352) 273-1971 (voice) (352) 846-0287 (fax) e-mail: dreed@flmnh.ufl.edu http://www.flmnh.ufl.edu/mammals/ dlreed@ufl.edu dlreed@ufl.edu

UGeneva FunctionalGenomeEvolution

We are looking for a highly motivated and innovative PhD student candidate (~4 years) to explore the wealth of genomic data from evolutionary perspectives using bioinformatics approaches. Our group has a broad range of interests related to the functional evolution of genomes, and actively contributes to international genome analysis consortia. The specific project aims and objectives will be developed together with the candidate to suit interests and skills.

The ideal candidate should have a strong background in bioinformatics, including programming skills (or the willingness and drive to acquire them), and a good understanding of molecular biology (preferably with some experience/background in molecular evolution). A Diploma or MSc degree in Biology or Bioinformatics, practical experience in the Unix environment, and fluency in English are required.

The project will be supervised by Prof. E. Zdobnov in the Department of Genetic Medicine and Development at the University of Geneva Medical School. We are also part of the renowned Swiss Institute of Bioinformatics, and offer a stimulating research environment with excellent facilities.

The international city of Geneva, described as 'the smallest of the large capitals', offers a vibrant city life within easy reach of the picturesque lake and stunning Alps.

Closing date for applications: 15 November 2009.

To apply: send your CV, statement of research interest, and names and contact details of at least two referees by e-mail to Evgeny.Zdobnov@isb-sib.ch

Further Information:

Computational Evolutionary Genomics Group, CEGG: http://cegg.unige.ch Swiss Institute of Bioinformatics, SIB: www.isb-sib.ch Online version of this advertisement: http://cegg.unige.ch/jobs/phd_2 Address: CEGG, CMU / 9022, Rue Michel-Servet 1, CH-1211 Geneva 4, Switzerland

Robert Waterhouse

Robert Waterhouse <robert.waterhouse@unige.ch>

ULaval SprucePopulationGenet

Hello,

Our group at Laval University in Québec City would like to post an offer for a graduate student scholarship in Forestry (Population genetics of wood properties in white spruce).

Graduate assistantship (M. Sc.) Population genetics of wood properties in white spruce. Center for Forest Research and Institute for Integrative and Systems Biology (IBIS) Laval University (Quebec, Canada) A graduate assistantship is available for a Master's degree in forest sciences at Laval University to investigate the genetic variability of wood properties among populations of white spruce trees (Picea glauca). The project is a partnership between the Canadian Wood Fibre Center (CWFC) (Dr J. Beaulieu), Laval University (Dr J. MacKay) and the Ministry of Natural Resources and Fauna of Quebec. The impact of genetics on the variability of wood properties will be investigated by comparing populations from several distinct eco-regions. The specific goals are as follows:

* Quantify the variability of wood fibre traits among white spruce populations from different ecoregions in Quebec;

* Investigate correlations between wood fibre traits and growth conditions such as the site index and stand structure in order to develop predictive models for wood quality;

* Verify the degree of relatedness between sampled trees by using DNA markers in order to: i) assess the potential impact of genetic relatedness on correlations between traits and growth conditions or ii) use it as a variable in the models.

Laboratory work mainly includes DNA extractions and genotyping of several markers to estimate the degree of relatedness between trees from different ecoregions. Statistical analysis of wood and fibre property data will assess if significant variation can be attributed to the origin of the trees (ecoregions) and to develop mathematical models to predict wood properties. The results will find application in applied tree breeding programs. A stipend of 16000 $ (CAN) per year is available for a two year period starting as early as January 2010. Laval University is a French language institution which welcomes many international students, and offers high quality graduate training and access to modern and well-equipped laboratories in the areas of forest genetics and genomics within the Institute for Integrative and Systems Biology (IBIS). Contact Dr John Mackay, by email john.mackay@sbf.ulaval.ca (Department of wood and forest sciences, Laval University, Quebec, Quebec, Canada, G1K 7P4, http://www.arborea.ulaval.ca/-project_team/principal_investigators/john_mackay/-index.html).

If you need any additional information, please do not hesitate to contact me.

Sincerely yours,

Claudia Careau Administrative assistant Centre for Forest Research Charles-Eugene-Marchand Building, office 2155 1030 avenue de la Médecine Laval University Quebec, Quebec G1V 0A6 Phone: 418-656-3703 Fax: 418-656-7493

claudia.careau@sbf.ulaval.ca

ULeipzig HumanOrigins

The Leipzig School of Human Origins, an International Max Planck Research School by the University of Leipzig and the Max Planck Institute for Evolutionary Anthropology, offers a unique interdisciplinary graduate program to study the evolutionary history of humans and great apes.

Graduate students are accepted into one of the following areas, but are encouraged to take part in courses and seminars from all three disciplines:

Comparative and Molecular Primatology - focusing on the evolution of social and cultural systems in the great apes, as well as other relevant mammals.

Evolutionary and Functional Genomics, Ancient DNA, Molecular Anthropology and Genome Bioinformatics - focusing on the evolutionary and functional genomics of humans and the great apes, as well as the retrieval of DNA from palaeontological remains.

Human Paleontology, Prehistoric Archaeology and Archaeological Science - focusing on computational approaches to the management and analysis of gene expression data.

We invite applications from all countries. Applicants must hold a Masters degree or equivalent in biology, biochemistry, anthropology, or related fields. If you hold an excellent BSc/BA (1st class honours) please contact us about possible accession.

It is not necessary to hold the degree at the point of application. However, you must have been awarded your degree prior to the start of the program in September.

Candidates have to be fluent in written and spoken English. German is not required but international students will be offered opportunities to take German courses.

Ph.D. students are supported by fellowships which are provided either by the Max Planck Institute for Evolutionary Anthropology or the University of Leipzig; or have been obtained by the student.

Term of Appointment: Fall 2010 Application Deadline: January 31, 2010

The language of the school is English. Visit www.leipzig.de for information on living in Leipzig, Germany, in the center of Europe.

Contact Information: Sandra Jacob Deutscher Platz 6 Leipzig, 04103, Germany Telephone Number: ++493413550122 Fax Number: ++493413550119 Website: www.leipzig-school.eva.mpg.de E-mail Address: leipzig-school@eva.mpg.de

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Sandra Jacob Max Planck Institute for Evolutionary Anthropology / The Leipzig School of Human Origins (Ph.D. Programme) Deutscher Platz 6, 04103 Leipzig, GERMANY phone: ++49 (0) 341 3550-122; fax: ++49 (0) 341 3550-119 http://www.eva.mpg.de/ http://www.leipzig-school.eva.mpg.de/

Sandra Jacob <jacob@eva.mpg.de>

UMassachusetts CiliateBiodiversity

GRADUATE STUDENT POSITION Biodiversity of Ciliates In Near-Shore Environments Smith College / UMass Amherst

We are looking for a highly motivated student to join our project, which aims to elucidate the patterns of diversity of ciliates from near-shore environments and to explore the ecological processes that underlie this diversity. The project is collaborative between Laura Katz's lab at Smith College and marine ecologist George McManus at the University of Connecticut. Work on the project combines culture-independent approaches with analyses of targeted morphospecies. Techniques include analyses of clone libraries, DGGE, and both light and fluorescence microscopy.

Graduate students in Laura Katz's laboratory join either through MS program at Smith College or the Ph.D. program in Organismic and Evolutionary Biology at the University of Massachusetts Amherst. Interested individuals should visit the web sites below and contact Dr. Laura Katz directly (lkatz@smith.edu)

Laura Katz, Smith College http://www.science.smith.edu/departments/Biology/lkatz/ OEB at UMass Amherst http://www.bio.umass.edu/oeb/ http://www.bio.umass.edu/oeb/admissions Smith College MS in biology http://www.science.smith.edu/departments/Biology/graduate.html http://www.smith.edu/gradstudy/ Collaborator George McManus, University of Connecticut http://microzooplankton.uconn.edu/ Laura A Katz <lkatz@smith.edu>

UMassachusetts CiliateGenomeEvol

GRADUATE STUDENT POSITIONS Genome Evolution in Ciliates Smith College / UMass Amherst

We are looking for highly motivated students to work on genome evolution in ciliates. All ciliates are defined by the presence of both a germline micronucleus and somatic macronucleus within each cell. Some ciliates, including those that are the focus of our work, extensively process their somatic genomes to generate gene-sized macronuclear chromosomes. We are looking at the patterns and processes that underlie these developmentally-regulated genome rearrangements. We are also exploring mitochondrial genomes from diverse ciliates to provide an evolutionary framework for our studies.

Graduate students in Laura Katz's laboratory join either through MS program at Smith College or the Ph.D. program in Organismic and Evolutionary Biology at the University of Massachusetts Amherst. Interested individuals should visit the web sites below and contact Dr. Laura Katz directly (lkatz@smith.edu)

Laura Katz, Smith College http://www.science.smith.edu/departments/Biology/lkatz/ OEB at UMass Amherst http://www.bio.umass.edu/oeb/ http://www.bio.umass.edu/oeb/admissions Smith College MS in biology http://www.science.smith.edu/departments/Biology/graduate.html http://www.smith.edu/gradstudy/
Laura A Katz <lkatz@smith.edu>

UNewBrunswick InvertebratePopulationGenetics

M.Sc. position: Marine invertebrate population genetics.

I seek a highly motivated and enthusiastic candidate to fill a fully funded MSc position in the Department of Biology at University of New Brunswick (Fredericton). The project will use DNA sequence variation to assess the level of genetic subdivision and patterns of gene flow among populations of the abundant marine amphipod Corophium volutator. The successful candidate will join a multi-disciplinary collaboration between researchers at UNB, Carleton University, and Mount Allison University. Our aim is to model the environmental interactions between climate driven processes and the population dynamics of C. volutator throughout the mudflats in the Bay of Fundy, Canada.

For more information about the Biology Department, see: http://www.unb.ca/fredericton/science/biology/ For information about Graduate Studies at UNB, see: http://www.unb.ca/gradschl/ For enquires, or to apply, email a CV or resume, a letter of interest, unofficial transcripts and contact information for 3 references to Jason Addison (jaddison@unb.ca). The review of applications will begin immediately and will remain open until the position is filled. Work could potentially begin anytime, but admittance to the Graduate Studies program is expected in January, May, or September of 2010.

Jason Addison

Jason Addison <jaddison@unb.ca>

UOklahoma DaphniaEvolution

Graduate Research Assistantship (GRA)/Ph.D. student position available: A Ph.D. student position is available in my laboratory to work on a new 3-year NSF-funded project entitled, -environment interactions V impact of cultural eutrophication on Daphnia tracked by genomics, physiology, and resurrection ecology.

In a planned 36-month project in collaboration with colleagues at Oklahoma State University and Indiana University, the PIs will use an integrated approach involving genetic/genomic, physiological, and ecology methods to examine how cultural eutrophication (i.e., enrichment of freshwater systems with nutrients such as phosphorus) influences evolutionary changes in organisms. The waterflea, Daphnia pulex, which plays a major role in freshwater food webs (i.e. it eats algae/bacteria and in turn is fed upon by fish), will serve as the model organism. Daphnia are ideal for such studies because they produce resting eggs that can lay dormant in lake sediments for long periods of time. Decades-old eggs can be induced to hatch (i.e. ecology) and viable DNA can be extracted from eggs that are centuries old. Moreover, the D. pulex genome has been sequenced and genetic/genomic methods (i.e. gene expression) are in place to study how changes in eutrophication (phosphorus-level) patterns over the past century have influenced how an organism like a daphniid can respond to ecosystem/environmental change. Results from this cross-disciplinary study will provide an excellent example of how man-made environmental changes (via eutrophication) influence natural (freshwater) ecosystems.

For more details and information, please contact:

Dr. Lawrence J. Weider, Professor of Zoology Director, The University of Oklahoma Biological Station (UOBS) University of Oklahoma Norman, OK 73019 Phone: 1-405-325-4766 or 325-7438 FAX: 1-405-325-0835 ljweider@ou.edu<mailto:ljweider@ou.edu> http://www.ou.edu/uobs/weider.html "Weider, Lawrence J." <ljweider@ou.edu>

UOslo MicrobialEvolution

Position as Doctoral Research Fellow (PhD-stipendiat) in microbial ecology/mycology is available at Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo, Norway.

The position is affiliated to a project initiated by the Microbial Evolution Research Group (MERG) in collaboration with Laboratory for microbial dynamics (LaMDda), University of Oslo. The position is available from November 1. 2009 for 4 years and includes 25% compulsory services, which typically includes lecturing and co-supervision of master students in the Department.

We seek a highly motivated and enthusiastic person with a good academic record and collaborative ability to work on a project dealing with microbial community ecology of mycorrhizal symbiosis. Focuses will be on the bacteria and fungi associated with the mycorrhizal symbiosis and the interplay between the plant host, fungal symbionts and the associated bacteria and possibly also transcriptional patterns in the symbionts in relation to selected, environmental and biotic factors. Both observational field studies and experiments will be conducted. The experiments will involve the establishment of an in vitro model system, where effects of bacterial and fungal species in the symbiotic relationship will be tested, including soil-borne species of Bacillus and available single gene mutants.

The project may involve field-work, green-house experiments, isolation of organisms and culturing, microscopy, metagenomics, DNA and cDNA libraries, and pro- and eukaryote transcriptomics. High throughput sequencing methods (e.g. 454 sequencing) as well as bioinformatics will play important roles in the project. The research group has access to a Roche 454 FLX Genome sequencer and extensive microscopy and bioinformatics infrastructures. The PhD student will be supported by collaborative students and faculty members within bioinformatics, microbial genomics, taxonomy and field-oriented evolutionary and ecological research.

The applicant must have a master's degree (or equivalent) within biology or related disciplines and excellent written and oral communication skills. Experience with any or all the following topics is highly desirable: microbiology, mycology, plant biology, molecular biology and molecular genetic techniques (e.g. PCR, sequence analysis, DNA-fingerprinting, gene expression studies, cloning), bioinformatics and microscopy.

For more details about the application, contact information, etc. see http://www.admin.uio.no/opa/ledige-stillinger/2009/vitenskapelige/doctoralresearchfellowBiology-2009-14863.html haavarka@ulrik.uio.no haavarka@ulrik.uio.no

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UOsnabrueck ParasitesInteractions

Graduate position: Parasites Interactions (Osnabrueck, Germany)

The Department of Biology at the University of Osnabrueck (Germany), invites applications for a PhD-position (E13/2), fixed-term position for 3 years on intra-host parasite interactions

Parasites interact with their host potentially leading to host-parasite coevolution, but different parasite genotypes infecting the same host may also interact, either by competition or by cooperation. The PhD project aims at characterising these interactions using the nematode Caenorhabditis elegans as a host and its bacterial microparasite Bacillus thuringiensis, including experimental evolution of parasite-parasite-host interactions. The main focus lies in the evolution of cooperation or competition, which in return should influence the evolution of virulence, resistance, associated costs and generation/maintenance of diversity. The project includes phenotypic and genetic analysis.

The project is funded by the German Science Foundation (SCHU 2522/1-1) and is part of the priority programme SPP 1399 on host-parasite coevolution. Thus, it interacts with other research groups across Germany and abroad, and in particular with projects using the same model organisms encouraging contact between PhD students working on related topics.

The project is supervised by Dr. Rebecca Schulte and it is based in the Department of Behavioural Biology at the University of Osnabrueck, Germany (head: Prof. Dr. Judith Korb). Research topics include conflicts and cooperation within and between species with special emphasis on evolutionary aspects.

Requirements

This position requires a Diploma/Master in Biology. Candidates should have a good background in evolutionary biology and knowledge of host-parasite interactions. Prior laboratory experience is required as well as handling of complex experiments and data (statistics). She/he should work well as member of a team and have good English skills. Knowledge of microbiology and/or experience with C. elegans is advantageous.

The University of Osnabrueck is committed to equal opportunity in employment and gender equality in its working environment. We strongly encourage applications from qualified women. Applications from appropriately qualified handicapped persons are also encouraged.

Applications

Please send applications with CV, one-page statement of research interests, and two references, as a pdf-file by email to Rebecca Schulte (rebecca.schulte@biologie.uni-osnabrueck.de). Alternatively, it can be posted to the Dean of the Department of Biology/Chemistry, University of Osnabrück, Barbarastraße 11, D-49069 Osnabrueck, Germany.

Deadline for applications: 20th November 2009. Start of position: as soon as possible.

For further information, please contact Rebecca Schulte (rebecca.schulte@biologie.uni-osnabrueck.de)

Rebecca Schulte, PhD Behavioural Biology University of Osnabrueck Barbarastr. 11 D-49076 Osnabrueck Germany e-mail: rebecca.schulte@biologie.uni-osnabrueck.de phone: +49 541 969 2458 fax: +49 541 969 2862

Rebecca.Schulte@Biologie.Uni-Osnabrueck.DE
Rebecca.Schulte@Biologie.Uni-Osnabrueck.DE

UOtago Genetics Cryptic Female Choice

Ph.D. Project Opportunity Available to Investigate the Genetic basis of Cryptic Female Choice in Chinook Salmon

We are currently seeking a student with interests in genetics, evolution, and behavioural ecology to conduct research into the genetic basis of possible cryptic female choice in Chinook salmon.

Project Description In many species females can control fertilisation after mating via behavioural, morphological, and physiological mechanisms - a process called cryptic female choice (CFC). While widespread, it is generally unknown, if and how CFC might be exerted in external fertilisers, where eggs and sperm are shed simultaneously into the surrounding water. Recently we demonstrated in salmon that ovarian fluid, a viscous substance released with eggs during spawning, differentially alters male sperm function in a female-dependent fashion, and thus that females may exert cryptic control of male reproductive success (Rosengrave et al.2008. A mechanism for cryptic female choice in chinook salmon. Behavioral Ecology 19: 1179-85). The rationale for this CFC is unknown, but our hypothesis is that ovarian-fluid-mediates sperm selection promoting favoured genetic combinations that enhance offspring fitness. We will test this hypothesis using a novel combination of CASA, compositional analyses, replicated paired-male competitive in vitro fertilisation experiments that mimic the gametic microenvironment, and genetic screens of MHC class I, class II and microsatellite loci to establish parentage. Using these approaches we will determine (i) the effects of a given female's ovarian fluid on a male's sperm function, (ii) how this male x female interaction influences male reproductive success, (iii) whether particular male and female genotype combinations (MHC I, II and microsatellites) are associated with greater or lesser sperm performance and male reproductive success, and (iv) whether any compositional differences among gametic fluids explain the patterns we observe. Our expectation is that the successful PhD student will focus on tasks ii), and iii), while contributing to the others.

The Ideal Candidate The ideal candidate will possess experience in molecular genetics, evolutionary genetics and behavioural ecology. They will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research programme. They will be a competent laboratory worker, with experience of all routine molecular genetic techniques, particularly microsatellite genotyping and sequencing, and should be computer literate with familiarity with database management and statistical analyses. Minimum qualifications: B.Sc. (Hons) and/or M.Sc. in Genetics, Molecular Biology, Molecular Ecology or equivalent.

Scholarship and Funding This project has no stipendiary award to support the student, but there is ample financial support for the research costs for the next three years via a Marsden grant that commences in 2010. Thus, we are seeeking a high achieving student with an A- average or better who we expect will be able to secure a University of Otago or Departmental scholarship to support their studies. Other avenues of support such as NZAID and NZIDR awards are also possibilities, but the deadline for many of these awards has passed for this year (see http://www.otago.ac.nz/study/scholarships/).

Eligibility The University of Otago and Departmental scholarships are open to all nationalities. However, candidates for whom English is not a first language must satisfy the English Language Requirements of the University to be eligible for study, see http://www.otago.ac.nz/international/postgraduate/english_requirements.html .Other eligibility criteria are detailed here http://www.otago.ac.nz/international/postgraduate/entrance_requirements.html . How to Apply Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmell, in the first instance. To apply, please send your Curriculum Vitae, a copy of your academic transcript, a sample of your written scientific work and the names of three referees with a covering letter to:

Professor Neil J. Gemmell Centre for Reproduction and Genomics (www.crg.org.nz) e-mail: neil.gemmell@otago.ac.nz

The closing date for the main round of UOtago Scholarships is 2 November 2009 so interested applicants should contact me as soon as possible to avoid missing this deadline.

Neil J. Gemmell Professor and Director Centre for Reproduction and Genomics Department of Anatomy & Structural Biology University of Otago, PO Box 913 Dunedin 9054 New Zealand

Phone: +64 3 479 6824 Fax: +64 3 479 7254 e-mail: neil.gemmell@otago.ac.nz

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UppsalaU Aging ExperimentalEvolution

Graduate position: UppsalaU.Aging.ExperimentalEvolution

PhD position in the evolutionary biology of aging is available at the Department of Animal Ecology, Uppsala University, Sweden.

The project will focus on two crucial yet poorly understood issues in the evolutionary biology of aging sex-specific selection and condition-dependence using animals with short generation time, such as the dioecious nematode worm /Caenorhabditis /remanei/// and the seed beetles (e.g. Callosobruchus maculatus//), as main model systems. The project will combine the experimental evolution with classical behavioural ecology approach. The main objective is to understand the evolution of sex differences in lifespan and reproductive aging. ///

/ /

/Applicants should have a MSc (or equivalent) in biology/ecology and a strong interest in evolutionary biology and behavioral ecology. Special interest in the evolution of life-histories and/or sexual selection is a plus. The project will be supervised by Alexei Maklakov (see http://www.iee.uu.se/zooekol/default.php?type=personalpage&id=87&lang=en < http://www.iee.uu.se/zooekol/default.php?type=personalpage&id=87&lang=en >) and the candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (EBC) (see http://www.ebc.uu.se/index_eng.php). The working atmosphere is international with English as working language. EBC 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./

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/This position is financed for four full years, and the successful candidate will receive a postgraduate fellowship the first year (15.500 SEK/month) and a postgraduate position year 2-4 (22.000 - 24.500 SEK/month)./

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/Important dates: The position is open until filled but all applications submitted by *November 15, 2009* will be given full consideration. The preliminary starting date is January 15, 2010, but is flexible./

/ /

/Applications should include: 1) short letter of interest / background (2 pages max); 2) complete CV; 3) a description of undergraduate training; 4) a copy of undergraduate degree and 5) the names and e-mail addresses of 2-3 referees. Applications should be sent by e-mail to Alexei.Maklakov@ebc.uu.se <mailto:Alexei.Maklakov@ebc.uu.se>. Alternatively, send hardcopies to the following address: /

/ /

/Alexei Maklakov /

/Animal Ecology/EBC /

/Uppsala University/

/Norbyvägen 18D, SE-752 36 /

/Uppsala, Sweden. /

/Please feel free to contact me by e-mail or by phone (+46-18-471 2702) for more information.///

/ /

/Note that there is another PhD position on a related topic available at EBC in the Department of Evolutionary Biology under supervision of Urban Friberg (see http://www.egs.uu.se/evbiol/Persons/Urban.html). This creates opportunities for discussions and collaborations between the research groups, which will be greatly encouraged!/

Alexei.Maklakov@ebc.uu.se
Alexei.Maklakov@ebc.uu.se

UppsalaU EvolutionaryGeneticsAgeing

PhD-position available at the Department of Evolutionary Biology at Uppsala University Sweden, within the project "Genomic distribution of sex-specific variation in ageing".

A striking pattern across the animal kingdom is that males and females of the same species often have different lifespan and rate of aging. Genetic variability for these traits also exists both between as well as within the sexes. Several theories aimed to explain these patterns have been put forward, but one of particular interest suggests that these differences are the result of sexual selection. The aim of the current project is to study the genomic distribution of sex-specific genetic variation in lifespan and ageing, to provide a better understanding of why and to what extent the sexes differ with respect to these traits. The project will focus on a Drosophila melanogaster model system, and will be conducted using classical Drosophila genetics in combination with modern systems biology and genomic approaches.

We are looking for a highly motivated student having a Master's degree or equivalent in biology, genetics or a related field, and a strong interest in evolutionary biology/genetics. Documented interest in statistics and experience with programming in R as well as Drosophila lab work is beneficial but not a required. He/she should work well both as a member of a group as well as independently, and also be proficient in both written and spoken English. The successful candidate will join a research group led by Urban Friberg (see http://www.egs.uu.se/evbiol/Persons/Urban.html) and will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (see http://www.ebc.uu.se/index_eng.php). This position is financed for four full years by a postgraduate fellowship the first year (15.500 SEK/month) and a postgraduate position year 2-4 (22.000 - 24.500 SEK/month). Applications should be written in English and include i) personal information/background, ii) a description of research interests (max 1-2 pages), iii) complete CV, iv) a description of undergraduate training, v) the names and email addresses of 2-3 referees. Applications should be sent to Dr. Urban Friberg, Dept. of Evolutionary Biology, EBC, Norbyv. 18D, Uppsala University, SE-752 36 Uppsala, Sweden. For more information please feel free to contact Urban Friberg by email (Urban.Friberg@ebc.uu.se) or by phone (+46-18-4716415). The position is open until filled, but for full consideration apply by the 20th of November. The ideal starting date would be January 2010.

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

Note that there is another PhD position on a related topic available at EBC in the Department of Ecology and Evolution under supervision of Alexei Maklakov (see http://www.iee.uu.se/zooekol/default.php?type=personalpage&id=87&lang=en). This creates opportunities for discussions and collaborations between the research groups, which will be greatly encouraged!

urban friberg <urban.friberg@ebc.uu.se>

UTasmania ConservationGenetics

PhD Scholarship (Australian Postgraduate Award Industry)

Conservation genetics and emerging wildlife disease

Project Title: Evolution, disease and extinction using ancient and modern Deoxyribonucleic acid (DNA) to investigate molecular evolution in the Tasmanian devil

Description:The aims of this project are to use comprehensive geographic and temporal genetic analyses to understand the origin, spread and impacts of an emerging wildlife disease, facial tumour disease, that threatens Tasmanian devils with extinction. Direct transmission of this unique infectious cancer is both facilitated by and likely to further erode already low genetic diversity in this species. This project involves using neutral genetic markers to estimate the timing and extent of loss of genetic diversity in Tasmanian devils and to evaluate the reasons for this loss. This study will provide critical genetic data and tools to monitor and prioritise conservation strategies aimed at preventing extinction. It will involve close interaction with the Hobart-based Save the Tasmanian Devil Program. The candidate should be interested in and capable of complex bioinformatics/data analysis, since large datasets are already available and new datasets will be used to address complex questions.

Location: The APAI will be based in the School of Zoology, University of Tasmania, Hobart, Tasmania, Australia. The candidate will spend periods of time in the Australian Centre for Ancient DNA, University of Adelaide.

Eligibility: Open. Must have Honours 1 / 2A or equivalent.

Supervision and contacts:Primary contact: Dr Menna Jones, School of Zoology, University of Tasmania. Phone: 0407 815606. Email: Menna.Jones@utas.edu.auChris Burridge, School of Zoology, University of Tasmania. Phone: (03) 6226 7653. Email: chris.burridge@utas.edu.auJeremy Austin, Australian Centre for Ancient DNA (ACAD), School of Earth & Environmental Sciences, The University of Adelaide. Phone: (08) 8303 4557 Mob: 0404 198 493. Email: jeremy.austin@adelaide.edu.au

Kathy Belov, Australasian Wildlife Genomics Group, Faculty of Veterinary Science, The University of Sydney. Phone: (02) 9351 3454. Email: kbelov@vetsci.usyd.edu.au

Menna.Jones@dpipwe.tas.gov.au

UTuebingen EvolutionaryBiology

International PhD Program Tuebingen, Spring 2010

The Max Planck Institute for Developmental Biology and the Friedrich Miescher Laboratory in Tuebingen, Germany, invite applications for PhD positions in: Evolutionary Biology, Ecological Genomics, Developmental Genetics, Animal Development , Plant Development, Quantitative Genetics, Molecular & Cell Biology, Biochemistry, Structural Biology and Bioinformatics

Highly qualified applicants from all countries are invited to apply. All applicants must hold or anticipate receiving a Diploma or Masters degree by the time of their start as a PhD student at our institutes. Candidates have to be fluent in written and spoken English. The positions are funded by Max Planck Fellowships.

Application form, evaluation forms (2 needed) and all details about our online registration are available at < http://www.eb.mpg.de/phd-program > www.eb.mpg.de/phd-program Application deadline is November 25, 2009. After the review of completed applications selected candidates will be invited for personal interviews in Tuebingen during February 10-12, 2010.

Thanking you for the posting in advance!

With kind regards,

Carolina Müller

Dr. Carolina Müller, PhD Program Coordinator

Tel: +49 7071 601 1354 Fax: +49 7071 601 1353 E-mail: carolina.mueller@tuebingen.mpg.de

PhD Program Office Max Planck Institute for Developmental Biology Spemannstr. 35; 72076 Tübingen

http://www.eb.tuebingen.mpg.de/phd-program Carolina Mueller <carolina.mueller@tuebingen.mpg.de>

UVermont EvolutionarySociogenomics

The Helms Cahan lab at the University of Vermont is seeking an energetic, motivated PhD student with an interest in evolutionary genomics, social evolution, or ecological genetics. We are broadly interested in the causes, mechanisms, and consequences of transitions in social structure, using ants as a model system. The student will join a brand-new NSF/ARRA-funded project investigating the genetic architecture of reproductive caste determination in harvester ants. We will be using high-throughput transcriptome sequencing and association mapping to identify genomic regions underlying the secondary loss of caste flexibility in ant populations displaying Genetic Caste Determination (GCD), an exceedingly rare mode of caste differentiation in which workers and queens are derived from genetically distinct mating crosses. The genomic resources developed over the course of the project will also be used to address evolutionary questions concerning the origin and causes of transitions in caste regulatory mechanisms. The student will be expected to develop his or her own dissertation project within the overall research program that reflect his or her interests; possible directions include comparative sociogenomics, evolution of development, phylogeography/population genetics, hybridization dynamics, or speciation. Summer support will be provided for four years; funding during the academic year will be in the form of teaching fellowships. Admission to the PhD program would be for Fall 2010, but support for summer field work could begin as early as June.

The Biology graduate program at the University of Vermont offers MS and PhD degrees across a wide range of disciplines from molecular biology to ecology. Our department has a particularly lively and productive group in Ecology and Evolution, with a strong focus on the integrative study of social insects (systematics, behavior, evolution, genetics, and ecology). To inquire about the position, please send an e-mail to Sara Helms Cahan (scahan@uvm.edu) indicating your research interests and experience.

To find out more about research in the Helms Cahan lab, go to: < http://www.uvm.edu/~biology/Faculty/Helms/Helms.html >http://www.uvm.edu/~biology/Faculty/Helms/Helms.html

To find out more about the Biology graduate program and faculty at UVM, go to: < http://www.uvm.edu/~biology/ >http://www.uvm.edu/~biology/

Dr. Sara Helms Cahan 307A Marsh Life Sciences Department of Biology University of Vermont Burlington, VT 05405 Tel: (802) 656-2962 Fax: (802) 656-2914 E-mail: scahan@uvm.edu

sara.cahan@uvm.edu sara.cahan@uvm.edu

UWisconsinMadison Evolution PlantHerbivore

Graduate Research Assistantship

Evolutionary Ecology of Plant-Herbivore Interactions University of Wisconsin, Madison

A Graduate Research Assistantship (M.S. - Ph.D. or Ph.D. only) is available for work with the research groups of Rick Lindroth and Eric Kruger at the University of Wisconsin-Madison. Funded by a new, five-year NSF grant, this research addresses genetic, ontogenetic and environmental factors that influence aspen defense (chemical resistance, tolerance, escape) against mammalian herbivores (e.g., deer). Primary objectives of the work are to: 1) characterize aspen chemical defense traits, 2) assess costs/benefits of resistance, tolerance and escape, and 3) evaluate the selective impact of browsing on the genetic structure of defense traits in an experimental population. Applicants must be interested in investigating both the chemical and population genetics aspects of plant-herbivore interactions. Applicants should pursue admission to the graduate program in Zoology (Ecology) or Forest and Wildlife Ecology.

For more information about the Lindroth and Kruger research groups, visit: http://entomology.wisc.edu/~lindroth/ http://forest.wisc.edu/facstaff/kruger.html The University of Wisconsin-Madison is a premier institution for research in ecology and evolution, and has ranked among the top five research universities in the

United States for each of the past 20 years.

Qualifications:

Highly motivated individuals with superior academic credentials and strong communication skills are encouraged to apply. Well-developed interpersonal skills are essential. Candidates must be able to work independently as well as part of a collaborative research team.

Stipend/benefits:

50% Research Assistantships currently provide a stipend of $ $20,184 (12 mo.), tuition waiver, and excellent medical/dental health plans.

Position available beginning in summer or fall of 2010.

Inquiries: Send preliminary e-mail letter of inquiry, describing research interests and academic qualifications, to:

Dr. Rick Lindroth Lindroth@wisc.edu

237 Russell Labs 1630 Linden Drive University of Wisconsin Madison, WI 53706 U.S.A.

Phone: 608-263-6277 Fax: 608-262-3322

lindroth@wisc.edu

UWyoming ProteinStructureEvolution

Ph.D. Position in Protein Structure Evolution

A PhD student position in structural bioinformatics in the Siltberg-Liberles Research Group at in the Department of Molecular Biology at University of Wyoming is available. Qualified applicants should have some skills in programming, knowledge of statistics, protein structure, biochemistry, and molecular biology, as well as an interest in evolution. The Siltberg-Liberles Group works in the field of comparative structural genomics, focusing on protein structure evolution. In many aspects this research program puts an emphasis on protein families involved in human disease but also on identifying general trends within protein structure evolution. For more details on research in the Siltberg-Liberles Research Group, please see http://www.wyomingbioinformatics.org/ . University of Wyoming is located in Laramie, WY, 2 hours north of Denver in the Rocky mountains. It is an ideal location for those with interests in skiing, rock climbing, hiking, and mountain biking.

To apply, please send a CV, statement of research interests, and contact information for three references, to jliberle@uwyo.edu. No GRE scores are required with an M.Sc. degree. Informal inquiries before application are welcome. Application deadline November 6, 2009.

Jessica Liberles <jliberle@uwyo.edu>

UZurich PlantEvolution

The PhD is quite ecological, but I would very much like to attract someone who is from an evolutionary background, as I think this would help the project considerably. Also, within the PhD I would like to extend the model into host-parasite interactions (hemiparasites) and then we can address such questions as optimal virulence etc. These are very clearly evolutionary questions.

Lindsay

Project:

A fully-funded PhD position is available to start immediately at the University of Zurich, Switzerland. http://www.uzh.ch/uwinst/ http://research.microsoft.com/en-us/people/dpurves/ Summary: we are looking to develop a general model of plant growth and decision-making which we can test and extend with real data. Questions include: how do plants invest carbon and nitrogen in different structures, which external factors influence these decisions, and what are the implications of this in terms of community ecology, the evolution of life-history strategies, and responses to climate change? This research will involve experiments with all kinds of plants and a good deal of modelling. Potential extensions include interactions of host plants with parasitic plants where questions include: what is the best strategy for the host and the parasite? How virulent should the parasite be and does this change when there are multiple parasites attached? We hope to include both ecological and evolutionary themes so that this position is suitable for anyone with an interest in both. The project has a great deal of flexibility, so it is also well-suited to an independent, imaginative and creative person who likes to choose their own research direction.

Location: The project will be based in the Institute of Environmental Sciences at the University of Zurich, Switzerland. Zurich is a wonderful city to live in, always features in surveys of cities with the best quality of life, and is in easy reach of the mountains during the winter. The project is co-supervised by Dr. Lindsay Turnbull (University of Zurich), Dr Andrew Hector (University of Zurich) and Dr. Drew Purves (Microsoft Research, UK) and requires an immediate start.

Qualifications required: We are looking for a well-motivated person to conduct this research over a 3-year period, culminating in a PhD from the University of Zurich, Switzerland. Applicants need to already hold a Master's degree and have some experience with computer modelling and plant ecology. The project is funded by Microsoft Research, UK and the successful candidate will receive extensive scientific and technical support from this source.

Contact: Please send your CV and application to: lindsayt@uwinst.uzh.ch. Please state why you are interested in the project in your application. Please label your attached CV file: "CV.applicant.name.doc"

Lindsay Turnbull Institute of Environmental Sciences Winterthurerstrasse 190 Zurich CH-8057

Lindsay Turnbull <lindsayt_ifu@yahoo.co.uk>

Vienna Drosophila ExperimentalEvolution

We are looking for an enthusiastic PhD student to work on experimental evolution in Drosophila. The successful candidate will work at the interphase of evolutionary theory of adaptation and experimental population genetics. By combining phenotypic and molecular changes during an experimental evolution the candidate will study adaptation from standing genetic variation. This PhD project is jointly supervised by J. Hermisson and C. Schlötterer. Candidates with interest in theoretical biology, modeling, phenotyping, and next generation sequencing are particularly encouraged to apply. The successful applicant will join the PhD program in Population Genetics at the VUW (http://i122server.vu-wien.ac.at/pop/PhD/projects.html).

Further information can be obtained from Joachim Hermisson: joachim.hermisson@univie.ac.at Christian Schloetterer: christian.schloetterer@vetmeduni.ac.at

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

VU Amsterdam SexualConflict

PhD-position in evolutionary ecology f/m Full-time (1.0 fte)

A 4-year NWO-funded PhD position is available in the group of Dr. Joris M. Koene within the section Animal Ecology of the Faculty of Earth and Life Sciences, VU University Amsterdam (The Netherlands). Vacancy number 1.2009.00293.

Project title "Evolutionary signatures of sexual conflict in hermaphrodites: Reproductive morphology and semen composition"

Description of the project The goal of the project is to investigate the role of sexual conflict in the evolution of simultaneous hermaphrodites. Within our integrative approach, this project will focus on comparing the evolution of reproductive morphology, mating system as well as seminal fluid composition. The project will fully exploit the knowledge already obtained with our model species Lymnaea stagnalis and will therefore concentrate on hermaphroditic fresh water snails (Basommatophora). The project is funded by the Netherlands Organisation for Scientific Research and may start very shortly.

Tasks - Executing scientific research as detailed in the project description. - Publishing results of the research in scientific journals as well as in a thesis. - Assisting in undergraduate courses given within the Department of Ecological Science. - Following the PhD educational programme as prescribed by the institute.

Required skills and education - MSc degree in Biology. - Advanced courses in molecular biology, evolution, animal physiology or equivalent. - Proficiency in both written and spoken English. - Excellent social skills, ability to work independently and high motivation will be assets.

Employment details The appointment will initially be for 12 months. After a successful evaluation the contract will be prolonged with 36 months. Employment will have to result in a written thesis by the end of this period. Gross monthly salary, based on experience, amounts to minimally 2,042 Euro during the first year up to 2,612 Euro during the fourth year. The university's fringe benefits of employment are available at www.vu.nl/vacatures . Information and applications

Further information and the complete project description can be obtained from the project leader, Dr. J.M. Koene (joris.koene@falw.vu.nl). Please mention the vacancy number in all your correspondence. Applications should include a covering letter motivating your interest (with a brief statement of your personal research aims and interests), a detailed curriculum vitae, a copy of your graduate work, reprints of published work (if available), and two reference names with contact details. Only complete applications will be considered and should be sent (preferably in one single file) by e-mail to falw-vacatures@falw.vu.nl or (only if necessary) by regular mail to Dr. J.M.R.M. Neutelings, Managing Director, Faculty of Earth & Life Sciences, VU University, De Boelelaan 1085, 1081 HV Amsterdam, The Netherlands. The deadline for application is 30 October 2009.

Dr. Joris M. Koene http://www.jkoene.dds.nl VU University - Animal Ecology De Boelelaan 1085, 1081 HV Amsterdam, THE NETHERLANDS tel: +31 (0)20 5987095; fax: +31 (0)20 5987123 joris.koene@falw.vu.nl http://www.falw.vu.nl/-animalecology University of Antwerp (Visiting Fellow) - Evolutionary Ecology Groenenborgerlaan 171, B-2020 Antwerp, BELGIUM http://www.ua.ac.be/joris.koene joris.koene@falw.vu.nl joris.koene@falw.vu.nl

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WashingtonStateU PlantEvolutionaryGenetics

The Busch lab at Washington State University is seeking independent, creative and highly motivated graduate students with interests in genetics, evolutionary biology, and ecological genetics. At the moment, there are positions open for two students at both the Ph.D. and M.S. level. To get an idea of the projects currently underway, please follow these links:

http://www.sbs.wsu.edu/faculty/?faculty/148

http://sbs.wsu.edu/facultypages/busch_lab.html Research in the Busch lab is broadly focused on the evolution and breakdown of self-incompatibility systems in angiosperms. The recurrent loss of self-incompatibility is a common evolutionary trend with dramatic consequences on the distribution of genetic diversity and the viability of natural populations. We are currently studying this question from classical genetic, ecological, and population genetic perspectives in a model genus (Leavenworthia). One current focus of work in the lab is the identification of mutations disabling self-incompatibility and their natural selection in the wild. We are also exploring the long-term consequences of close inbreeding by studying the genetic basis of heterosis and incipient speciation in selfing species. Other projects currently underway in the laboratory involve: modeling the breakdown of self-incompatibility during bottlenecks or pollinator disappearance, examining the demographic and ecological factors influencing selfing rate, and studying the effects of habitat fragmentation on genetic diversity in endemic species. Following the expected completion of genome sequencing in our study organism (Leavenworthia) in 2010, opportunities will abound for students interested in studying adaptive and non-adaptive processes using population genomics approaches.

Washington State University is located in Pullman, WA in the beautiful Palouse region. Surrounded by rolling wheat fields and abundant outdoor opportunities, the university is found in a small rural setting in the Inland northwest. The School of Biological Sciences at WSU has a strong history of training excellent researchers in ecology and evolution, and has many internal funding opportunities for students with specific research interests in plant biology. The University of Idaho is 8 miles away and there are many social and scientific activities that solidify interactions between these two vibrant research communities.

Students interested in pursuing a Ph.D. or M.S. at WSU are asked to contact Jeremiah Busch via email to discuss their interests that could be pursued in the laboratory. For information on the School of Biological Sciences and guidelines for applying to the program, please see:

http://www.sbs.wsu.edu/ http://www.sbs.wsu.edu/-grad-studies/ Jeremiah W. Busch Assistant Professor School of Biological Sciences Washington State University Pullman, WA 99164 jwbusch(at)wsu(dot)edu)

Jobs

Bergen LabTech MarineComparativeSpecies

Job: Laboratory Department Engineer, Sars International Centre for Marine Molecular Biology, Bergen, NORWAY

The Sars International Centre is a partner of the European Molecular Biology Laboratory (EMBL) and a department of Unifob AS, affiliated with the University of Bergen. The Sars Centre focuses on genome scale research in vertebrate and invertebrate biology, using comparative and genetic molecular studies of marine species.

The Sars Centre has available a full time position as Laboratory Department Engineer in a new evolutionary developmental biology group. The position is initially for 2 years with the possibility of extension and the start date is early 2010. Work in this group focuses on studies of developmental biology of different marine and fresh water invertebrate animals using morphological and molecular tools. The person holding this position will be trained by and work in close association with the Group Leader. Major tasks will include DNA cloning, PCR, microinjections, time lapse and confocal microscopy, in situ hybridization, and tissue sectioning for histology and electron microscopy, depending on the evolution of the lab projects. Other responsibilities include the daily management of lab equipment and consumables and purchasing.

Applicants should have at least an engineering college degree (høyskole) or equivalent qualifications based on education and professional experience. Experience in molecular biology including cloning and PCR is expected. Prior experience in cell and developmental biology with model or non-model animal systems would be desirable. The salary level for Department Engineer (code 8430) begins at NOK 310.000 and is negotiable based on prior experience. Unifob has employee insurance and pension agreements and is an equal opportunity employer. Further information may be obtained from Andreas Hejnol, Group Leader, at andreas.hejnol@sars.uib.no, phone +47 55 58 43 28.

Written application in English, including a CV containing all information about education and work experience and the names and contact information of two references should be marked 09Sars15 and sent to: Sars Centre, Head of Administration, Thormøhlensgt. 55, NO-5008 Bergen, Norway, no later than 10 November 2009. Please note that applications sent by e-mail will not be considered.

andreas.hejnol@sars.uib.no andreas.hejnol@sars.uib.no

CentreCollege PopulationGenetics

TENURE-TRACK POSITION IN BIOLOGY

CENTRE COLLEGE invites applications for a tenure-track position for a population geneticist/conservation biologist at the assistant professor level to start in fall 2010. The successful applicant will have a Ph.D. in the biological sciences with expertise in population genetics, population ecology and/or conservation biology and must demonstrate a commitment to excellence in teaching and scholarship at a nationally-ranked liberal arts college. Teaching duties include courses in evolutionary genetics, ecology, introductory biology, senior seminar, and special topics courses in area of specialty. Collaborative research with undergraduates is expected and supported. Participation in Centre's study abroad program is also encouraged.

Centre College is a highly selective liberal arts college of 1,200 students, listed by U.S. News in the top fifty liberal arts colleges in the nation. Classes are small and academic standards are high. The College is located in Danville, Kentucky, a town of 18,000 recognized for its high quality of life. It is within easy driving distance of Lexington, Louisville, and Cincinnati. Centre College is committed to hiring a diverse faculty of teachers/scholars. For information concerning the college, visit our web site at www.centre.edu . To apply, please submit letter of application, statement of teaching philosophy, statement of research interest, CV, transcripts, and three letters of recommendation to: Dean Stephanie Fabritius, Vice President for Academic Affairs, Centre College, 600 West Walnut St., Danville, KY 40422. Review of applicants will begin November 1, 2009 and continue until position is filled. Centre College is an Equal Opportunity Employer.

Margaret G. Richey Professor, Biology and Biochemistry/Molecular Biology Centre College Danville, KY 40422 859-238-5319

CENTRE COLLEGE Personal education. Extraordinary success. http://www.centre.edu Peggy Richey <peggy.richey@centre.edu>

CNRS France FieldAssistant LizardPopulationConnectivity

Field Assistant Landscape effects on common lizard population connectivity La Station d'Ecologie Experimentale du CNRS a Moulis.

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 in predicting observed connectivity between populations of 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 quantify relative habitat preferences, the data from which will be used to parameterise least-cost path models of landscape connectivity. No salary is associated with this position but accommodation will be provided.

This position is ideal for a 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 15^th December 2009. Candidates will be notified by the 15^th January 2010

Dr Colin Bleay,

Station d'Ecologie Experimentale du CNRS

09200 Moulis

France.

Colin.Bleay@EcoEx-moulis.cnrs.fr

CornellU Bioinformatics Programmer

PROGRAMMER POSITION in Computational Biology at Cornell

A position is now available for a programmer, to serve as an integral part of the computational genomics research laboratory of Jason Mezey (http://mezeylab.cb.bscb.cornell.edu/) at Cornell University. Our group focuses on the development of novel statistical and computational methods for addressing fundamental questions in complex trait / disease genomics and in the application of these methods with our collaborators in molecular and medical fields. The duties of the position will include implementing and improving the computational speed of algorithms, building analysis pipelines, database construction and management, and software development.

The Mezey group has a dual appointment in the Department of Biological Statistics and Computational Biology at Cornell University (Ithaca, NY) and in the Department of Genetic Medicine at Weill Cornell Medical College (New York City), with members at both locations. We are looking for a programmer who would primarily be at our Ithaca location.

Ideal candidates will have a computer science background, proven programming skills in C/C++ and PERL, experience with relational databases (mysql or similar), basic knowledge of web programming, familiarity with probability and theoretical statistics, and experience working with publically available genomic data. The position is available immediately. To apply, please go to the following link:

https://cornellu.taleo.net/careersection/10164/jobsearch.ftl and search for job #11422 (Programmer Analyst III; job posting date 09/26/09) If you have any additional questions please contact Jason Mezey at jgm45@cornell.edu.

jgm45@cornell.edu jgm45@cornell.edu

Edinburgh Bioinformatician

Bioinformatician MRC Human Genetics Unit, Edinburgh

The MRC Human Genetics Unit is seeking to recruit a new member of staff to specialise in the analysis of high-throughput sequencing data. This post is associated with the development of the new MRC Regional Sequencing Hub to be established at the University of Edinburgh, and will deliver a high-level analysis service to the Institute of Genetics and Molecular Medicine (IGMM) research community. It offers an excellent opportunity to work with a variety of distinguished scientists on a wide range of cutting edge problems. Further information on the research interests of IGMM groups is available on the IGMM web site (http://www.igmm.ac.uk/).

The full advert is at http://www.nature.com/naturejobs/science/jobs/114851 Candidates should hold a PhD in Biology, Bioinformatics, Statistics, Computer Science or a closely related discipline and have extensive experience in computational biology, genetics, molecular biology or a related field. Informal enquiries can be made to Personnel@hgu.mrc.ac.uk or to Colin.Semple@hgu.mrc.ac.uk . Closing Date: 2 November 2009

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

HarvardU EvolutionOfPrimateBehavior

TENURE TRACK JOB IN PRIMATE BEHAVIOR HARVARD UNIVERSITY

The Department of Human Evolutionary Biology at Harvard University is seeking to make a full-time tenure-track appointment at the assistant or untenured associate professor level in the field of non-human primate behavior, and seeks candidates who will complement the current strengths of the program. We are particularly interested in candidates whose interests in behavior extend to cognitive evolution, ecology, genetics, or physiology, and whose primate behavioral studies are explicitly related to human evolution. A strong doctoral record is required and the Department seeks candidates with exceptional promise as scholars and teachers to offer courses at the undergraduate and graduate levels. The Department administers a large and successful undergraduate concentration in Human Evolutionary Biology, hence excellence in undergraduate teaching is a priority. Our Doctoral program stresses integration of laboratory and field research and the cooperative training and mentoring of Ph.D. candidates. Harvard University is an Equal Opportunity/Affirmative Action employer, and applications from women and minorities are particularly encouraged. The appointment is expected to begin on July 1, 2010. Interested candidates should send a CV, example publications, teaching evaluations if available, and the names and addresses of three potential references, by November 13, 2009 to: Prof. Richard Wrangham, Search Committee Chair, Department of Human Evolutionary Biology, Harvard University, 11 Divinity Avenue, Cambridge, MA 02138 USA, or by email to mlynch@fas.harvard.edu.

Charles Nunn <cnunn@oeb.harvard.edu>

India SocialPhenomenaEvolution

The Complex Systems group at the Institute of Mathematical Sciences (IMSc), Chennai, has been examining, in collaboration with the Ecology, Evolution and Behaviour Group of the National Institute of Advanced Studies (NIAS), Bangalore, theoretical approaches to understand the structure and evolution of social interactions in nonhuman primates. This involves (i) reconstructing the social networks of such animals from field-observation data using techniques from complex network theory, and (ii) developing agent-based models, with individuals following set of "strategies" to interact with other members in the group, which can reproduce many of the observed features of the empirical networks. Such a study should not only illuminate how primate groups work as a cohesive society, but may also shed light on the evolution of complex societies with hierarchical organisation in humans.

We are currently looking for a candidate motivated to apply mathematical and modeling techniques to understand evolution of social phenomena to work as a Project Assistant/Research Assistant on the above problem. It may also be possible for such a candidate to subsequently register for a doctoral degree. The candidate should necessarily have a background in mathematical/quantitative sciences, have some experience in using analytical and computational techniques, and have a strong interest in evolution of biological systems. Knowledge of MATLAB or equivalent scientific software is desirable but not essential. Interested candidates are requested to contact Dr Sitabhra Sinha (sitabhra@imsc.res.in) at IMSc, Chennai and Dr Anindya Sinha (asinha@nias.iisc.ernet.in) at NIAS, Bangalore.

Debapriyo Chakraborty <boomsthebest@gmail.com>

InstForestGenetics Germany Genomics

At the Institute of Forest Genetics in Grosshansdorf of the Johann Heinrich von Thünen-Institute (vTI), Federal Research Institute of Rural Areas, Forestry and Fisheries, is a vacancy for the permanent position in Genomics of a

scientific employee in part-time (19.5 regular working hours/week).

Tasks:

. Planning, initialisation and analysis of large scale DNA-sequencing of genomes of trees and their pathogens (insects, fungi) using classical Sanger- and new generation sequencing techniques. . Development of SNPs in coding and non-coding regions in genomes of trees and their pathogens (insects, fungi) . Application of SNPs for genetic diversity studies, tree breeding and species identification as well as provenance identification . Analysis of sequence and population genetic data . Development and maintenance of data bases on sequences and population genetic data

Professional requirements:

. PhD in biology, forest science, agricultural science or related fields, doctoral thesis on a subject in genomics or bioinformatics, broad experience in molecular biology, bioinformatics and population genetics. . Skills in programming (C++, Java or Perl).

Personal requirements:

. Ability to analyze complex facts . Ability for team orientated networking . Very good knowledge of English and good knowledge of German . Readiness to go on business trips lasting several days

The employment complies with the terms of the contract for Public Service (TVÖD). Payment will be according the German pay scale TOVD 13; a bonus can be granted according to the pay scale 14, when personal and pay scale conditions exist.

A take over to civil service status is possible later on, but a claim can not be asserted.

The vTI promotes the professional equality of women and men and therefore asks specially women to apply. Severely handicapped persons will be especially considered by equal aptitude. A minimum of physical aptitude is required.

Please submit your application with the usual supporting documentation until October 23rd, 2009 to

Dr. Bernd Degen (Phone: 04102-696 101) E-Mail: bernd.degen@vti.bund.de Johann Heinrich von Thünen-Institut (vTI) Institut für Forstgenetik Sieker Landstraße 2 D-22927 Grosshansdorf, Germany

Bernd Degen <bernd.degen@vti.bund.de>

Marseilles EvolutionaryBiology

A Position of Professor in evolutionary biology will open soon at Marseilles (start october 2010) a strong back ground in animal gentics and bioinformatics is required The choosen candidate will have to develop her/his own research in close collaboration with the other members of the lab

for more information contact : Pierre Pontarotti

Pierre Antoine Pontarotti

Directeur de Recherche CNRS

UMR 6632 Université de Aix Marseille/CNRS . Equipe Evolution biologique et Modélisation , case 19 3 place Victor Hugo 13331 Marseille Cedex 03 France tel 33491106489

we are organizing the 14th Evolutionary Biology Meeting at Marseilles http://sites.univ-provence.fr/evol-cgr/ Pierre PONTAROTTI <Pierre.Pontarotti@univ-provence.fr>

MNHN Paris Systematics

The Muséum National d'Histoire Naturelle (MNHN) of Paris will be recruiting researchers from different scientific disciplines beginning in 2010. These disciplines include but are not limited to systematics and evolution both in botany and in zoology. For example, between 2010 and 2011, the museum plans to recruit a Professor specializing in plant systematics and phylogenetics and an Assistant/Associate Professor specializing in plant adaptive radiation.

If you are interested in a tenure-track position of Assistant/Associate Professor or Professor at the MNHN of Paris, please be advised that you must have completed the French mandatory procedure (qualification list) by 2010 in order to be considered.

The initial registration to apply to the qualification list for the position of Professor and/or Assistant/Associate Professor (Maître de conferences) of MNHN is open from September 15 until October 29, 2009 via the Ministère de l'Education Nationale website (https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/candidats.html), under the heading GALAXIE. We are sorry but the website is written only in French.

We invite all interested researchers to register. About mid-December, the persons registered will receive an email asking them to send to two reviewers a CV and copies of 3 to 5 publications. The deadline to send this documentation is December 14, 2009. Those who qualify may apply between 2010 and 2013 for MNHN positions.

For more information about the opportunities in botany and the procedure to follow, please contact PH Gouyon (gouyon@mnhn.fr) or JN Labat (labat@mnhn.fr).

labat@mnhn.fr

NSFProgramDirector BiologicalInformatics

Dear SSE Member,

NSF Announcement for Permanent Program Director Position in Advances in Biological Informatics

The National Science Foundation (NSF) is looking to fill a permanent position of Program Director in the Advances in Biological Informatics (ABI) program, Division of Biological Infrastructure (DBI). ABI seeks to encourage new approaches to the analysis and dissemination of biological knowledge for the benefit of both the scientific community and the broader public. The ABI program is especially interested in the development of informatics tools and resources that have the potential to advance, or transform, research in biology supported by the Directorate for Biological Sciences at the National Science Foundation. The Program Director for the ABI Program is responsible for the planning and administration of the program within the framework of legislation, agency policies, missions, objectives, and resources. This is an exciting opportunity for experienced individuals to have a profound impact on furthering the biological sciences in the U.S. Details of the position and its responsibi lities can be found at http://jobview.usajobs.gov/GetJob.aspx?OPMControl=1663370 . Details about the ABI program can be found at http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=5444&org=DBI&from=home Deadline for applications is 15 October 2009.

Please direct questions about the position to Peter Arzberger, Division Director, DBI, parzberg@nsf.gov or Peter McCartney, Program Director, ABI, pmccartn@nsf.gov

Judy Stone (Secretary of SSE) and SSE Executive Council - jstone@colby.edu

Judy Stone via Bill Dahl <wdahl@botany.org>

OregonStateU ResAssist PopGenetics

Mike Blouin in the department of Zoology at OSU wants to hire someone to study disease resistance genes in snails. The position can be hired as a faculty research assistant, research associate or Post Doc, depending on the applicant's degree and qualifications. The position may be either part-time (at least a .50 FTE) or full time (1.0 FTE), 12-month, fixed-term. There is currently funding for one year of full-time work, but I hope to extend that.

The candidate will conduct molecular biology and population genetics research in Michael Blouin's laboratory at OSU (http://people.oregonstate.edu/ ~ blouinm/index.htm). We study the genetics of resistance by snails to infection by parasites. We are using candidate gene and linkage mapping approaches. The mapping methods will involve next generation sequencing (Illumina) to develop and score SNPs. Candidate would also be involved in supervising students and maintaining inbred lines of snails. Candidate might also be involved in Illumina-based studies on gene expression in hatchery and wild salmon. Experience with bioinformatics or statistical genetics would be desirable.

Search the OSU jobs site (http://oregonstate.edu/jobs/) for posting number 0004835. The search closes 10/23/09.

Feel free to contact me if you have questions.

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

blouinm@science.oregonstate.edu

PortlandStateU PlantEvolution

The Department of Biology at Portland State University invites applications for a tenure-track Assistant Professor in Plant Biology. We seek an innovative scientist asking fundamental questions in any area of plant evolution/ecology. Areas of special interest include development, phylogenetics, plant-animal interactions, or plant-microbial interactions. Appointment at a more senior level may be considered for exceptional candidates with records of outstanding accomplishment. Applicants must have a Ph.D., with priority given to candidates with postdoctoral experience and who have demonstrated success in developing a productive research program. We encourage applications from individuals whose interests complement existing departmental strengths in ecology, physiology, evolution, and genetics (see the departmental web site: http://www.bio.pdx.edu/). The successful candidate will be expected to develop a strong externally-funded research program, be effective in teaching at the undergraduate level, and participate in the training of graduate students in our growing doctoral program. This is a tenure-track 9Vmonth appointment to begin in the fall of 2010. Review of applications will begin 26 October, 2009, and will continue until the position is filled. A curriculum vitae, statements of research and teaching interests, and three letters of reference should be sent to: Sarah Eppley, Chair, Plant Biology Search Committee, Department of Biology, P.O. Box 751, Portland State University, Portland, Oregon 97207 or via email (plants@pdx.edu). /Portland// State University is an Affirmative Action, Equal Opportunity institution and welcomes applications from diverse candidates and candidates who support diversity./

Sarah Eppley Assistant Professor Department of Biology Portland State University P.O. Box 751 Portland, OR 97207

Phone: 503-725-8986 Fax: 503-725-3888

Sarah Eppley <eppley@pdx.edu>

PurdueU StatisticalBioinformatics

The Department of Statistics, Purdue University invites applications for a tenure-track position beginning August 2010 at the Assistant Professor level in the area of statistical bioinformatics. This hire will join an exciting and established group in statistical bioinformatics.

The Department of Statistics offers a stimulating and nurturing academic environment. More than 35 tenured and tenure-track faculty members direct research programs in a broad range of areas complementary to statistical bioinformatics. Further information about the department is available at

http://www.stat.purdue.edu All applicants should hold a Ph.D. in Statistics or a related field, be committed to excellence in teaching, and have demonstrated strong potential for excellence in research. Salary and benefits are highly competitive. For all positions in Statistics, please visit

http://www.stat.purdue.edu/hiring/ to apply.

Review of applications will begin on December 1, 2009, and will continue until the position is filled. Purdue University is an Equal Opportunity/Equal Access/Affirmative Action employer fully committed to achieving a diverse workforce.

doerge@purdue.edu

RoyalBotanicGardens Kew ComparativeMorphology

Senior Researcher in Morphology/Anatomy (Band E)

The Royal Botanic Gardens, Kew

Job status: Permanent

Salary per annum: starting salary in the region of £30,742, depending on skills and experience

JOB DETAILS: The Royal Botanic Gardens Kew is seeking to recruit a researcher based in the Jodrell's Micromorphology Section. The new postholder will carry out comparative research in plant structure to address key questions in systematic and evolutionary biology, paying particular attention to morphological trait evolution in relation to conservation and climate change.

http://www.kew.org/about-kew/jobs/ deadline: November 23 2009

Paula Rudall PhD DSc Head of Micromorphology, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, UK

Paula Rudall p.rudall@kew.org

RoyalBotanicGardens Kew MycologySystematics

Senior Researcher in Mycology Systematics

The Royal Botanic Gardens, Kew

Job status: Permanent

Salary per annum: up to £40,864

Job Details: The main purpose of this role is to conduct research on mycological systematics and/or conservation/restoration ecology of fungi consistent with the mission and objectives of the Royal Botanic Gardens, Kew. In addition the post holder will be expected to raise funding externally to support research of the Section and to build the quality of Kew's collections through field meetings, exchange programmes and effective herbarium curation.

http://www.kew.org/about-kew/jobs/-ref_SeniorResearcherMycology.htm "Martin I. Bidartondo" <m.bidartondo@imperial.ac.uk>

RoyalBotanicGardens Kew PlantEvolutionaryBiologist

JOB TITLE: Plant Evolutionary Biologist (Band E)

REF: 298

HOURS OF WORK: Full Time (36 hours net)

JOB STATUS: Fixed Term Appointment (3 years)

SALARY PER ANNUM: £30,742 - £34,116

DEPARTMENT AND LOCATION: Jodrell, RBG Kew

JOB DETAILS:

The main purpose of this role is to establish a research program on the evolution of plants and plant systematics / classification complementing the current strengths of the Molecular Systematics Section of the Jodrell Laboratory (see Kew's Science Directory for current projects; http://www.kew.org/science/directory/-index.html). In addition you will be expected to raise funding externally to support research and provide core relief.

ESSENTIALS:

Ph.D. plus one previous post-doctoral post desirable. Training in molecular biology techniques/plant systematics/evolutionary biology. Previous relevant experience in plant molecular systematics/evolutionary biology. Excellent written and oral skills (publication record and presentations at international meetings). Must be able to organise own time and research programme. Excellent standard skills in computing, plus phylogenetic analysis expertise. Excellent judgement and capacity to make independent decisions. Excellent problem solving skills. Good self motivation (supervision will be limited). Excellent team working. Good knowledge of specialist background literature and other available resources. Knowledge of health and safety regulations, and good laboratory practice.

CLOSING DATE: Wednesday 4th November 2009

INTERVIEW DATE: Friday 20th November 2009

For full role details and information on how to apply please visit http://www.kew.org/about-kew/jobs/-index.htm Felix Forest <F.Forest@kew.org>

Salem Oregon YuccaEvolution

Dear Colleagues,

A one-year, NSF-funded research technician/lab manager position is available in the Smith lab at Willamette University. The project focuses on population genetic and ecological processes in the Joshua tree / Yucca moth pollination system. Competitive salary and benefits are available, commensurate with the applicant's background and experience. Secured funding is currently available for one year; the position may be extended for additional years contingent upon the availability of funding and satisfactory performance. The job responsibilities will include (but are not limited to) genotyping of yucca moth and joshua tree individuals, and participation in field research in the Mojave desert in the early spring.

Willamette University is a selective, liberal-arts college located in Salem, Oregon. Salem is a progressive, multicultural and multiethnic community, located 47 miles south of Portland. Salem is within an easy drive of the Oregon coast, Eugene, the Cascade Mountains, Mt. Hood, and the Columbia River Gorge. Seattle, Washington, Vancouver, BC, and the Olympic peninsula are all reachable within a day's drive.

The official position announcement is pasted below, and can viewed at the Willamette University Human Resources website:

http://www.willamette.edu/dept/hr/employment/-admin/Biol_Research_Asst_2009/index.html Christopher Irwin Smith Assistant Professor Department of Biology Willamette University Salem, OR 97301 ph: 503-370-6181 fax: 503-375-5425

www.willamette.edu/ ˜ csmith/ChrisSmith.htm email: csmith@willamette.edu csmith@uidaho.edu chris_smith@post.harvard.edu

Research Assistant / Lab Manager in Evolutionary Ecology - Department of Biology As part of a research project funded by the National Science Foundation, the Research Assistant extracts DNA from plant and insect specimens, genotypes these using microsatellite DNA markers and DNA sequencing, records the methods used and experimental results. The Research Assistant will participate in field research, including assisting in the design and implementation of field experiments and travelling to field sites for several weeks. The Research

Assistant analyzes experimental data using computer software packages for genetic and statistical analysis and graphing and assists in the preparation of material for publication. The Research Assistant manages and oversees day-to-day laboratory functions, including assisting undergraduates completing research in the Principal Investigator's laboratory, ordering laboratory equipment and supplies, arranging for repair of laboratory equipment, and maintaining a database of plant and insect collections and genomic DNA materials.

The Research Assistant plans and performs technical experiments that require training in certain basic laboratory skills. In addition, the Research Assistant manages the day-to-day operation of the laboratory in a way that maximizes the number of days dedicated to collection of research data while ensuring that the physical components and clerical operations of the laboratory are also maintained. Thus the position requires a degree of organizational skill and an ability to work independently with a minimal of supervision. The position requires a certain knowledge of University policies and procedures as well as strong interpersonal, written and verbal communication skills. Completion of job duties includes travel to field sites in the Mojave Desert (Nevada, California, and Arizona), and the completion of field experiment. Thus, the ability to live and work in semi-primitive conditions is required.

This is a full-time one year position which includes full benefits. Extension of this position is dependent upon continuation of funding.

Duties and Responsibilities:

The duties and responsibilities of the Research Assistant include, but are not limited to, the following functions, which are not listed in any particular order of importance or significance:

Research Assistant:

1. Extracts genomic DNA from plant and insect tissues using DNA extraction kits and evaluates DNA concentrations and quality using a gel electorphoresis and spectrophotomtery.

2. Genotypes plant and insect samples using microsatellite genotyping by electrophoresis and analysis of electropherogram data.

3. Sequences DNA from samples using PCR amplification and Sanger sequencing with dye-labeled terminators.

4. Analyzes raw microsatellite and DNA sequence data using standard softwares, including Gene Mapper and CodonCode.

5. Participates in weekly lab meetings, including reading and discussing current scientific literature in the topics of coevolution,

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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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SmithCollege ResAssist GenomeEvolution

Research Assistant Position at Smith College

The research technician will use molecular and bioinformatics tools to explore genome evolution within the ciliate Chilodonella uncinata, and to elucidate evolutionary relationships among ciliates. The technician will PCR, clone and sequence multiple genes from ciliate micronuclear and macronuclear genomes. The technician will also characterize genes from ciliate mitochondria using both traditional and walking PCR. Further, the technician will track cultures using light microscopy and ultimately work with the PI to develop fluorescence microscopy for these systems. Finally, the technician will need to maintain data in a well-organized database, with attention paid to details of completeness and quality, while also supporting general lab functions.

Requirements: Bachelor's degree plus at least one year lab and informatics experience.

Skills: Must be highly motivated to collect and catalog DNA sequence data, and to perform bioinformatics tasks. Experience with basic molecular skills, including PCR, cloning and sequencing; knowledge of biopython, ClustalW, PAUP, RaxML, and other informatics tools designed to analyze DNA sequence data would be ideals. Also need basic microscopy skills to maintain ciliate cultures.

This is a full-time, one year grant funded position with the possibility of renewal. Smith College is an equal opportunity employer encouraging excellence through diversity.

Please contact Laura Katz (lkatz@smith.edu) with questions.

More information on the Katzlab can be found at: http://www.science.smith.edu/departments/Biology/lkatz/ Official Job posting can be found at: https://jobs.smith.edu/ –

Laura A. Katz, Elsie Damon Simonds Professor Department of Biological Sciences lkatz@email.smith.edu 44 College Lane Smith College Northampton, MA 01063 Phone: 413-585-3825 (office) 413-585-3750 (lab) Fax: 413-585-3786 http://www.science.smith.edu/departments/Biology/lkatz/

Loans that change lives: http://www.kiva.org/ Donate free: http://www.hungersite.com Laura A Katz <lkatz@smith.edu>

Syngenta Biotech

Dear List Members, The following positions are open at Syngenta Biotechnology in Research Triangle Park, NC. Syngenta was recently named one of the top biotechnology employers by Science. http://sciencecareers.sciencemag.org/career_magazine/previous_issues/articles/2009_10_02/science.opms.r0900079 Genome Annotation Specialist (#1434): This individual will be responsible for implementing automated annotation pipelines for genome, transcript, and proteins sequences. Advanced knowledge of sequence analysis tools is required. Experience with modern high throughput sequencing analytics is desirable. A strong competency with Unix and scripting in a language such as Perl is required.

Genomic Database Specialist (#1435): This individual will be responsible for maintaining and optimizing database systems for genome annotation and related information. Experience overseeing database systems is required and experience with Oracle and PostgreSQL is desirable. The ideal candidate will have a solid understanding of genomics and a background in a life sciences setting. Strong competency with Unix and Perl is required.

Genomic Platform Technology Team Leader (#1183): This individual will lead a team of experienced scientists to generate and deliver high quality omics data and constant platform evolution. The role provides leadership in technical and experimental design, investigation of new genomic technologies, optimization of selected technologies and the development/implementation of regular process improvements. Success will involve collaboration with IT/bioinformatics to ensure optimal data integration and analysis, regular education on platform capabilities and ensuring platform access by global R&D scientists. Experience in the management of Affy and/or Illumina GAIIx platforms is essential. As a team leader, this individual will help define Integrated Genome Biology group strategy through membership in the iGB Integration Team.

Lead discovery scientist (#1224): The incumbent will develop and apply systematic and integrative approaches to support data mining and analysis of genomic, transcriptomic, metabolomic, proteomic, genetic and public literature in order to accelerate the discovery of genes and biomarkers for trait improvement. Ph.D. in biological sciences and hand on experience in applying statistical and computational methodology to predict gene functions from complex data sets are required. Knowledge of plant biology is desirable.

Large Scale Data Analyst (#1433): Apply statistical and machine learning methods to extract value from complex integrated "omics" datasets, including traditional and digital expression, genomic variation, metabolomic, and phenotypic data.

Read more and apply at http://www.syngentacareers.com/listing/

UArizona ComputBiol PopulationGenomics

STAFF SCIENTIST IN COMPUTATIONAL BIOLOGY AND POPULATION GENOMICS, UNIVERSITY OF ARIZONA

A Staff Scientist position in computational biology and population genomics is available in Michael Hammer's group at the University of Arizona. The focus of the position will be on the analysis of genomic-scale population genetic data gathered from humans and nonhuman primates; in particular, we are interested in a computational scientist who can focus on the modeling and analysis of next generation sequencing data. On-going projects in the lab are aimed at distinguishing the forces that shape patterns of genomic variability, including demographic processes, sexual selection, and natural selection. The primary project is a collaborative, NIH-funded research project to collect large-scale DNA sequence data from eight primate species to study the influences of mating system, sex-biased migration patterns, and chromosomal effective population size on patterns of polymorphism and rates of divergence. While the NIH-funded research project provides intellectually exciting and challenging computational and statistical problems, the candidate will have some flexibility in choosing projects that best match career goals. The position is open to masters or PhD level candidates. The salary will be competitive and based on level of experience, and may well exceed salary levels found on the NIH postdoctoral scale.

Our research group hosts geneticists, computational biologists, applied mathematicians, and anthropologists under this broad research agenda, and provides a working interdisciplinary research environment. The project provides opportunities to work with an active community of researchers in Ecology and Evolutionary Biology, Math, Anthropology, and Computer Science at the University of Arizona, and with Jeffrey Wall and his collaborators at UCSF.

Preference will be given to applicants who have a PhD and experience in the following fields: computational biology, statistical genetics, evolutionary genetics, computer science, or applied mathematics; and who have knowledge of probability theory, stochastic processes, and theoretical/computational statistics. Proficiency in programming is required.

The ideal candidate will have the skills to develop innovative statistical and modeling methodology. Additional capabilities that the lab and project are seeking include mining publicly available data, and bioinformatic methods to design targeted capture arrays for large-scale next generation sequencing of both genic and intergenic regions.

The expected start date is negotiable. This position includes outstanding UA benefits including health, dental, and life insurance; paid vacation, sick leave, and holidays; UA/ASU/NAU tuition reduction for the employee and qualified family members; access to UA recreation and cultural activities; state retirement; and more.

All applicants must apply on-line by completing an appointed personnel application and include a cover letter, curriculum vitae, and contact information for three references. To view the on-line posting and to apply, go to www.uacareertrack.com/applicants/Central?quickFind6097 or go to www.uacareertrack and search postings using job #44065.

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, perspectives and backgrounds M/W/D/V.

Michael Hammer <mfh@email.arizona.edu>

UArizona LabTech MulticellularEvolution

A RESEARCH TECHNICIAN POSITION is available in the laboratory of Dr. Richard E. Michod (http://www.eebweb.arizona.edu/Michod/) in the Department of Ecology and Evolutionary Biology at the University of Arizona (Tucson, AZ; http://www.eebweb. arizona.edu/).

We are looking for a motivated, enthusiastic and independent individual with a strong background in evolutionary biology and/or genomics and/or molecular biology to address questions concerned with the evolution of multicellularity, using the green algal group Volvocales as a model-system. Current projects in the lab address the genetic basis for the evolution of germ-soma differentiation, life history trade-offs as a function of colony size, the role of DNA damage in the evolution of sex.

Minimal requirements are a bachelor's degree in biology or a related field or a minimum of four years laboratory experience. Preferred qualifications include familiarity with molecular lab techniques (DNA extraction, PCR, etc.), sterile technique, basic statistical analyses, and microscopy. Experience working with green algae is not critical, but applicants should have experience in and familiarity with basic laboratory techniques; experience with the Comet assay is a plus but not a necessity.

To apply, please e-mail Pierre Durand (pdurand@email.arizona.edu) with the following information: a statement detailing your research interests and qualifications, a CV, and the names and contact information of three references. The position is funded by an NSF grant. Salary range is $22,602 - $28,144, with specific salary to be dependent on education and previous experience. The start date is flexible (as early as November 1, 2009). The University of Arizona is an EO/AA Employer.

– Matthew D. Herron Ph.D. candidate Dept. of Ecology & Evolutionary Biology University of Arizona mherron@email.arizona.edu http://www.eebweb.arizona.edu/grads/mherron/ 520-621-1844

xprinceps@gmail.com

UBuffalo EvoDevo

Please note that evolutionarily-oriented developmental genomicists, working on ANY organismal system, are encouraged to apply.

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Developmental Genomics

The Department of Biological Sciences (http://www.biology.buffalo.edu) at the University at Buffalo is seeking outstanding applicants for a tenure-track Assistant Professor position in the field of Developmental Genomics. Applications from candidates with interests in whole-genome approaches to study fundamental biological processes including embryonic development, nervous system development, and creation/maintenance of specific organs and tissues are encouraged to apply. This position is offered as part of an ongoing initiative at UB in the area of Molecular Recognition in Biological Systems and Bioinformatics.

UB is the largest and most comprehensive campus in the SUNY system. We offer outstanding research facilities with opportunities for interdisciplinary interactions within UB, Roswell Park Cancer Institute, and the NYS Center of Excellence in Bioinformatics and Life Sciences. A generous startup package will be provided. The successful candidate will be expected to maintain an externally funded research program and to participate in graduate and undergraduate teaching. Applicants should have a Ph.D. (or other doctorate degree), at least three years of postdoctoral experience, a scholarly publication record and fluency in both spoken and written English.

To apply, a curriculum vitae, description of current and future research interests, and reprints of at least three recent or in press publications must be electronically submitted to: www.ubjobs.buffalo.edu/applicants/Central?quickFindR921. In addition, three reference letters should be sent under separate cover, either electronically to devgenomics-search@buffalo.edu, or by mail to Developmental Genomics Search Committee, Department of Biological Sciences, 109 Cooke Hall, University at Buffalo, Amherst, NY 14260. We will begin reviewing applications on November 1, 2009 and continue until the position is filled. Please consult our website for information about UB, our department and our community.

The University at Buffalo is an Equal Opportunity Employer/Recruiter.

– Victor A. Albert Empire Innovation Professor of Biological Sciences University at Buffalo (SUNY) http://biology.buffalo.edu/Faculty/Albert/albert.html "Victor A. Albert" <vaalbert@buffalo.edu>

UCaliforniaLosAngeles DirectorCenter

**Evolutionary Biologists, we strongly encourage you to apply to the following position:

Director, UCLA Center for Society and Genetics

The UCLA Center for Society and Genetics seeks a highly qualified candidate to serve in the position of the Center's Director. The appointee will hold a full-time appointment at the Associate or Full Professorial level in the Center, as well as a joint appointment in a UCLA department appropriate to the appointee's disciplinary research interests. The appointment as Center Director will be for a five-year renewable term, after which time the appointment will continue as a normal faculty appointment. Salary is commensurate with education and experience.

The UCLA Center for Society and Genetics (CSG) is a Center for Interdisciplinary Instruction with a strong research and teaching emphasis, 14 core and affiliated faculty, and plans for continued growth. Our multidisciplinary program seeks to understand the burgeoning biological sciences and their complex interactions with the social world. The Center thus seeks to generate new knowledge about the co-evolution of science and society by promoting innovative and socially relevant research and education. Applications are welcome from either life science or human science scholars whose research focuses on the intersection of the biological and the social. The ideal candidate will be an intellectual leader, with strong disciplinary grounding, strong extramural funding record, and the ability to work closely with colleagues across a variety of fields in the humanities, social sciences, natural sciences and medicine. The new Director of the Center should enhance the national and international profile of the Center, guide the development of a new Human Biology and Society Major housed within CSG, and continue the Center's strong commitment to diversity, public education, and outreach.

Please send letter of application, C.V., statement of research and teaching interests, and names of referees to CSG Director Search Committee c/o Ana Wevill, CSG Manager, UCLA Center for Society and Genetics, Box 957221, 1323 Rolfe Hall, Los Angeles, CA 90095-7221. Electronic applications will be accepted at ana@socgen.ucla.edu –please place CSG Director Search in the subject heading. Posting #:3022-0910-01. For procedural questions, contact Ana Wevill ana@socgen.ucla.edu. For all other questions, contact the Chair of the Search Committee: Soraya de Chadarevian (chadarevian@history.ucla.edu), CSG Co-Director Norton Wise (nortonw@history.ucla.edu) or CSG Co-Director Ed McCabe (emccabe@mednet.ucla.edu). Initial review of applications will begin November 9, 2009 and will continue until the position is filled. UCLA is an Equal Opportunity/Affirmative Action Employer. The Center has a strong commitment to the achievement of excellence and diversity among its faculty and staff. For further information on CSG, visit: http://www.socgen.ucla.edu/

Ana Wevill MSO II, Supervisor UCLA Center for Society & Genetics 1323 Rolfe Hall ph: 310-267-4990 fax: 310-206-1880 email: ana@socgen.ucla.edu www.socgen.ucla.edu Ana Wevill <Ana@socgen.ucla.edu>

UCaliforniaMerced Computational Evolutionary Genomics

The Ardell Lab at UC Merced invites applications from qualified scientists and engineers for a

Senior Research Associate in Computational Biology and Evolutionary Genomics

A full-time bioinformatics research associate / systems administrator position is available to support a small network of innovative and interdisciplinary computational biology and genomics laboratories. The individual Senior Research Associate (SRA) will be responsible for creative, supervised design, development, and integration of bioinformatics databases and software — both alone and in collaboration with computational biologists. The SRA will be given opportunities to participate directly in research and be published. Additional responsibilities will include administration and maintenance of a Mac OS X/UNIX-based workgroup, web server, and high performance computing cluster with a user-load of about 8 users or less. For more information on our groups please see

http://qsb.ucmerced.edu/faculty/dardell/lab/ (Ardell Lab)

http://granada.ucmerced.edu/ ˜ cfrank/webb/Home.html (Frank Lab)

The position is available immediately. Initial appointment will be one year, with possible renewal on a year-to-year basis. Renewal of appointment is contingent on performance and availability of funds.

Qualifications:

A bachelors degree in Computer Science or related fields, Masters preferred, and a minimum of two years of professional experience in systems administration or computational research support including Perl, Apache, MySQL and administration of Mac OS X or UNIX-based systems and/or networks. Experience with MPI, XGrid, and SGE is highly desirable. Other technologies of interest: PHP, CSS, Wordpress, CGI, and Python. An interest in database and algorithm design and open source software engineering is essential. Prior experience in bioinformatics is highly desirable, but not required. Training in bioinformatics will be provided as necessary. Demonstrated ability to maintain accurate database files and library and script documentation.

To apply:

https://jobs.ucmerced.edu/n/staff/position.jsf?positionId=2264 – David Ardell 5200 North Lake Road, School of Natural Sciences, University of California, Merced CA 95343 office: (209) 228-2953 // fax: (209) 228-4675 // dardell@ucmerced.edu

dardell@ucmerced.edu dardell@ucmerced.edu

UCentralFlorida EvolutionaryOrganismal Biologist

Innovative Approaches to Evolutionary and Organismal Biology The Department of Biology at the University of Central Florida (UCF) invites applications for a tenure-track position at the rank of Assistant Professor. The candidate's research will use innovative molecular approaches to address questions in evolutionary or organismal biology. Candidates must have a demonstrated ability or strong potential to establish and maintain a vigorous, extramurally-funded research program. Preference will be given to candidates who complement departmental strengths in conservation biology, ecology, evolution, and organismal biology, and facilitate collaborations. See http://biology.cos.ucf.edu/ for department details. The successful candidate must have an earned Ph.D. and appropriate post-doctoral training. S/he will contribute to our Ph.D. program in Conservation Biology and M.S. program in Biology, and teach graduate and undergraduate courses. UCF has a strong research emphasis and provides competitive startup funds and teaching loads. Applicant must fill out an online job application (please do not upload any materials here, see below) at: https://www.jobswithucf.com/-applicants/jsp/shared/frameset/Frameset.jsp?time=-1255461062403 Then, applicants should send a single Adobe Acrobat PDF document that includes a letter of intent, curriculum vitae, a two-page statement of research plans and a one-page teaching philosophy to: bio-search@mail.ucf.edu and arrange for three letters of recommendation to be sent either to the above email or to: Dr. C. L. Parkinson, Chair, EOB Search Committee, Department of Biology, 4000 Central Fl. Blvd., University of Central Florida, Orlando, FL 32816-2368. Review of applications will begin December 1, 2009, with an anticipated start date of August 2010. UCF is in the top five national universities in the "Top Up-and-Coming Schools" list published by U.S. News & World Report. The University of Central Florida is an Affirmative Action/Equal Opportunity Employer. Minorities and women are encouraged to apply. As an agency of the State of Florida, all application materials and selection procedures are available for public review.

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>

UChicago 2 Tech ChIP-chip

We are looking to hire two technicians to help generate ChIP-chip and ChIP-seq data for the ModEncode project with molecular biology and Drosophila genetics experience.

Thanks very much. Rebecca

https://jobopportunities.uchicago.edu/applicants/-jsp/shared/frameset/Frameset.jsp?time=-1255475504700 Rebecca Spokony, PhD Kevin White's Lab Department of Human Genetics CSLC Room 431 920 E 58th St University of Chicago Chicago, IL 60637 Tel. (773)-834-0074

"Spokony, Rebecca [BSD] - HGD" <rspokony@bsd.uchicago.edu>

UCLondon ResTech SexAntagonismQTL

Dear all,

I am seeking to hire a high grade research technician to work on the genetic basis of sexual antagonism in Drosophila melanogaster. The post is funded by a grant from the Natural Environment Research Council to myself (PI) and Kevin Fowler (Co-I). The position is available for 3 years, starting in January 2010 (negotiable).

The position is Grade 7 and for a highly qualified individual to work in an enabling role but with some responsibility and independence. We are looking for somebody who either has experience as a technician or has worked as a researcher but is looking for an alternative career in academia.

The official advert is pasted below. For more information and to apply, please visit http://tinyurl.com/-reuter-tech. The application deadline is Wednesday 11th November 2009. Interviews will take place in the second half of November.

Best regards, Max

RESEARCH TECHNICIAN (GRADE 7)

Analysing quantitative trait loci of sexual antagonism in fruitflies

A research technician post is available at University College London to work with Max Reuter and Kevin Fowler on the genetic basis of sexual antagonism in fruitflies. The position is part of a project funded by the Natural Environment Research Council, the aim of which is to identify and characterise quantitative trait loci of sexual antagonism in Drosophila melanogaster. The project combines evolutionary and molecular genetic approaches to fine-map QTL of sex- specific fitness and identify candidate genes underlying sexual antagonism. The post-holder will assist a postdoctoral researcher in phenotypic and molecular analyses and will have primary responsibility for a suite of hemiclonal lines and recombinants. Duties will include fitness assays, genotyping via SNP genomic markers, resequencing of genomic regions of interest, data entry/analysis, insect husbandry and laboratory management. The project will be based in a thriving research group within UCL's GEE. For further information on this project and the group, see http://www.homepages.ucl.ac.uk/~ucbtmre/Labsite .

This position is an opportunity for a highly motivated, independent and reliable individual who enjoys working in a team. The candidate will need good organisational and research skills and to be positive about using, developing and troubleshooting new methods. Molecular skills are essential. Experience of large-scale experiments with insects and behavioural assays would be advantageous. Education to B.Sc. Hons. level or higher and work experience as a technician or researcher in a relevant discipline is required. The post is available from 1st January 2010 (flexible) for 36 months, with a starting salary at Grade 7, point 29 on the UCL salary scale: £31,620 (£28,839 plus £2,781 London Allowance).

Application Process: For more information and to apply using the online application process please vitis the post's page on the UCL HR website, accessible throughhttp://tinyurl.com/reuter-tech. It is essential that candidates ensure that their skills and experience meet the post's criteria outlined before applying. In case you have difficulties with the online system, plase email ian.evans@ucl.ac.uk, Ian Evans, Divisional Staffing Officer, Faculty of Life Sciences, University College London, Room 122, Darwin Building, Gower Street, London, WC1E 6BT. Telephone: 020 7679 4486.

The closing date for applications is Wednesday 11th November 2009, 4:30pm. Interviews will take place in late November.

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London 4 Stephenson Way London NW1 2HE, UK

Phone: +44-20-76795095 Fax: +44-20-76795052

http://www.homepages.ucl.ac.uk/~ucbtmre/Labsite/
m.reuter@ucl.ac.uk m.reuter@ucl.ac.uk

UEdinburgh LanguageEvolution

THE UNIVERSITY OF EDINBURGH COLLEGE OF HUMANITIES AND SOCIAL SCIENCE SCHOOL OF PHILOSOPHY, PSYCHOLOGY AND LANGUAGE SCIENCES

LECTURER IN EVOLUTION OF LANGUAGE

SALARY SCALE: £36,532 - £43,622 GRADE: UE08 CLOSING DATE: 4 DECEMBER 2009

VACANCY REFERENCE: 3011813

The University of Edinburgh seeks to appoint a permanent, full-time Lecturer in Evolution of Language within the School of Philosophy, Psychology and Language Sciences. More information here:

http://www.jobs.ed.ac.uk/-
vacancies/index.cfm?fuseaction=-
3Dvacancies.furtherdetails&vacancy_ref=3011813
n.barton@ed.ac.uk n.barton@ed.ac.uk

UFlorida DiseaseEvolution

The Department of Biology, University of Florida, seeks a tenure-track faculty member working at the interface between evolutionary biology and infectious disease, who will be expected to have an adjunct appointment in the UF Emerging Pathogens Institute (EPI). We seek applicants who develop quantitative and theoretical tools to advance our understanding of the evolution of emerging pathogen systems (e.g., host-pathogen coevolution, drug resistance, pathogen response to global change), and may also use such tools to inform broader domains of biological inquiry (e.g. evolutionary genetics, ecology, animal behavior). Host and pathogen taxonomic foci are open. Instruction at both undergraduate and graduate levels is expected. The Department of Biology fosters a collegial, collaborative, interdisciplinary environment with strong ties to EPI, the Florida Museum of Natural History, the UF Genetics Institute, and other UF centers in biomedical, veterinary, environmental and agricultural sciences. For more information and to submit an electronic application consisting of a cover letter, curriculum vitae, statements of research and teaching interests, three reprints, and names of three referees, please go to http://www.biology.ufl.edu/Administration/Jobs.aspx (position #00025351). The appointment is at the rank of tenure- track Assistant Professor; however, appointment at the Associate Professor rank is possible for an exceptional candidate. Ph. D. or equivalent in a relevant discipline is required; postdoctoral research experience is preferred. Salary is commensurate with experience. The anticipated starting date is August 16, 2010. Review of applications will begin on 1 December 2009 and will continue until the position is filled. The selection process will be conducted under Florida's "Government in the Sunshine" and Public Records Laws. Our department is committed to diversity as a component of excellence. Women, minorities and members of other under-represented groups are encouraged to apply. The University of Florida is an equal opportunity institution.

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://web.me.com/mlwayne/Wayne_Lab/The_Wayne_Lab.html mlwayne@ufl.edu mlwayne@ufl.edu

UFlorida InsectEvolution

We have just posted a new tenure-track job in the Entomology and Nematology Department at the University of Florida. The primary focus will be teaching and undergraduate advising, but there is also a substantial research component. The focus of the candidate's research is completely open, as long as it includes insects or other terrestrial arthropods that entomologists might recognize (e.g., mites, spiders, etc.). The University of Florida has a strong interdisciplinary community of people studying ecology and evolution that collaborate across several departments including Entomology and Nematology (http://www.entnemdept.ufl.edu/), Biology (http://www.biology.ufl.edu/), Wildlife Ecology and Conservation (http://www.wec.ufl.edu/), the UF Genetics Institute (http://www.ufgi.ufl.edu/), and more. Individuals with research interests in evolution or ecology are encouraged to apply. Please see the official advertisement below for more information.

Subject: Faculty position available in Entomology at the Univiersity of Florida

A faculty position in Entomology, with a primary emphasis on undergraduate teaching, is available at the University of Florida. Please see the job description below. Questions about the position can be directed to Heather McAuslane (hjmca@ufl.edu<mailto:hjmca@ufl.edu>). Application should be made online using the UF Jobs web site (https://jobs.ufl.edu/applicants/Central?quickFind=62552).

Job Description: This is a 12-month tenure-accruing position that will be 80% teaching (College of Agricultural and Life Sciences) and 20% research (Florida Agricultural Experiment Station) in the Department of Entomology & Nematology, Institute of Food and Agricultural Sciences, at the University of Florida. The principal responsibilities will involve teaching undergraduate non-major courses in insect science, serving as the coordinator of the undergraduate program, and actively recruiting and supporting undergraduate majors. The successful candidate will engage in scholarly activities related to instruction, including teaching undergraduate courses, advising and mentoring undergraduate students, supervising undergraduate student research and creative work, participating in curriculum revision and enhancement, seeking funding for the teaching program, publishing teaching-related scholarship, producing learning tools, and engaging in professional development activities related to teaching and advising. The incumbent is also expected to supervise and advise graduate students, obtain significant grant support for the research program, and publish research results in refereed journals. Tenure will accrue in the Department of Entomology & Nematology. This assignment may change in accordance with the needs of the unit. Faculty are encouraged to support and participate in the CALS Honors Program, distance education, and international education. All IFAS faculty are expected to demonstrate commitment and responsibility to the three functions of the Land Grant mission.

Minimum Requirements: An earned doctorate in Entomology or a closely related discipline is required. Experience and demonstrated excellence in undergraduate instruction is required. Candidates should have demonstrated skills in verbal and written communication, interpersonal relationships, computer-based instructional methods, and procurement of extramural funding. The candidates must be supportive of the mission of the Land-Grant system. The candidate must also have a commitment to IFAS core values of excellence, diversity, global involvement, and accountability.

Preferred Qualifications: Postdoctoral experience is desirable.

Special Instructions to Applicants: To ensure full consideration please apply online and submit additional materials by December 15, 2009. Position will remain open until a viable applicant pool is determined. Nominations are welcome. Nominations need to include the complete name and address of the nominee. This information should be sent to the address below. Individuals wishing to apply should go online to https:/-

/jobs.ufl.edu (referencing requisition # 0803264) and submit:

- Faculty Profile - short application - Cover letter that states applicant's interest in the position and qualifications relative to the credentials listed above - Complete vita (which includes statement of current position and responsibilities); - Statement of teaching philosophy (as 'References') - Statement of research or extension interests (as 'Other Document') - PDF files of 2-3 of your most important publications (as 'Work Sample')

Also, official transcripts showing receipt of the doctoral degree, and three letters of recommendation should be sent to:

Heather McAuslane

— / —

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

UFlorida LepidopteraCollectionManager

Thanks so much. The announcement is inserted below.

COLLECTION MANAGER FOR LEPIDOPTERA McGuire Center for Lepidoptera and Biodiversity, Florida Museum of Natural History, University of Florida, Gainesville, FL

The Florida Museum of Natural History invites applications for a collection manager position at the McGuire Center for Lepidoptera and Biodiversity. The Center has one of the worldâs largest lepidopteran collections with a large staff and active research programs in systematics, evolutionary biology, ecology and biodiversity conservation.

Requirements include a degree in the biological sciences, preferably M.S. or Ph,D., with appropriate experience in a museum or similar collection-based background, and a broad knowledge of lepidopteran classification. Primary responsibilities will include curation and management of collections (acquisitions, accessions, loans, public inquiries, etc.), and supervision of associated preparators and other staff.

Individuals wishing to apply should visit https://jobs.ufl.edu (referencing requisition # 0803166) and submit an online application which must include a curriculum vitae, three letters of recommendation and a description of your collections managementexperience and knowledge of Lepidoptera. The application deadline is November 16, 2009 and the anticipated start date is January 2010.

"celiazar@flmnh.ufl.edu" <celiazar@flmnh.ufl.edu>

UKentucky MolEvolution

ASSISTANT PROFESSORS OF BIOLOGY UNIVERSITY OF KENTUCKY

The Department of Biology at the University of Kentucky seeks 2 tenure- track Assistant Professors interested in molecular bases of evolution and/or molecular approaches to environmental response. Other areas of modern biological thought will be considered. We are particularly interested in programs that integrate empirical approaches with theoretical, statistical, or computational methods. Model systems for research are open, ranging from microbes to plants and animals, as are levels of biological organization studied, ranging from molecular genetics and epigenetics of cells to genomics of populations. Applicants must have an earned doctorate and have completed postdoctoral training, and previous research by the successful applicants must be published in premier scientific journals. Evidence of an ability to obtain extramural grant support is preferred. Responsibilities for the successful candidates include establishment of an independent research program that is supported by awards from extramural agencies and contribution to the teaching mission of the Biology Department. For more details on the department and the university, visit our website (http://biology.uky.edu) or contact Dr. Vincent Cassone, Chair, Department of Biology, vincent.cassone@uky.edu or (859) 257-6766.

Applicants should send a letter of application, a curriculum vitae, statements on teaching philosophy and experience, and a description of the applicant's research program electronically to biosearch@uky.edu. Applicants should also arrange for three signed letters of recommendation in pdf. format on official letterhead to be sent to the same electronic address. The review of applications will begin November 1, 2009.

The University of Kentucky is an Affirmative Action/Equal OpportunityUniversity that values diversity and is located in an increasingly diversegeographical region. It is committed to becoming one of the top public institutions in the country. Women, persons with disabilities, and membersof other underrepresented groups are encouraged to apply. The University also supports family-friendly policies.

David Weisrock <dweis2@uky.edu>

UMassachusetts Amherst EvoDevo 2

Assistant Professor Position in Evolutionary Developmental Biology (Evo/Devo)

The Department of Biology at the University of Massachusetts Amherst (< http://www.bio.umass.edu/biology >www.bio.umass.edu/biology) invites applications for a tenure-track assistant professorship in the area of Evolutionary/Developmental Biology (Evo/Devo). The UMass Biology Department provides an interactive and broad research environment, with faculty research spanning levels of biological organization. Especially strong research clusters focus on the areas of Neural Developmental, Cell Biology, Plant Biology, Functional Morphology, and Evolution. Successful candidates will have a Ph.D., postdoctoral experience, and the potential to develop and maintain an extramurally funded research program. New faculty members will have the opportunity to participate in strong graduate training programs in Molecular and Cellular Biology (< http://www.bio.umass.edu/mcb >www.bio.umass.edu/mcb), Organismal and Evolutionary Biology (< http://www.bio.umass.edu/oeb >www.bio.umass.edu/oeb), Plant Biology (< http://www.bio.umass.edu/plantbio >www.bio.umass.edu/plantbio), and Neuroscience and Behavior (< http://www.umass.edu/neuro >www.umass.edu/neuro).

The candidate should have a strong record of research examining molecular/cellular mechanisms of development that are of fundamental importance for evolutionary biology. We are interested in candidates whose research addresses issues such as the origin and diversification of body plans, the functional divergence of regulatory pathways into novel developmental systems, or the evolution of body structures. Work with model systems, including nematodes, flies, or fish is encouraged, but outstanding applicants who work on other systems will also be considered. Successful candidates should compliment and bridge current departmental research strengths in neural development, evolutionary biology, and functional morphology.

Evaluation of applications will begin on October 26, 2009 (Extended deadline) and continue until the position is filled. Position to be filled contingent upon University funding.

Please send application materials to: Evo/Devo Search #R36699, Biology Department, Attn: Karen Nelson, 611 North Pleasant Street, University of Massachusetts, Amherst, MA 01003. Application materials should include a curriculum vitae, research plan, teaching statement, plus the names, phone numbers, and email addresses for 3 referees. 3 letters of recommendation can either be included in the packet or sent electronically to: evodevosearch@bio.umass.edu . The University is part of the 5 College Consortium (< http://www.fivecolleges.edu/ >www.fivecolleges.edu) in the beautiful Pioneer Valley in Western Massachusetts, just 2 hours from Boston and 3 hours from New York City.

The University of Massachusetts is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups are encouraged to apply. The Biology Department is aggressive in its efforts to hire candidates who will enhance the diversity and general balance of the faculty and the sciences.

Duncan J. Irschick Associate Professor Department of Biology 221 Morrill Science Center University of Massachusetts at Amherst Amherst MA 01003

Phone: 413 545 1696; FAX: 413 545 3243 E-mail: irschick@bio.umass.edu http://www.bio.umass.edu/biology/irschick/

Duncan J Irschick <irschick@bio.umass.edu>

UMassachusetts MolecularEvolutionBioinformatics

MOLECULAR EVOLUTION / BIOINFORMATICS ASSISTANT PROFESSOR UNIVERSITY OF MASSACHUSETTS BOSTON

The Department of Biology at the University of Massachusetts, Boston seeks applicants for a full-time tenure track Assistant Professor who specializes in molecular evolution, phylogenetics, bioinformatics or a closely related field starting in September 2010. Applicants should be well versed in evolutionary and ecological theory. Applications will be particularly welcome from candidates who utilize creative experimental approaches that combine molecular biology, genetics and bioinformatics to address complex environmental problems and who can participate in an interdisciplinary Ph. D. program. The research specialty of the applicants could include molecular evolution, phylogeography, phylogenetics, modeling or other cross-disciplinary fields. The successful applicant is expected to establish an externally funded research program, direct the research of students at the undergraduate, masters and doctoral levels, and interact with a dynamic group of ecologists, environmental, evolutionary and computational biologists. Excellence in teaching at the undergraduate and graduate levels is expected. A Ph.D. and postdoctoral training (or equivalent professional experience) are required. Members of underrepresented groups and women are strongly encouraged to apply.

Applicants should send a statement of teaching and research interests and goals, curriculum vitae, 3-5 representative reprints, and three letters of reference. We prefer application material be sent electronically to biology@umb.edu. If e-files exceed 15mb, please break into smaller segments and send as multiple emails. Hard copies can be sent to Bioinformatics/Molecular Evolution Search, Biology Department, University of Massachusetts, 100 Morrissey Blvd., Boston, MA 02125. For further information, visit the Biology Department website at www.bio.umb.edu, or contact Ron Etter, Chair of Search Committee, at ron.etter@umb.edu or (617)-287-6613. Target date for receipt of applications is Nov. 15, 2009, but applications will be reviewed until the position is filled.

UMass Boston is an Affirmative Action, Equal Opportunity, Title IX employer.

Ron J. Etter Professor Biology Department University of Massachusetts 100 Morrissey Blvd. Boston, MA 02125 Voice 617-287-6613 FAX 617-287-6650 email ron.etter@umb.edu

Ron Etter <ron.etter@umb.edu>

UMichigan ComputationalEvolBiol

Computational Evolutionary Biology Assistant Professor University of Michigan

The Department of Ecology and Evolutionary Biology (EEB) at the University of Michigan invites applications for a tenure-track assistant professor position in computational evolutionary biology. This position is part of a coordinated effort to enhance existing strengths in computational sciences across multiple departments. We seek outstanding individuals with primary research and teaching interests in any area of computational evolutionary biology, including, for example, molecular evolution, evolutionary genomics, evolutionary systems biology, population and quantitative genetics, phylogenetics and phylogeography, and evolutionary theory. Computational biologists with or without an empirical laboratory component to their research programs are encouraged to apply. Opportunities also exist for using the large collections of the Museum of Zoology and Herbarium. For further information about EEB, please see http://www.eeb.lsa.umich.edu . To apply, please email cebsearch@umich.edu a single PDF file that includes a complete curriculum vitae, a statement of current and future research plans, a statement of teaching philosophy and experience, evidence of teaching excellence, and copies of publications. Please also arrange to have three letters of recommendation sent directly to the above email address. Review of applications will begin on November 15, 2009. Women and minorities are encouraged to apply, and the University is supportive of the needs of dual career couples. The University of Michigan is an equal opportunity/affirmative action employer.

Jianzhi George Zhang Professor of Ecology and Evolutionary Biology University of Michigan jianzhi@umich.edu

jianzhi@umich.edu jianzhi@umich.edu

UMississippi Population Genetics

The University of Mississippi, Department of Biology, invites applications for an Assistant Professor position (tenure-track) in population genetics. The appointment requires a Ph.D. in biological sciences or a related discipline. We seek an individual with strong quantitative skills who uses contemporary mathematical and molecular techniques in the study of population genetics. Teaching duties will include genetics, population genetics, and courses in area of specialization. The incumbent will be expected to establish an extramurally funded research program involving graduate and undergraduate training.

The Department of Biology consists of 16 faculty and educates 500 undergraduate biology majors and 36 graduate students (M.S. and Ph.D.). Although the department's strength historically has been in ecology, current research interests span all levels of organization from the cell to the ecosystem. Recent hires include faculty in the areas of cell physiology, conservation biology, evolutionary genetics and phylogeography, microbial ecology, neurobiology, and symbiotic systems. More detailed information concerning the department is available at http://olemiss.edu/depts/biology. The University of Mississippi is located in Oxford, Mississippi, one of the top college towns in the U.S., and a community known for outstanding educational and cultural opportunities.

To apply, please visit our Online Employment Service at jobs.olemiss.edu. Applications should include: (1) cover letter outlining interest and suitability for the position, (2) curriculum vitae, (3) a one-page statement of teaching experience and interests, including a list of potential graduate and undergraduate courses, (4) a statement of research interests, (5) reprints of up to 5 recent publications or submitted papers, and (6) names and contact information for three references. Review of applications will begin November 1 and continue until the position is filled or an adequate applicant pool is established. The University of Mississippi is an EEO/ AA/Title VI/Title IX/Section 504/ADA/ADEA employer.

Brice Noonan

The University of Mississippi Department of Biology, Box 1848 University, MS 38677 Ph: 662-915-6705 Fax: 662-915-5144

http://bnoonan.org bnoonan@olemiss.edu

bnoonan@olemiss.edu bnoonan@olemiss.edu

UNC ResearchTech FlyPopulationGenetics

Research Technician in Fly Population and Evolutionary Genetics University of North Carolina - Chapel Hill

I am seeking a full time technician to assist in fruit fly research addressing fundamental questions in population and evolutionary genetics. Specifically, we are developing comparative genomic resources to facilitate our understanding of the interplay between DNA polymorphism, divergence, and recombination. This position would begin November 2009 and continue for at least a year. This is an ideal position for recent graduates interested in taking time off prior to attending graduate school. Chapel Hill, NC is a delightful location with a vibrant town center and academic community.

Ideal applicants have a BA in biology or related field, prior independent research experience, an understanding of the fields of genetics and evolution, independence, motivation, and the ability to work well in a multidisciplinary, multi-institutional research team. In addition, experience working with fruit flies is desirable.

Please note that due to time and institutional constraints, only US citizens and permanent residents will be considered. Also, post- doctoral applications are strongly discouraged. Preference will be given to local candidates.

To Apply: Please email a CV, a cover letter describing your qualifications and interests, and the names and contact information for three references to Corbin Jones cdjones@email.unc.edu If you have any questions or would like clarification please feel free to contact before applying.

Review of applications will begin October 14th and continue until a successful candidate is found. This project was made possible by Funds from the ARRA.

Corbin D. Jones, Ph.D. Department of Biology Carolina Center for Genome Sciences Campus Box 3280, Coker Hall UNC-Chapel Hill Chapel Hill, NC 27599-3280

cdjones@email.unc.edu cdjones@email.unc.edu

UNebraska ViralEvolution

Tenure Track Virologist Position

Tenure track Assistant Professor at the University of Nebraska-Lincoln Center for Virology and the School of Biological Sciences. Candidates will be expected to develop a nationally recognized research program in virology. Specific area of research is open; appropriate examples of research interests include viral evolutionary genetics, comparative genomics and proteomics, viral-host interactions, pathogenesis or epidemiology of diseases. Candidates must show excellent capacity to develop and coordinate interdisciplinary collaborative research with other Center and departmental researchers. Candidates will be expected to teach courses at the undergraduate and graduate levels. A Ph.D. and postdoctoral experience in related area is required. Salary is commensurate with qualifications and experience.

Desired start date is Spring/Summer 2010. The position will remain open until a suitable candidate is selected. The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers.

To be considered for this position go to http://employment.unl.edu and use requisition #090545 and complete the Faculty/Administrative Information Form and attach CV; cover letter; statement of teaching and research philosophy in three separate documents, up to 3 reprints; and names, addresses, and phone numbers of three references. Arrange for three letters of reference to be sent to Dr. Alan Kamil, School of Biological Sciences, University of Nebraska-Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118 by October 30, 2009. Review of applications will begin November 2, 2009 and continue until a suitable candidate is selected.

Jay F Storz <jstorz2@unlnotes.unl.edu>

UNotreDame ResTech Genomics

Job: Research Technician Position

Description: A Research Technician position is available in the Notre Dame Genomics Core Facility in the Eck Institute for Global Health. The Genomics Core Facility performs DNA sequencing and microarray experiments. The successful applicant will interface with Genomics Core users, perform sample preparations for microarray and DNA sequencing experiments, and operate/maintain microarray and DNA sequencing equipment. In particular, this technician will run full-service NimbleGen microarray experiments, assist with operating/maintaining the ABI 3730xl sequencer, and assist with the operation of next-generation sequencers. Familiarity with these techniques is desired but candidates with basic molecular biology experience will be considered. Applicants must be organized and work well with others. This is an opportunity to join a team that is growing into an integral component of Notre Dame's research community and aims to bolster it through providing access to new technologies, methods, and expertise.

Salary range for this position will be $28,000 - $40,000 commensurate with applicant's genomics experience level.

Information on the Eck Institute for Global Health, the Department of Biological Sciences, and other college faculty and facilities can be found at http://globalhealth.nd.edu/, http://biology.nd.edu and http://science.nd.edu. Review of applications is ongoing and will continue until a suitable candidate is identified. Qualified individuals should send (pdf format requested) a cover letter, curriculum vitae, and contact information for three references to: John Tan, jtan1@nd.edu<mailto:jtan1@nd.edu>.

The University of Notre Dame is a private, Catholic university and is consistently ranked in USN&WR as a top-twenty national university. The South Bend area has a vibrant and diverse economy with affordable housing and excellent school systems, and is within easy driving distance of Chicago and Lake Michigan. The University of Notre Dame is an Equal Opportunity, Affirmative Action Employer.

Michael E. Pfrender Associate Professor Department of Biological Sciences 109B Galvin Life Science Center Notre Dame, IN 46556 USA

Eck Institute for Global Health (http://globalhealth.nd.edu/)

Michael Pfrender <Michael.Pfrender.1@nd.edu>

Uruguay 4 EvolBiodiversity

The Universidad de la República - Uruguay, invites applications for three positions at the rank of Assistant Professor, and one at the rank of Full Professor, of the Department of Ecology, Evolution and Biodiversity, to be created in the city of Punta del Este (DEEB - CURE). Candidates are expected to lead an independent group with a strong research program on any topic related to biological diversity, at any organisational level and focal system. The areas of coastal ecology and fisheries are of high priority for one of the Assistant Professor Positions.

Screening of applications is already under way and the positions are expected to start between Jaunuary and March, 2010. For inquiries about these positions and assistance with the application process, please contact Dr. Omar Defeo (odefeo@dinara.gub.uy) and include a curriculum vitae (preferrably in pdf format).

= = = La Universidad de la República - Uruguay, llama a postulantes para tres posiciones de Profesor Adjunto (Asistente) y una posición de Profesor Titular, en el

Departamento de Ecología, Evolución y Biodiversidad, a ser creado en la ciudad de Punta del Este (DEEB - CURE). Los aspirantes deberán demostrar capacidad para llevar adelante líneas de investigación propias y para formar recursos humanos en temas relacionados con la diversidad biológica, a cualquier nivel de organización y sistema de estudio. Se valorará una demostrada capacidad de trabajo en equipos de investigación. Las áreas de ecología costera y pesquerías son de alta prioridad para uno de las posiciones de Profesor Asistente.

La búsqueda de candidatos esta en marcha y se espera que las posiciones sean ocupadas entre Enero y Marzo de 2010. Por consultas sobre estos cargos y asistencia con los trámites de inscripción, comunicarse con el Dr. Omar Defeo (odefeo@dinara.gub.uy), adjuntando un curriculum vitae (preferentemente con formato pdf).

Dr. Daniel E. Naya Profesor Adjunto (Assistant) de Evolución Facultad de Ciencias, Universidad de la República Iguá 4225, Montevideo 11400 URUGUAY tel (+598 2) 525 8618 ext (7) 136 http://-evolucion.fcien.edu.uy/daniel/daniel.html Investigador Asociado al Centro de Estudios Avanzados en Ecología y Biodiversidad, Pontificia Universidad Católica de Chile, CHILE http://www.bio.puc.cl/caseb/ "Daniel E. Naya" <dnaya@fcien.edu.uy>

USouthFlorida DiseaseEvolution

The University of South Florida Department of Integrative Biology (http://biology.usf.edu/ib/) in Tampa, FL is searching for a tenure track Assistant Professor of disease biology (broadly defined) with interests in interdisciplinary ecological, evolutionary, and/or environmental questions. We seek a colleague who will complement our department's research strengths in environmental microbiology, conservation biology, ecology and evolution, and marine biology, and who will develop a vigorous, externally-funded research program. Applicants working with any taxon or on relevant theoretical problems, including epidemiology, are encouraged to apply. Research interests that complement newly formed biomedical, global change, or computational research clusters in the School of Natural Sciences and Mathematics are also desirable.

Duties will include research, mentoring graduate students, and teaching graduate and undergraduate classes. Our strong graduate program offers Ph.D and M.S. degrees in Biology. The Department and University research facilities include an Ecological Research Area, computing facilities, animal housing facilities, molecular biology/ microbiology laboratories and access to freshwater and marine study sites. Applicants must have a Ph.D in Biology or related discipline, and postdoctoral experience is preferred.

To apply, please visit https://employment.usf.edu/-applicants/Central?quickFind=50882, and have three recommendation letters emailed to bioibsearches@cas.usf.edu. Applications will be accepted until December 11, 2009. University of South Florida is an Affirmative Action/Equal Opportunity/Equal Access Institution. Applications from minorities and women are encouraged. For disability accommodations, please call Mary Parrish (813) 974-6210. According to Florida law, applications and meetings regarding them are open to the public.

Dr. Gordon A. Fox Voice: (813)974-7352 Fax: (813)974-3263 Dept. of Biology ((for US mail:)SCA 110) ((for FedEx etc:)NES 107) Univ. of South Florida 4202 E. Fowler Ave. Tampa, FL 33620, USA http://-foxlab.cas.usf.edu < http://foxlab.cas.usf.edu > "Trying is the first step towards failure." – Homer Simpson "Fox, Gordon" <gfox@cas.usf.edu>

UWisconsinMadison HumanPopulationGenetics

I would like to make you aware of our effort to hire a leading Professor of Human Genetics at the University of Wisconsin-Madison, in the context of the NIH-supported Institute for Clinical and Translational Research (ICTR). Applications are invited for an Associate or Full Professor to develop and direct a human genetics group. The position will serve as an anchor for recruitment of up to five additional hires. Candidates with expertise in human genetics, population genetics, genetic epidemiology, genomics, or computational biology, and strong translational interests, are especially encouraged to apply. Further details are available under PVL# 62591 at < http://www.ictr.wisc.edu/-employment >.

For more information, contact Professor Christina Kendziorski, hiring committee chair, at <kendzior@biostat.wisc.edu> or 608-262-3146.

Please reply directly to the sender at

<info@uwictr.wisc.edu>. Thank you.**

Carol Eunmi Lee <carollee@wisc.edu>

UYork EvolutionaryBiology

We are currently advertising for a lecturer in any aspect of evolutionary biology (a tenured position, equivalent to assistant professor) here in the Biology Department at York.

The closing date is 8 October, and details can be found at https://www22.i-grasp.com/fe/tpl_YorkUni01.asp?newms=jj&id=28579 (sorry for the short deadline - I have only just become aware of EvolDir)

Many thanks

Peter Young

– – Prof J P W Young Department of Biology University of York PO Box 373 York YO10 5YW UK

Direct phone: +44 1904 328630 Department: +44 1904 328500 Fax: +44 1904 328505 www.york.ac.uk/depts/biol/staff/jpwy/jpwy.htm jpy1@york.ac.uk

Peter Young <jpy1@york.ac.uk>

WilliamsCollege EvolutionaryGenetics

ASSISTANT PROFESSOR Tenure-Track Faculty Position in Evolutionary Genetics Biology Department Williams College

The Biology Department at Williams College, a premier liberal arts college with a long-standing tradition of excellence in the sciences, invites applications for a tenure-track position at the rank of Assistant Professor, to begin July 2010. We seek an evolutionary geneticist to teach genetics, evolution and other courses at the introductory and advanced level that effectively integrate the fields of molecular evolution, organismal biology and genetics. Faculty members teach one course and two laboratory sections, or the equivalent, each semester. Start-up funds and internal funding for research are available, and a research program that attracts extramural funding and involves talented undergraduates is expected. A Ph.D., postdoctoral experience, and a strong research record are required. Applicants should submit curriculum vitae, brief statements of teaching and research interests, and arrange for three letters of recommendation to be sent, to: Judy Uryniak, Academic Assistant, Department of Biology, Williams College, Williamstown, MA 01267, Judith.A.Uryniak@williams.edu Applications will be considered as they are completed with a deadline of November 23, 2009.

– Judy Uryniak Academic Assistant Biology Department 59 Lab Campus Drive Williams College Williamstown, MA 01267 tel: 413-597-2126 fax: 413-597-3495

Judith.A.Uryniak@williams.edu Judith.A.Uryniak@williams.edu

YeshivaU ComputationalBiol

Department of Systems and Computation Biology Albert Einstein College of Medicine of Yeshiva University

Multiple Tenure Track Faculty Positions

The Albert Einstein College of Medicine, one of the leading medical schools in New York City, is seeking to fill multiple tenure track faculty positions in the newly formed Department of Systems and Computational Biology. Established in April 2008, the main goal of the new department is to advance our understanding of living systems by developing theoretical, computational and experimental approaches to study complex biological systems.

The College has 750 medical students, 325 graduate students and 360 post-doctoral fellows in training and boasts a strong research faculty covering broad areas of experimental biology, offering outstanding opportunities for collaborative interactions. The 200,000 square foot Center for Genetic and Translational Medicine at Einstein, which opened in late 2007, locates computational, systems and experimental scientists in physical proximity to foster interdisciplinary communication and collaboration. Highly competitive start-up packages are available.

Job Requirements

We seek outstanding scientists with broad experience and demonstrated collaborative interactions with experimental or clinical investigators. Candidates should have strength in a physical, mathematical or computational field at the Ph.D. or equivalent level. Experience applying these skills to a biological or biomedical area (demonstrated through publications or support) is also required. Areas of interest include, but are not limited to: Modeling cellular processes, such as signaling, transcriptional regulation and immune response; Pathway analysis; Genetic networks; Functional proteomics and genomics; Evolution of structure and function; Computational neuroscience; Mathematical and computational modeling of complex traits and diseases.

Applicants should send a letter of interest, C.V., statement of research and teaching interests, and names of three referees, in electronic format to:

Systems and Computational Biology Search Committee Albert Einstein College of Medicine Jack and Pearl Resnick Campus 1300 Morris Park Ave. Price Center, Rm. 153 Bronx, New York 10461 E-mail Address: SysBio@aecom.yu.edu Subject line should be: SCB Faculty Search

EOE

Heather Hughes <h.hughes@jobtarget.com>

Yukon 5techs RedSquirrels

Five field technicians are needed to work as part of a long-term project run by researchers at the University of Alberta, McGill University and University of Guelph, studying the ecology and evolution of red squirrels near Kluane Lake, Yukon, Canada. Details on the project and area can be found at www.redsquirrel.ca. Technicians will be responsible for monitoring the survival and reproduction of red squirrels during the 2010 breeding season. Duties will include live-trapping, handling and tagging of red squirrels, assessing reproductive condition, radio-collaring and telemetry, and performing behavioral observations.

Successful applicants will have a biology or wildlife background, exhibit sound decision making abilities, and will be prepared to live at our remote field camp in the winter. Field technicians must be prepared to complete fieldwork using snowshoes under northern winter weather conditions. Previous field experience with small mammals and winter field experience will be considered assets. Applicants must be eligible to work in Canada (i.e., citizens, permanent residents or visa holders), have up-to-date first-aid training, a valid driver's license and a clean driving record.

Four technicians are needed between February 22 and August 27, 2010 and one position is needed between January 15 and May 10, 2010, but end dates are negotiable. Salary will depend on experience, but will start at $1,400 per month. In addition, food and accommodation will be provided in the field.

Applicants should send a resume and cover letter, including references by e-mail to Ainsley Sykes at the University of Alberta (asykes@ualberta.ca). Please indicate in your cover letter when you will be available to start and when you would like to end. Review of applications will begin immediately. Under-represented groups are particularly encouraged to apply.

Dr. Andrew G. McAdam Department of Integrative Biology University of Guelph Guelph, ON, Canada, N1G 2W1

ph: 519-824-4120 ext. 56826 fax: 519-767-1656 www.uoguelph.ca/~amclab/ www.redsquirrel.ca amcadam@uoguelph.ca amcadam@uoguelph.ca

Other

AFLP linkage

I have read several papers that have mentioned that polymorphic AFLP markers from the same primer combination are often tightly linked on a specific chromosome. However, I can not find any of these references at the moment. If anybody knows of such a reference, please send it to me.

Thanks, Greg gdouhan@ucr.edu

Greg W. Douhan, Assistant Professor Department of Plant Pathology and Microbiology Fawcett Lab RM 238 University of California Riverside, CA 92521-0122 Office (951) 827-4130 Fax (951) 827-4132

Greg Douhan <gdouhan@ucr.edu>

AlleleFreq Fst

I would like to calculate pairwise FST values for a dataset of around 20 populations for which I only have the allele frequencies at 6 microsatellite loci, not the raw genotypic data. All the software programs that I would normally use to calculate FST (FSTAT, Genepop etc) require raw genotypes as the input file, and Arlequin only appears to allow a single locus at a time to be analysed when frequency data is used. Can anyone suggest a way around this problem? Thanks, Hilary

Dr Hilary Miller Research fellow, Allan Wilson Centre for Molecular Ecology and Evolution School of Biological Sciences Victoria University of Wellington PO Box 600, Wellington New Zealand Ph: +64 4 463 7432 Fax: +64 4 463 5331 email: hilary.miller@vuw.ac.nz

Hilary.Miller@vuw.ac.nz Hilary.Miller@vuw.ac.nz

ALU simulations

“simulations of microevolutionary scenarios with ALU data”

We are working on a broad panel of alu loci in human populations produced by Mark Batzer’s lab. We would like to apply a simulation approach in order to test some evolutionary scenarios regarding sub-Saharan populations. Unfortunately currently available software (e.g. simcoal, popABC) do not implement a mutational model fitting that of ALU loci. Therefore we wonder whether anyone could provide us with info regarding simulation approaches and software which could be applied to our particular dataset. Our ideal target is a software for coalescent simulations allowing for 100 RFLP-like unlinked loci which follow an infinite site mutation model.

Giovanni Destro Bisol Universita’ di Roma La Sapienza Dip.to di Biologia Animale e dell’Uomo sede di Antropologia P.le A. Moro 5 - 00185 Roma tel 0039 06 49912273 fax 0039 06 49912771

Four stages of acceptance: i) this is worthless nonsense; ii) this is an interesting, but perverse, point of view; iii) this is true, but quite unimportant; iv) I always said so. J.B.S Haldane, Journal of Genetics 1963

Giovanni.Destrobisol@uniroma1.it

Ant samples

Dear Colleagues,

My group and I would be extremely interested in just a few samples of the small black (dark brown) formicine garden ant Lasius niger (workers e.g.) from Russia, Kazakhstan, Mongolia, Ukraine, Rumania, Georgia, Greece, Finland, Portugal, Spain, or Norway.If any one is in possession of such samples (even just a few workers) and would out of great kindness allow us to have some, we would immensely appreciate it. Alternatively, if you know any one who may be in possession of such, or is likely to be, or might grab a few in spring, or might know someone who might grab a few (local entomological associations?), please let me know. L. niger is very widespread in meadowlands, grassy areas, parks, lawns, along pavements, and its colonies are rather large (up to 50,000 workers, often building soil mounds when in long grass). It is also a non-aggressive ant, in the sense that, try as it may, it cannot pierce human skin and has no sting.Many thanks in advance, for any and all help,

Best regards,Else Fjerdingstad

else.fjerdingstad@qc.cuny.edu

Bark beetle samples

≪ Dear colleagues,

we are looking for bark beetles from Europe and Asia of two species : Ips typographus and Dendroctonus micans. We are also interested in the ulstraspecific predator Rhizophagus grandis, often found in the galleries of D. micans.

Would it be possible for you to send me beetles (put alive in alcohol 100%)?

We can provide the material if necessary (eppendorfs and ethyl alcohol) and will naturally cover any related expenses.

We need the location where the samples were collected and eventually the tree specie attacked (Picea sp.or Pinus sp.).

We need around then individuals by country, preferentially catched in different sites but we will be grateful with any beetles found.

Sample could be sent to: François Mayer

Laboratoire de Lutte biologique et Ecologie spatiale (LUBIES), CP 160/12

Université Libre de Bruxelles 50 av FD Roosevelt, 1050 Bruxelles/Brussels

Belgium

Many thanks for

Ir. François Mayer

Research Fellow, FNRS-FRIA / PhD student Biological control and Spatial ecology Lab (LUBIES) Université Libre de Bruxelles

fmayer@ulb.ac.be

Bgee GeneExpressionDatabase

We would like to introduce to the evolutionary biology community Bgee, a database for gene expression evolution:

http://bgee.unil.ch/ Bgee allows you to query expression patterns of homologous genes in homologous organs between animal species. The latest release includes human, mouse, xenopus, and zebrafish, as well as preliminary data for Drosophila.

Bgee is in continuous development, and we welcome all feedback. Please contact us also if you wish to be informed of future developments.

We hope that Bgee will be useful for animal Evo-Devo, evolutionary functional genomics, and other comparative studies.

Example query on mouse HoxA5: http://bgee.unil.ch/bgee/bgee?page=gene&action=summary&gene_id=ENSMUSG00000038253 Best regards, Marc, for the Bgee team

Marc Robinson-Rechavi Department of Ecology and Evolution Biophore 3219, University of Lausanne, 1015 Lausanne, Switzerland tel: +41 21 692 4220 fax: +41 21 692 4165 http://bioinfo.unil.ch/ Swiss Institute of Bioinformatics http://www.isb-sib.ch/groups/lausanne/evolutionary-bioinformatics-m-robinson-rechavi.html La liberte ne s'use que quand on ne s'en sert pas marc.robinson-rechavi@unil.ch

Biological domains and kingdoms for kids

My son's elementary-school class is learning the five-kingdom system of classification. His teachers are open to updating their teaching materials and have asked for recommendations of books that reflect a more modern taxonomy. I think something along the "six-kingdom" approach is best ... I'm not sure that kids this young (6-9 years) need to be able to distinguish among all of the protists!

Can any of you recommend children's books along these lines that would be suitable? The teachers would like something between the first- through fifth-grade reading level.

Thanks! -Leah

– Leah Larkin, Ph.D. Assistant Professor Department of Biological Sciences University of the Pacific 3601 Pacific Avenue Stockton, CA 95211 (209) 946-2182 (Office)

Leah Larkin <llarkin@pacific.edu>

Determining k in STRUCTURE

The STRUCTURE manual describes an "ad hoc" method of evaluating k by computing the posterior probability of any given k from the "Estimated Ln Prob of Data,$B!I(B which is printed out by default in each run's output.

This can be a real chore if 1) you are testing a broad range of possible k or 2) your LnPr (k) absolute values are large. I hope that this can be worked into a future release of STRUCTURE.

In the meantime, has anyone out there in the community written a simple computer program to do this?

alan.meerow@ars.usda.gov

EasternGreySquirrel samples

Dear Colleagues,

I have a student student studying genetic variation in the Eastern Grey Squirrel for his senior thesis. I am seeking tissue samples or DNA from both the native and introduced range that he could use for PCR. Please let me know if you have material that would be usable.

Best regards,

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

www.willamette.edu/ ˜ csmith/ChrisSmith.htm email: csmith@willamette.edu csmith@uidaho.edu chris_smith@post.harvard.edu

csmith@willamette.edu

EvolutionBlog TravelAward

I'm sending an announcement about a travel fellowship that may be of interest to the evolutionary biology community. Please consider posting this to evoldir.

Thank you! -the folks at NESCent

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Blog about evolution and win $$$ to attend ScienceOnline2010 Application deadline: December 1, 2009

Calling all science bloggers: The National Evolutionary Synthesis Center (NESCent) is offering two travel awards to attend ScienceOnline2010, a science communication conference to be held January 14$B!>(B17th, 2010, in North Carolina$B!G(Bs Research Triangle Park.

The awards offer the opportunity to travel to North Carolina to meet with several hundred scientists, educators, writers and editors to explore how online tools are changing the way science is done and communicated to the public. Each winner will receive $750 to cover travel, lodging, and other expenses to attend the conference. In addition, winners are invited to spend the morning of Friday January 15th interacting with scientists at NESCent, and to attend a lunch in their honor.

The purpose of this contest is to encourage the best of evolutionary writing on the Web. To apply for an award, writers should submit a blog post that highlights current or emerging evolutionary research.

To learn more about the contest, visit: http://-www.nescent.org/news/TravelAward.php –

*** Robin Ann Smith, Ph.D. Communications Manager Science Education and Outreach National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC 27705 Tel: 919-668-4544 Fax: 919-668-9198 www.nescent.org Robin Smith <rsmith@nescent.org>

Gel double peaks

I have a question about specific restriction enzyme activity and T-RFLP analysis.

I have a NED marked PCR product which is digested with one of the three restriction enzymes Cfo I, Hae III or Taq I and the corresponding buffer. The products are analyzed with an Applied Biosystems 3730xl DNA Analyzer and the T-RFLP profiles analyzed with the software GeneMapper v4.0.

In the T-RFLP profiles the products cut with Cfo I result in clear single peaks at a certain size. But Hae III and Taq I sometimes produce a kind of double peaks (I attached an example). There are two peaks which are 1 bp away from each other. We first thought there might be variations in the fragment lengths of the PCR products but as this only appears for two of the three enzymes it might have an enzyme specific reason? Had anyone similar problems or is there an explanation how this double peaks can evolve? They are repeatable but their total height varies.

Thanks a lot for your ideas and suggestions!!!

Chrisitin Koch and Svante Holm Department of natural Sciences, engineering and mathematics Mid Sweden University 850 71 Sundsvall Sweden svante.holm@miun.se<mailto:svante.holm@miun.se> +46 60148537

Svante.Holm@miun.se

Genotyper Windows

Dear evoldir members,

I am try to run Genotyper (version 3.7 NT) software in Windows xp, and windows vista. However, I always received an error message “Could not start the application because there is not enough memory”. I know that Genotyper software was never tested on the Windows XP operating system, and that the error states that there is insufficient memory, but the fix is actually to reduce the amount of virtual memory on the computer:

(Go to Control Panel > System> Advanced tab> in the performance options pane, select settings> select advanced tab> in the virtual memory pane, select change > select de customize radio button> set initial size to 500> set maximum size to 700.)

This work in my old computer (Microsoft Windows XP, 3.21Ghz, 1Gb RAM) but not in the new one (Microsoft Windows XP, 2.33Ghz, 3.49Gb RAM), and never worked in the computers with Windows vista operating system.

Know anybody the way to run Genotyper software on Windows XP and/or Windows Vista?

Thank in advance,

Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología Universidad de Las Palmas de Gran Canaria Campus Universitario de Tafira 35017 Las Palmas de Gran Canaria Canary Islands Spain Phone: (+34) 928 454 543 Fax: (+34) 928 452 922 email: mgonzalez@proyinves.ulpgc.es

canariensis750@hotmail.com

Goby samples

Dear EvolDir members,

we are currently starting a project on the phylogeography of some goby species from the Mediterranean Sea. For this project, we are looking for tissue samples of the following species : Pomatoschistus microps,

P. marmoratus and P. knerii. If one of you can provide us with some samples, please contact me at the following address.

Best regards, Christelle Tougard.

Christelle Tougard Institut des Sciences de l'Evolution - UMR CNRS 5554 Equipe "Métapopulations, Conservation & Coévolution" Université Montpellier II Place E. Bataillon - CC065 34095 Montpellier cedex 05

Telephone : +33 (0)4 67 14 47 17 Fax : +33 (0)4 67 14 36 22 E-mail : christelle.tougard@univ-montp2.fr

http://www.isem.cnrs.fr/ http://www.cnrs.fr/inee/recherche/actionsincitatives-RTP-Paleogenetique.htm Christelle Tougard <Christelle.Tougard@univ-montp2.fr>

InsectDiversity paper

Hi, I was looking for the following paper but my faculty doesnt have access to this journal. I would very much appreciate is someone with access it could sent it to me.

Jones, O. et al., 2009. Using taxonomic revision data to estimate the geographic and taxonomic distribution of undescribed species richness in the Braconidae (Hymenoptera: Ichneumonoidea). INSECT CONSERVATION AND DIVERSITY, 2(3), 204-212.

Please reply to viktor.nilsson@emg.umu.se

Thanks, Viktor Nilsson

–

Viktor Nilsson, PhD student Ecology & Environmental Science, Umeå University S-901 87 Umeå, Sweden

Phone: +46 90 786 97 77 E-mail: viktor.nilsson@emg.umu.se Mobile: +46 70 293 69 02

viktor.nilsson@emg.umu.se viktor.nilsson@emg.umu.se

Linkage disequilibrium calculation

Hello all,

I am trying to obtain a probability associated with a linkage disequilibrium calculation. I am using the work of Hill 1974 to calculate LD between a codominant marker and several dominant markers. I have estimates of LD associated with my data, but I'm not sure how to determine whether my calculations of LD are significantly different from 0. If anyone has solved this problem before and could give me some advice, I would greatly appreciate it.

Thanks, Julie

Julie B. Hébert PhD Candidate BEES Program (Behavior, Ecology, Evolution, and Systematics) Department of Entomology University of Maryland 4172 Plant Sciences 301-405-8919

byrdie@umd.edu byrdie@umd.edu

Longworth traps wanted

Hi, I'm after around 80 Longworth traps to supplement those I already have for a PhD project involving the St Kilda fieldmouse. I'm sure there must be hundreds around the UK sitting unused, if anyone would be willing to put some on long term loan (3 years) I'd be very grateful.

Thanks, Tom Black

T.W.Black@sms.ed.ac.uk

Wild Evolution Group Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road Edinburgh EH9 3JT

Tel: +44 (0) 131 651 3612 Fax: +44 (0) 131 650 6564

T.W.Black@sms.ed.ac.uk T.W.Black@sms.ed.ac.uk

Methods Ecology Evolution Journal

Methods in Ecology and Evolution [http://bes.homeftp.org:11111/www.methodsinecologyandevolution.org/] is a new online only journal that the British Ecological Society have launched in collaboration Wiley-Blackwell. MEE aims to make full use of online enhancements to papers, such as audio clips, video, flash video as well as computer code and tutorial materials. We also host a dedicated blog. MEE is actively seeking submission of manuscripts in the field of evolutionary ecology. For more information, please visit our website at Methods in Ecology and Evolution [http://bes.homeftp.org:11111/-www.methodsinecologyandevolution.org/] . Graziella Iossa Journal Coordinator,Methods in Ecology and Evolution

The British Ecological Society 26 Blades Court Putney London SW15 2NU UKTel. +44 (0)7794 333168 Fax +44 (0)20 88719779 Email mee@britishecologicalsociety.org Web http://-www.methodsinecologyandevolution.org/

mee@britishecologicalsociety.org
mee@britishecologicalsociety.org

Pear samples

Dear Colleagues,

I am looking for samples of seed or fruits of Pyrus calleryana (Callery Pear) from Asia, including the Chinese region around Jingmén and Yichang in Hubei Province. Such samples are needed for a genetic study comparing genetic diversity of introduced, invasive populations in the US with those in the native range. Although I would certainly welcome seed or fruit from any region of Asia (Japan, Korea, etc.), I am especially interested in China because that is where the seed for this species was originally obtained by US plant explorers in the early 1900's.

If possible, I would like to obtain samples from several trees per site, but any number of samples would be much appreciated. I will provide supplies necessary for collecting samples and will cover any incurred expenses. Please contact me at theresa.culley@uc.edu for further information. Thank you.

Sincerely, Dr. Theresa Culley Department of Biological Sciences University of Cincinnati 614 Rieveschl Hall Cincinnati, OH USA 45221-0006

culleyt@ucmail.uc.edu culleyt@ucmail.uc.edu

RFAM alignments

Hi,

I would like to know what are the different options for building trees from ncRNA alignments, like e.g. the ones in RFAM. Ideally, software that takes into account the secondary structure of these RNA sequences.

Thanks,

Albert.

Albert Vilella <avilella@ebi.ac.uk>

RFAM alignments answers

Upon request, here is the link with all the RNA phylogenetic analysis tools available, updated with answers to my query email:

http://openwetware.org/wiki/-Wikiomics:RNA_phylogenetics Cheers,

Albert Vilella <avilella@ebi.ac.uk>

Salmonid MHC micros

Hi,

I'm looking for linked microsatellite primers for MHC class II in salmonids. Can anyone help me? I have searched extensively through references but only found linked microsatellite primers for class I.

Many Thanks

Roseanne Miller

Roseanne Miller <roseanne_miller@yahoo.com>

Simulated haplodiploid hybrids

Dear Evoldir members,

I wish to simulate hybrids from standard population genetic multilocus microsatellite genotypes, but my populations are haplodiploid (bumblebees) rather than diploid. Are there any programs available that can simulate F1, F2 and backcross hybrid genotypes from haplodiploid parental populations? Something akin to Nielsen's HybridLab (http://www.dfu.min.dk/ffi/uk/-populationgenetic/hybridlab/) would be great.

Kind regards, Tomás

Dr. Tomás Murray Postdoctoral Fellow Crops Research Centre Teagasc Oak Park Carlow Ireland

Tel.: +353-59-9170218 Fax: +353-59-9142423 Email: tomas.murray@teagasc.ie Web: www.agresearch.teagasc.ie/oakpark/ tomas.murray@teagasc.ie tomas.murray@teagasc.ie

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Simulation tool serial sampling

Dear All,

I am looking for a simulation tool with the following features: - forward in time OR backward in time with serial sampling (like Serial Simcoal) - has a mutation model suitable for microsatellites (SMM or GSMM) - includes recombination - able to simulate complex demographies, including admixture

I know it's a lot to ask for but if anyone is aware of such tool please let me know.

Thank you!

Kati

– Katalin Csilléry TIMC-IMAG, équipe TIMB, Université Joseph Fourier, F 38706 Tel.: + 33 456 52 00 65

Katalin.Csillery@imag.fr

Simulation tool serial sampling answers

Dear All,

recently, I posted a request "looking for simulation too with serial sampling". I had many responses, thank you all for getting back to me. However, most of you who wrote back to me, were also looking for such a tool!

Basically, it seems that two possibilities exist to do the job: i.e. - forward in time OR backward in time with serial sampling (like Serial Simcoal) - has a mutation model suitable for microsatellites (SMM or GSMM) - includes recombination - able to simulate complex demographies, including admixture

1. quantiNEMO http://www2.unil.ch/popgen/-softwares/quantinemo/ Thanks to Samuel Neuenschwander, author of quantiNEMO, who wrote back to me. quantiNEMO was originally developed to simulate quantitative traits, however, it allows also to simulate genetic data, including microsatellites. Loci are placed on a genetic map with any chromosomes. It is individual-based, forward in time, and allows to obtain samples from any generations. A very attractive feature is that parameters can change with time, thus allowing for sampling from any user defined generations. quantiNEMO allows to simulate highly complex demographic histories including selection.

I found it very easy to learn to use. The only drawback is speed... but we can forgive for the slowness given all the features!

2. simuPOP A very general and flexible simulation environment, written in Python. Very attractive, however, its use requires quite a bit of coding in Python. The SimuPOP community, however, might be able to help (see very positive response from Bo Peng below). If anyone would try and finds it faster than quantiNEMO I would be interested to hear from you!

"If you cannot find a program that fits your need, you can use simuPOP, a general-purpose individual-based population genetics simulation environment, to write your simulation, provided that you or someone in your group can program in Python. Please refer to the simuPOP website (simupop.sourceforge.net) for more information and feel free to discuss your simulation in the simuPOP mailing list. We might even be able to help you implement your simulation if your project is interesting enough."

Hope this helps many...

All the best Kati

Katalin Csilléry, post-doc TIMC-IMAG, équipe TIMB, Université Joseph Fourier, F 38706 Tel.: + 33 456 52 00 65

Katalin.Csillery@imag.fr

Software Archaeopteryx TreeViewer Editor v0 951

Archaeopteryx version 0.951 beta (2009.10.28) has the following major improvements over previous versions:

* (Re)Introduction of tree topology editing (cut, copy, paste, delete, new).

* (Re)Introduction of node data editing (covering most phyloXML data fields).

* A "New" menu item (under "File") for manual tree creation.

* Various display types (rectangular, unrooted, circular, etc.).

* Interactive overview feature when zoomed in.

See: http://www.phylosoft.org/archaeopteryx/ – Christian

czmasek@burnham.org

Software TESS update

A new version of TESS by Eric Durand is available online at:

http://www-timc.imag.fr/Olivier.Francois/tess.html TESS 2.3 implements a Bayesian clustering algorithm for the inference of spatial population genetic structure. The new features are:

- an improved admixture model using trend surfaces and spatial autocorrelation - modeling of dominant markers - inclusion of geographic distance - possibility to export to CLUMPP format directly - possibility to start from a NJ tree - computation of model choice indices: DIC - better GUI

Specifically, the new admixture model uses a CAR (conditional autoregression) model based on the Delaunay tessellation. The new version allows the user to weight the TESS spatial network by exponentially decreasing geographic great circle distance. This new model could be considered more reliable than the TESS 1.x admixture model which was based on an approximation of the model implemented in STRUCTURE. TESS 2.3 allows to use dominant markers. It also improves the admixture model implemented in TESS 2.0. Various GUI bugs have been corrected since 2.0. In addition, TESS 2.3 implements a variant of the CAR model, called the BYM model. The manual is up-to-date. The without-admixture model is unchanged.

best regards Eric Durand

Eric Durand <eric.durand@imag.fr>

Spagedi Phist vs Fst

Hello all.

I've been having trouble getting the program Spagedi to successfully run Phist vs Fst analyses of sequence data. I've tried everything I can think of but have not been able to get it to run. I was wondering if someone would be willing to send me an input file they have used successfully for this purpose. I'd like to compare it with mine, see if I can spot mistakes.

Thanks in advance, Giselle Perdomo

PhD Candidate School of Biological Science Monash University - Clayton Campus Melbourne, Victoria 3800, Australia Phone: +61-3-9905-5680 email: giselle.perdomo@sci.monash.edu.au

Gisselle Perdomo <gisselle_p@yahoo.com>

STRUCTURE HARVESTER

I have asked the author if I could post the info about this program on evoldir and he has graciously given permission. It is a wonderful tool.

Dent A. Earl at UC Santa Cruz has created a Web-based tool called STRUCTURE HARVESTER which takes as input a zip file of your Structure output (follow instructions online), and plots likelihood and variance against K. It can also plot the Evanno et al. delta K method, and generate CLUMPP infiles for you. Finally it allows you to download a txt file with the numbers used to create the plots. The Web version of the program is found at: http://taylor0.biology.ucla.edu/struct_harvest/ <http://owa.gla.ac.uk/exchweb/bin/redir.asp?URL=3Dhttp://taylor0.biology.u cla.edu/struct_harvest/> . You can download the PERL scripts for local use at: http://users.soe.ucsc.edu/ ˜ dearl/software/struct_harvest/ .

There is one small bug on the Web version which Dent will be fixing soon. The program timer assumes that your results will be complete in 3 seconds. If the server is under load, or if your data require more time, you will be directed to an empty page or an HTML error page. I've worked around this by hitting the back button on my browser, allowing the reloading of the submission data and then clicking the forward button on my browser. My results than appear. Your results will remain on the server for 7 days after they are generated.

Alan

Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: 786-573-7075; FAX: 786-573-7110 email: alan.meerow@ars.usda.gov

Alan.Meerow@ARS.USDA.GOV

STRUCTURE log likelihoods

In some current analyses with STRUCTURE, I am receiving Ln(Pr) score with absolute values in excess of 30,000, even > 50,000. Is it reasonable of me to conclude that the information content of my data in these cases, relative to the model assumptions of the program, is abysmal?

Thanks,

Alan

Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: 786-573-7075; FAX: 786-573-7110 email: alan.meerow@ars.usda.gov <mailto:alan.meerow@ars.usda.gov>

"Meerow, Alan" <Alan.Meerow@ARS.USDA.GOV>

Transgenic Drosophila

Subject: Transgenic Drosophila Species

We would like to call your attention to the availability of new transgenic stocks of ten species.

Drosophila melanogaster: 38 stocks Drosophila simulans: 13 stocks Drosophila yakuba: 19 stocks Drosophila erecta: 14 stocks Drosophila sechellia: 1 stock Drosophila pseudoobscura: 15 stocks Drosophila willistoni: 13 stocks Drosophila mojavensis: 2 stocks Drosophila mercatorum: 8 stocks Drosophila virilis: 29 stocks

Please visit the stock center website for details about each stock. https://stockcenter.ucsd.edu/index.php?table=Transgenic Therese Ann Markow, Professor Amylin Chair in Life Sciences Section of Ecology Behavior and Evolution Division of Biological Sciences Muir Biology Building 2215 9500 Gilman Drive University of California at San Diego La Jolla, CA 92093-0116

Email: tmarkow at ucsd.edu Phone: (858) 246 0095 Laboratory: (858) 246 0402 FAX:(858) 534-7108

http://biology.ucsd.edu/labs/markow/ http://stockcenter.ucsd.edu Therese Markow <tmarkow@ucsd.edu>

Trends Evol Biol

Trends in Evolutionary Biology is a new online-only Open Access peer-reviewed journal publishing articles that span the breadth of modern evolutionary biology. Articles can range in scope from the origin of life to the evolutionary diversification of life and of biomacromolecules, from experimental evolution to evolutionary bioinformatics. Trends in Evolutionary Biology publishes original articles, brief reports, editorials and commentaries, review articles, and book reviews.

Trends in Evolutionary Biology has now published its first three pieces, including two articles and a book review, as listed below. We welcome new submissions at http://www.pagepress.org/journals/index.php/eb. Thank you for considering us for your next publication.

David Liberles Editor-in-Chief

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UMichigan Volunteer GeladasConservation

ONE camp manager needed for The University of Michigan Gelada Research Project, a study of the behavior, communication, endocrinology, and conservation of wild geladas (Theropithecus gelada) V a close relative of baboons. All research is conducted at a field station located in the Simien Mountains National Park of Ethiopia. Directors of the project are Drs. Thore Bergman and Jacinta Beehner, faculty at the University of Michigan. The camp manager will be responsible for (a) collecting basic demographic and reproductive data as part of routine monitoring of the well-habituated study population, (b) conducting focal animal samples and collecting fecal samples from individually- recognized geladas (for later laboratory steroid hormone analysis in the USA), (c) recording GPS readings of gelada ranging locations, (d) managing the computer database, and (e) equipment upkeep and personnel management. The gelada population has been studied on a near-daily basis since 2006 and we currently recognize approximately 150 individuals. The camp manager will live in a stone hut located in the national park with 0-3 graduate students (depending on the time of year), and 1-2 Ethiopian staff. Our camp includes one stone house with 3 bedrooms, a full kitchen set-up (including a propane-powered stove and oven), solar panels to power computers and lights, a generator (for electricity during the rainy season), a satellite telephone and modem (for email), a Mitsubishi 4x4 pickup truck, a shower tent (hot showers can be had by heating up water on the stove). There is no running water at the fieldsite, but fresh water can be fetched from a nearby spring. Also, there is no refrigeration at the fieldsite, but we have a project freezer at a nearby eco-lodge (about a 30-minute drive away) where we can store things. For more information on the project directors, the project publications, and some photos of the fieldsite, please see the following websites: http://sitemaker.umich.edu/jacinta.beehner/home , and http://sitemaker.umich.edu/thore.bergman/home . Qualified applicants will have a B.S. or B.A in Biology, Zoology, Biological Anthropology, or a related field. Prior travel and/or field experience in Africa or mountainous regions of Asia or South America preferred. Applicants must be fluent in English and eager to learn Amharic (the national language of Ethiopia). Good physical fitness is essential - the terrain is hilly, the air is thin (due to the high elevation), and the temperatures can get quite cold during the rainy season (nights are sometimes below freezing and days can be cold). Good organizational skills and experience with basic database management a must. Must be able to drive a stick-shift 4x4 truck over rough terrain. Experience with leadership also a plus V as you will be managing several graduate students and field assistants.

Salary/funding: Round-trip airfare and living support provided for the volunteer (travel, meals, lodging). Volunteer will be provided with basic accommodation, food and other basic supplies while at the field site. However, the volunteer is responsible for any additional expenses incurred while traveling in Ethiopia. The project will provide travel health insurance, but the volunteer is required to acquire the necessary vaccinations prior to entry to Ethiopia. The volunteer will need to provide their own winter/alpine condition clothing, footwear and sleeping bag. Advice about what items are necessary for life in the Simien Mountains will be provided to the successful applicant.

Appointment: 1-2 years beginning late January 2010. Because the training process requires 2-4 months, the successful applicant must be willing to work for a minimum of 1 year. Applicants committing to a longer period will receive one round-trip flight to their home country halfway through their internship.

Deadline: Position will remain open until filled.

Application: Please email the following materials to Dr. Jacinta Beehner at jbeehner@umich.edu: (1) a letter of interest stating how and why this position satisfies your interest and future career goals, explaining your suitability for this project, plus a time frame during which you are available to work, (2) a CV or resume detailing relevant experience, (3) a summary of college courses taken and the grades received, to be followed by an official transcript, and (4) contact information for at least two references, preferably at least one academic reference as well as one person who has worked closely with you or who has closely supervised your work. The subject heading of the email message should read: for field research position.

Jacinta C. Beehner Assistant Professor of Psychology and Anthropology

— / —

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

Used LiCor wanted

Dear Evoldir members,

if you possess a LiCor 4200L automated sequencer, which is no longer used, please read on. Otherwise please delete the message. My sincere apologies for the spam.

We are looking for a used spare part for our LiCor sequencer. It needs a 'new' power supply. If you have such a machine that is out of use or broken down with a different problem, you might wish to contact me directly. We would take either the spare part or an entire machine, if it is cheap and shipment is feasible, and dismantle it ourselves.

Thank you.

Best wishes,

Gregor

Dr. Gregor Kölsch Zoological Institute Department of Molecular Evolutionary Biology University of Hamburg Martin-Luther-King-Platz 3 20146 Hamburg GERMANY Tel. +49 (0)40 42838 3933 Fax +49 (0)40 42838 3937

Gregor.Koelsch@uni-hamburg.de

PostDocs

Bergen Flatworm EvoDevo

Postdoctoral Researcher: Evolutionary Developmental Biology of acoel flatworms

The Sars Centre in Bergen (Norway) is offering one postdoctoral position for two years in the Comparative Developmental Biology of Animals group (Group Leader Andreas Hejnol). The group is interested in the evolution of the organ systems and studies the development of different invertebrate taxa at the cellular and molecular level. Research in the group combines the use of advanced microscopical techniques with molecular approaches in diverse marine organisms. Primary focus of the research is on the development of acoels, marine worms which form the sister group to all remaining bilaterian animals. Their phylogenetic position in the tree of life makes them key organisms for studying the evolution of body axis formation, germ layer specification and nervous system centralization.

The position/project involves the use of established molecular methods, as well as the development of functional approaches to address specific questions regarding organ system evolution and germ layer specification. Although the primary focus of the project will be on acoel development it is not limited to this animal group. Applicants should have a strong interest in evolutionary developmental biology and a solid background in molecular and/or cell biology. Prior experience with the use of experimental methods to manipulate gene expression such as RNA interference, morpholinos etc. is desirable. Additional skills in genomics and bioinformatics are a clear plus. The position is available immediately; the start date is negotiable.

The Sars International Centre is a partner of the European Molecular Biology Laboratory (EMBL), www.embl.de and a department of Unifob www.unifob.no , affiliated with the University of Bergen www.uib.no. The Centre is focused on basic research in marine molecular biology, developmental biology and evolution, through genetic and comparative studies of invertebrates and vertebrates.

Salary for Postdoctoral Researcher (code 8151) start at NOK 436.800 depending on seniority. Unifob has employee insurance and pension agreements and is an equal opportunity employer. For further information regarding the position and scientific content of the project please contact Dr. Andreas Hejnol, Group Leader: andreas.hejnol@sars.uib.no , or see our website www.sars.uib.no . Written application, in English, should include a C.V., a summary of educational and work experience, a brief statement of research interest and contact information for two references. Please mark application “09Sars16” and mail to: Head of Administration, Sars Centre, Bergen High Technology Centre, Thormøhlensgt. 55, N-5008 Bergen, Norway. Deadline for applications is 15. November 2009. Please note that applications sent by e-mail will not be considered.

hejnol@hawaii.edu hejnol@hawaii.edu

BigelowLabs Maine Phylogenomics

Position Description

Post-doctoral position in phylogenomics / bioinformatics 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 January 2010. Primary duties include plastid DNA isolation, EST library construction, phylogenomics and bioinformatics analysis. Candidates 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. Salary and benefits will be commensurate with experience. 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 three references to jobs@bigelow.org. Please reference #PD10-1 in the subject line. For full consideration, the application should be received by November 7th, 2009. Bigelow Laboratory is an Equal Opportunity Employer.

Jane Gardner <jgardner@bigelow.org>

CNRS Paris ButterflyWingPatternEvolution

Postdoctoral position on the evolutionary genetics of butterfly wing patterns.

CNRS / Museum National d'Histoire Naturelle, Paris

Duration: up to 3 years Funding: European Research Council Net monthly salary: 2200-2800â¬*Deadlineforapplication* : 26*November*2009

A postdoctoral position is available to work on the evolutionary genetics of a balanced polymorphism for wing-pattern mimicry in the Amazonian butterfly Heliconius numata. The project is devoted to characterise the genomic organisation and annotation of a wing pattern-determining âsupergeneâ locus, and to understand the evolutionary history of chromosomal rearrangements associated with mimicry polymorphism and balancing selection. The research will involve various approaches ranging from linkage mapping to molecular evolution, genomics/bioinformatics and evo-devo, and will take advantage of a rich comparative framework with closely related species. A rich and rapidly increasing amount of genomic resources is now available for this and other Heliconius species. The full genome sequencing of a closely related species is underway. A flavour of our current research in Heliconius butterflies can be found here: http://heliconius.zoo.cam.ac.uk/-joron/ http://www.heliconius.org . The successful candidate will join a new team lead by Mathieu Joron and funded by the ERC and the CNRS at the Natural History Museum in Paris. A PhD and a strong background in genetics or evolutionary biology are required. Good skills in molecular genetics are essential. Fluency in French is not required. The postdoc will have the opportunity to collaborate closely with local evolutionary biologists, postgraduate students, as well as with international collaborators from the Heliconius Genome Consortium.

The Natural History Museum (www.mnhn.fr) is situated right in the centre of Paris, next to UniversitÃ© Pierre & Marie Curie (Paris 6 Jussieu), Ecole Normale SupÃ©rieure, and Institut Jacques Monod. The Natural History Museum has recently enjoyed an intensive campaign of recruitment of young researchers in all aspects of biodiversity and evolutionary research, and Paris as a whole has a vibrant research community in the life sciences.

The position is for up to 3 years depending on starting date (January 2010 or soon thereafter). Net monthly salary is EUR 2300-2800 depending on experience.

Interested candidates are strongly encouraged to make informal contact with Mathieu Joron as soon as possible (joron@mnhn.fr). Applicants should send a 1-2-page application letter stating research interests and date of availability, a detailed CV, and the names and contact details of at least two referees, preferably by email, by 26 November 2009, to Mathieu Joron (joron@mnhn.fr):

Mathieu Joron (joron@mnhn.fr) MusÃ©um National d'Histoire Naturelle, Origins, Structure and Evolution of Biodiversity lab CNRS UMR 7205, case postale 39, 16 Rue Buffon, 75005, Paris, France Tel. +33(0)140-79-33-27 http://heliconius.zoo.cam.ac.uk/joron/ Mathieu Joron <joron@mnhn.fr>

CornellU ComputationalGenomics

Multiple postdoctoral positions in the areas of computational and medical genomics are now available in the laboratory of Jason Mezey (http://-mezeylab.cb.bscb.cornell.edu/) at Cornell University. Our group focuses on the development of novel statistical and computational methods for addressing fundamental questions in complex trait / disease genomics and in the application of these methods with our collaborators in molecular and medical research.

The Mezey group has a dual appointment in the department of Biological Statistics and Computational Biology at Cornell University (Ithaca, NY) and in the department of Genetic Medicine at Weill Cornell Medical College (New York City), with members at both locations. We are currently looking for postdocs for the Weill location to work in collaboration with Dr. Ronald G. Crystal (http://www.med.cornell.edu/-research/ronaldcrystal/). There will be ample opportunity to collaborate with research groups located at Cornell and at Weill. Specifically, we are looking for people to work in the following areas:

1) Next generation sequence analysis. The successful applicant will develop algorithms for novel applications of these data to questions in medical genomics, including the causes and consequences of somatic mutation events. This individual will work on a number of ongoing projects employing next generation sequencing

data.

2) Genome-wide association analysis. This individual will work on the development and assessment of algorithms for GWA analysis. This individual will be expected to interact with group members working on related genome-wide feature selection problems.

3) Network discovery and modeling. The successful applicant will develop graphical modeling approaches for discovering network structure using a variety of genomic data. This individual will be expected to work on existing projects, as well as on their own development of novel methods and applications.

Ideal candidates will have a statistics, computer science, and/or bioinformatics background, strong programming skills, and experience working with publically available data and/or computationally intensive problems in genomics fields. The positions are available immediately. To apply for these positions, please send an email with a single collated PDF including (1) CV, (2) names and contact information of three references, (3) statement of research interests, to Beatrix Johnson <bj11@cornell.edu>.

jgm45@cornell.edu jgm45@cornell.edu

CornellU PlantPopulationGenetics

USDA-ARS at Cornell University

Postdoctoral Position in Quantitative/Population/Computational Genetics for Plant Breeding

Postdoc to analyze data from the Barley Coordinated Agricultural Project. The Barley CAP is a groundbreaking effort to apply association genetics to crop improvement in US elite barley germplasm. Over 2,500 barley lines from ten breeding programs have already been genotyped at high density (~3,000 SNP) and extensively phenotyped. More data is on the way. To analyze this data, we are assembling and adapting methods from plant, human and livestock genetics. These methods include association mapping using single-marker and haplotype block methods, association-based marker imputation, genomic selection, and GxE analysis. We are a pioneering lab in many of these methods and look to train postdocs in the basics and perform research to extend the analyses. Many directions of cutting edge research are open and with the data in hand can rapidly lead to publications. The environment at Cornell includes nationally recognized research programs in population genetics, genomics and plant breeding, which will provide additional resources and stimulation.

Incumbents will work in the labs of Jean-Luc Jannink and Peter Bradbury on efforts to

- Identify and make use of haplotypes in SNP data from barley inbreds, representative of North American elite and breeding pools. - Scale-up genomic selection methods to datasets involving possibly tens of thousands of lines and markers - Extend genomic selection methods to better design training populations, reduce loss of genetic diversity, and capture epistatic effects - Use extensive existing data to empirically validate genomic selection Preferred applicants should have a Ph.D. in quantitative, population, or computational genetics; knowledge of plant breeding; proven written and spoken communication skills and ability to work collaboratively. US citizens or Green Card holders are also preferred (others may apply but initial employment will be delayed). An excellent postdoctoral salary will be offered. Positions are for two years, extendible up to four. The positions will remain open until good candidates are identified.

A letter of interest in the position, C.V., and contact information for three references should be emailed to Jean-Luc Jannink and Peter Bradbury at:

JeanLuc.Jannink@ars.usda.gov

Peter.Bradbury@ars.usda.gov

Official job posting at:

http://jobview.usajobs.gov/GetJob.aspx?JobID=-3D84201814 jeanluc.work@gmail.com

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DublinCityU MolecularEvolution

Dear Evolutionary Biologists,

The Bioinformatics and Molecular Evolution Group at Dublin City University, Ireland are inviting interested parties to contact us regarding postdoctoral fellowships.

These fellowships are competitive and will be awarded to those applicants with excellent track records. There are 2 strands for this funding:

(1) EMPOWER: candidates must be within 3 ^{3}academic years^{2} from the award of PhD and propose pursuing their work for 24 months at an

Irish research laboratory. See http://www.ircset.ie/-Default.aspx?tabidx And

(2) INSPIRE: These are linked to the Marie Curie International Mobility Fellowships. Candidates must be within 5 ^{3}academic years^2 from the award of PhD or equivalent. They must propose pursuing their work for 18 months at a research laboratory in any country of their choice worldwide, followed by a 12 month reintegration period at an Irish research laboratory. See http://www.ircset.ie/Default.aspx?tabidw Our research group is multidisciplinary, our focus is on mammal protein evolution.

Interested parties please contact Dr Mary O'Connell (details below), with a brief introduction to yourself, your research interests, and your CV.

Best wishes,

Mary

– Dr Mary J. O'Connell, Bioinformatics and Molecular Evolution Group leader, School of Biotechnology, Dublin City University, Glasnevin, Dublin 9.

Phone: +353 1 700 5112 Fax: +353 1 700 5412 Email: mary.oconnell@dcu.ie website: http://bioinf.dcu.ie dr mary o'connell <mary.oconnell@dcu.ie>

GeorgiaInstTech BrainEvoDevo

A POSTDOCTORAL POSITION in evolutionary developmental biology of the brain is available in the laboratory of Todd Streelman, at the Georgia Institute of Technology. Candidates for this position will be expected to carry out independent research contributing to our understanding of how brains diversify, using the cichlid fish model. Experience in developmental biology, genetics, and/or high-throughput analyses of gene expression, is desired.

More information on Streelman's lab can be found at the following site: http://www.biology.gatech.edu/-faculty/todd-streelman/. The Georgia Institute of Technology offers exciting avenues for collaboration with engineers and computational scientists. Georgia Tech was recently voted one of the best places to work, and Atlanta is consistently ranked among the top ten places to live for young professionals.

The start date for this position is flexible; funding is available for at least two years but is contingent upon satisfactory progress in year one. The salary will be competitive and commensurate with experience. Interested individuals should send informal queries or an application consisting of a (i) CV, (ii) a brief description of research and professional goals, and (iii) the names and addresses of 2 references to Todd Streelman, by e-mail (todd.streelman@biology.gatech.edu).

J.T. Streelman Associate Professor School of Biology Georgia Institute of Technology 310 Ferst Drive Atlanta, GA 30332-0230 404-385-4435 (office) 404-385-4436 (lab) 404-385-4440 (fax) E-mail: todd.streelman@biology.gatech.edu http://www.biology.gatech.edu/faculty/todd-streelman/ todd.streelman@biology.gatech.edu todd.streelman@biology.gatech.edu

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HarvardMedSchool Human StatGenomics

A post-doctoral position in human/statistical genomics is available to be supervised jointly by Dr. Philip de Jager and Dr. Barbara Stranger, in the Departments of Neurology and Medicine, Brigham & Women's Hospital, and Harvard Medical School.

We are looking for an enthusiastic and energetic individual to join our research effort investigating the functional consequences of human genetic variation in the immune system. Specifically, disease-related genetic variation and genome-wide CNV and SNP data will be analyzed in relationship to immunologic profiles derived from RNA expression as well as cytometric and proteomic data generated from several different cell types. The project is an NIH-funded study focusing on the genetic basis of transcript regulation in differentiated immune cell states in large population cohorts comprising multiple ethnicities. The position provides opportunity for integrated analysis of genetic variation (SNPs and copy number variation) with whole-genome gene expression data from multiple immune cell lineages.

The qualified candidate should be highly motivated, with experience in genomics, bioinformatics, computational biology, human population genetics, or a related field, with experience in statistics. He or she should have experience analyzing high-throughput genomic datasets derived from microarray and/or other high-throughput technologies (e.g., experience with GWAS, eQTL, ChIP-Seq, ChIP-chip, or CNVs) and skills in one programming language (R, Perl, Java, or C/C++). An excellent understanding of genetics is required. Because our work involves multiple collaborators, a good balance between independence and team spirit is essential, and effective communication skills are necessary.

The position offers a stimulating and multi-disciplinary environment and the opportunity to work with researchers at Harvard Medical School, Brigham and Women's Hospital, and the Program in Medical and Population Genetics of the Broad Institute of MIT and Harvard.

Requirements: Ph.D. in Biology, computational biology, statistics, computer science, or related area.

Application and inquiries should be submitted by e-mail to Barbara Stranger (bstranger@rics.bwh.harvard.edu) or Phil de Jager (pdejager@rics.bwh.harvard.edu). Along with your CV, please include a cover

For more information please see: http://dejager_lab.bwh.harvard.edu/ and http://strangerlab.bwh.harvard.edu/

Barbara Stranger <bstranger@rics.bwh.harvard.edu>

INRA France IntraspecificHybridization

Dear all,

We are offering a postdoc position in order to work on links between intraspecific hybridization and biological invasions.

The full description can be found by following this link :

http://www2.sophia.inra.fr/perso/fauvergue/accueil/postdoc.pdf Please do not hesitate to forward this message to potential candidates.

Thank you,

Xavier

Xavier Fauvergue

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

Tel 33 4 92 38 64 63

xavier fauvergue <xavier.fauvergue@sophia.inra.fr>

Maryland EvolutionaryBioinformatics

Post-doc in evolutionary bioinformatics: Origin of protein folds

Qualified individuals are invited to apply for a postdoctoral position at CARB in computer-based analysis of protein evolution. Apparently novel protein folds continue to be discovered, undermining the old conventional wisdom that there are just a few thousand primordial folds. With funding from NIH, we are developing and applying computer-based approaches to estimating what fractions of apparently novel folds are attributable to de novo origins, to sub- domain chimaerism, to lateral transfer from uncharacterized genomes, and so on. The successful applicant will join an energetic and collaborative team led by John Moult (structural biologist) and Arlin Stoltzfus (evolutionary biologist).

Applicants must have: a Ph.D. in a relevant field, and at least 2 years experience (at the grad or post-doc level) in computer-based research (e.g., biooinformatics, statistical data analysis, simulation, phylogenetic inference). Expertise is desireable in one or more of the following: developing and applying models of evolution; testing hypotheses using statistical methods; integrating sequence, structure, and other data; designing and implementing web-based data resources.

The position is a renewable one-year appointment (with probable renewal for a second year), to begin as soon as possible, and with a salary commensurate with experience. Women and minority candidates are especially encouraged to apply.

To apply, email a letter of application (referencing position #301022), curriculum vitae, and contact information for three personal references to carbsrch@umbi.umd.edu . Review of applications will begin November 22 and continue until the position is filled. Questions should be directed to:

Dr. Arlin Stoltzfus (stoltzfu@umbi.umd.edu) Center for Advanced Research in Biotechnology 9600 Gudelsky Drive, Rockville, Md 20850 Tel: (240) 314-6208

Arlin Stoltzfus <stoltzfu@umbi.umd.edu>

MaxPlanckInst EVA PrimateGenetics

MPI-EVA Primate population genetics

Applications are invited for a two-year postdoctoral position investigating the population histories of wild primate populations in the molecular genetics lab in the Primatology department of the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany. The project will involve high-throughput sequencing and analysis of large DNA sequence datasets, and relevant experience would be advantageous. Starting date is January 2010 or soon thereafter. Support is provided in the form of a tax-free stipend; the exact amount depends upon age and years of post-Ph.D experience. Leipzig is a charming city with a lively cultural scene and a low cost of living and the MPI-EVA is an outstanding place to do research. For more information on research in this group, see http://www.eva.mpg.de/primat/files/genetics.htm Enquiries and applications in the form of a cv, brief statement of research interests, relevant publications and contact information for three references should be sent via email to Linda Vigilant at vigilant@eva.mpg.de

Linda Vigilant Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig Germany http://email.eva.mpg.de/%7Evigilant/ Linda Vigilant <vigilant@eva.mpg.de>

MaxPlanckInst Leipzig HumanOrigins

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

*Leader of an Independent Junior Research Group on *

* *

The Origin of Human Subsistence.

Over the last several million years, hominins have developed diverse strategies to extract energy from their environment. New questions and models have arisen to address the relationship between this evolution and the evolution of life histories, technological adaptations and, more broadly, social organization and economy of ancient humans. From the origin of meat consumption to the intensification of the environmental exploitation by late paleolithic hunter-gatherers, subsistence involves the continuous interaction between cultural and biological changes.

* *

For the new group, multidisciplinary approaches, with a broad range of methods ranging from classical zooarchaeology, to isotopic studies and modelling, are preferred.

The Max Planck Institute for Evolutionary Anthropology has five departments, including the Department of Human Evolution (Director: Jean-Jacques Hublin) with which the Independent Junior Research Group will be associated. More 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. Funds for conducting research, including salaries for a second post-doctoral scientist (13/14 TVöD) and two technical assistants are available. The appointment will be for a term of 5 years.

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, and the names of three referees and must be received at the address below by *December **31**, 2009*:

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

rowney@eva.mpg.de rowney@eva.mpg.de

MaxPlanck NematodePopulationGenetics

MAX-PLANCK INSTITUT FÜR ENTWICKLUNGSBIOLOGIE

Max-Planck Institute for Developmental Biology

The Department for Evolutionary Biology (Director Ralf J. Sommer) invites applications for a Postdoctoral Position on Nematode Population Genetics.

The Department has an active research program in evolutionary ecology and evolutionary developmental biology studying the nematode model organism Pristionchus pacificus, the genome of which has recently been sequenced (Dieterich et al., Nature Genetics, 40, 1193-1198 (2008)). Our research aims for an integration of evo-devo with population genetics and ecology (see Sommer, Nat. Rev. Genet. 10, 416-422 (2009).

P. pacificus lives in close association with scarab beetles and feeds on microbes that grow on the carcass of the dead beetle. Our model species is cosmopolitan and we have currently more than 160 wild isolates representing an enormous resource for natural variation.

We are starting a population genetic analysis of P. pacificus with a particular emphasis on La Réunion in the Indian Ocean. The Max-Planck Institute provides large-scale sequencing facilities, including next generation sequencing technology.

Experience in population genetics is absolutely required.

The position is for two years with a possible extension for one more year.

Funding would be available from 1. February 2010.

Closing date for applications: 15. November 2009

Please submit applications to:

Ralf J. Sommer Dept. for Evolutionary Biology Max-Planck Institute for Developmental Biology 72076 Tübingen, Germany ralf.sommer@tuebingen.mpg.de http://www.eb.tuebingen.mpg.de/dept4/home.html http://www.pristionchus.org dmerrill@ksu.edu dmerrill@ksu.edu

NESCent CallForProposals

POSTDOCTORAL FELLOWSHIPS IN EVOLUTIONARY BIOLOGY AND RELATED FIELDS We are now accepting proposals for Postdoctoral Fellowships at The National Evolutionary Synthesis Center (NESCent). We are looking to fund innovative approaches to outstanding problems in evolutionary biology. Proposals are due December 1. For more information, please see our website at https://www.nescent.org/science/proposals.php . CALL FOR PROPOSALS - SABBATICAL SCHOLARS AND COLLABORATIVE WORKING GROUPS Proposals for Sabbaticals and for collaborative working groups (Working Groups and Catalysis Meetings) are now being accepted at The National Evolutionary Synthesis Center (NESCent). We are looking to fund innovative approaches to outstanding problems in evolutionary biology. In particular, proposals that have a clear interdisciplinary focus, or involve evolutionary concepts in non-traditional disciplines, are strongly encouraged, as are proposals that demonstrate international participation and a mix of senior and emerging researchers, including graduate students. Proposals for Working Groups and Catalysis Meetings are accepted twice a year, with deadlines on June 10 and December 1. Proposals for Sabbaticals may be one semester to a full year (deadlines June 10 and December 1) or they may be for short-term visits (2 weeks to 3 months; deadlines on January 1, April 1, July 1 and September 1). For more information, please see our website athttps://www.nescent.org/science/proposals.php . Craig McClain <cmcclain@nescent.org>

NewMexicoStateU ExperimentalEvolution

The Department of Biology at New Mexico State University invites applications for a postdoctoral research associate interested in experimental evolution using evolved Vibrio bacteria involved in a squid beneficial symbiosis. The position is available for 2 years, (renewable up to 3 years). This postdoctoral position is involved with an NSF funded project to examine the effect on both host and environmental selection pressures molding the association between Vibrio bacteria and sepiolid squids. In addition, the successful candidate will be expected to supervise and mentor both graduate and undergraduate students in the laboratory and in the field. A Ph.D. in biology with emphasis in microbial evolution or ecology is recommended. Experience with genome analysis, bioinformatic tools, and 454 sequence technology is desirable. Send a curriculum vitae and contact information for at least three references to: Dr. Michele Nishiguchi, Biology Department MSC 3AF, Box 30001, Las Cruces, NM. 88003. E-mail: nish@nmsu.edu. Screening of applications will begin on November 1st, 2009 and will continue until filled. New Mexico State University is an equal opportunity/affirmative action employer. Offer of employment is contingent upon verification of individual's eligibility for employment in the United States and upon completion of a criminal history check. Requisition # 2009011521. –

Michele K. Nishiguchi, PhD Professor Department of Biology - MSC 3AF New Mexico State University PO Box 30001 Las Cruces, NM 88003-8001 575-646-3721 (office) 575-646-4123 (lab) 575-646-5665 (FAX) email: nish@nmsu.edu http://biology-web.nmsu.edu/-nish/index.html "Well behaved women rarely make history" Laurel Thatcher Ulrich

"Michele K. Nishiguchi" <nish@nmsu.edu>

NIST MolecularEvolution

NRC post-doc in molecular evolution

On short notice, a competitive Recovery-Act-funded fellowship program has opened at NIST. This provides the opportunity for a 2-year NRC post-doctoral fellowship in computational studies of the evolution of genes, proteins or genomes. The project area is flexible and depends on the applicant's interests and abilities, but the applicant must be a citizen of the U.S. The base salary is approximately $63K. The deadline to apply for the first round of awards is November 1– for those who have a proposal idea ready to go. A second and final round of awards will be made next year, with a deadline of May 1, 2010.

For further information, contact:

Arlin Stoltzfus (arlin.stoltzfus@nist.gov), Research Biologist, NIST tel 240 314 6208, fax 240 314 6255, www.molevol.org/camel Arlin Stoltzfus <stoltzfu@umbi.umd.edu>

NorthCarolinaStateU EvolutionaryEcology

Postdoctoral Research Position in Evolutionary Ecology

A postdoctoral position is available in the laboratory of Dr. Brian Langerhans, in the Department of Biology at North Carolina State University. The lab's research focuses on the importance of major ecological factors (e.g., predation, competition, abiotic agents) in driving predictable (and unpredictable) phenotypic evolution and speciation. While the lab primarily centers on the evolutionary ecology of fishes and lizards, the selected postdoc will have great latitude in selecting their specific research foci. Rather than being tied to a particular project, the goal of this postdoctoral position is to recruit a strong, innovative researcher to investigate any research topic closely aligned to the focus of the Langerhans Lab.

The successful candidate will have the opportunity to contribute to a variety of projects (including both lab and field work), and will be encouraged to develop an independent research program related to the central topic of better understanding the causes, consequences, and predictability of phenotypic evolution. Research could be empirical (e.g., lab or fieldwork on Gambusia fishes or other study organisms), theoretical (e.g., statistical or computational inquiries and developments), or both.

Requirements: The postdoctoral researcher should have a Ph.D. in evolution, ecology, behavior, or a closely related field, demonstrate a record of successful publications, possess excellent analytical and communication skills, and excel at both independent and collaborative research. Specific skills required for this position depend on the research topics chosen by the applicant, but might include ecological/evolutionary experiments in aquatic systems, geometric morphometrics, biomechanics, multivariate analyses of phenotypic selection, population genetics, theoretical modeling, or quantitative genetics.

Research Topics: The successful candidate can investigate a wide range of topics under the umbrella of evolutionary ecology, including ecological speciation, evolutionary consequences of anthropogenic impacts, morphological and locomotor evolution, predictability of phenotypic evolution, functional morphology of locomotion, predator-prey coevolution, genital evolution in livebearing fishes, phylogeography, phenotypic plasticity, neutral genetic diversity and adaptive potential, adaptive constraints of gene flow, sensory bias, evolution of sexual dimorphism, and links between locomotor, feeding, and life history evolution.

Start Date / Position Details: The position will begin approximately September 1st, 2010 (negotiable), and continue for 24 months. Salary will be highly competitive and commensurate with experience and qualifications (~$40K). The position will also include research funds ($3000 per year), health insurance, and benefits.

Application: To apply, please send a cover letter, CV, two letters of recommendation, and pdfs of up to three relevant papers to Dr. Langerhans (langerhans@ncsu.edu). In the cover letter, please include a general description of the proposed research topic(s), and how the work would fit into the overall focus of the lab. Review of applications will begin immediately, and continue until filled.

Location: North Carolina State University is located in Raleigh, North Carolina's state capital. The campus is home to a vibrant research community, with faculty members studying related topics within numerous departments (e.g., Biology, Plant Biology, Genetics, Entomology, Statistics), and multiple integrative research centers (e.g., Keck Center for Behavioral Biology, Bioinformatics Research Center). The university is also conveniently located within a 30-minute drive of UNC Chapel Hill, Duke University, the National Evolutionary Synthesis Center (NESCent), Research Triangle Park, and the North Carolina Museum of Natural Sciences. Raleigh is a culturally diverse city with excellent restaurants, parks, museums, and theaters. The city is conveniently located approximately 2 hours from both the ocean and the mountains.

More information on research in the lab can be found at: http://faculty-staff.ou.edu/L/Randall.B.Langerhans-1/ More information on the Department of Biology at NCSU can be found at: http://harvest.cals.ncsu.edu/biology/ langerhans@ncsu.edu langerhans@ncsu.edu

Okinawa Bioinformatics

Evolution of secondary metabolism in bacteria

A postdoctoral researcher position is available in the Evolutionary Systems Biology Unit at the Okinawa Institute of Science and Technology (OIST). The unit's research focuses on the evolution of secondary metabolism in bacteria using computational biology as well as experimental approaches. The aim is to get a better understanding of evolutionary processes by generating and analysing data on the systems level. This will include genome analysis, sequencing, proteomics, comprehensive phylogenetics, metabolic and regulatory networks reconstruction, study of protein-protein interactions and modelling.

The successful applicant will be responsible for designing and carrying out analysis of sequence information, different types of "omics" data and modelling of biological networks. This will include database management, application of mathematical and statistical methods like Bayesian Networks and programming. Candidates should hold a PhD in a relevant discipline (bioinformatics, computer science, mathematics or similar) and have a strong background in computational methods, mathematics/statistics and programming. Basic knowledge in biology would be an asset, but is not absolutely necessary. It is more important to have a strong interest in applying mathematical and computational methods to molecular biology data.

Initial contracts will be for two years and can be prolonged within the project period. Starting dates are negotiable.

OIST offers competitive salaries and additional allowances for relocation, housing and commuting.

Applications will be reviewed as they arrive, and will continue until the positions are filled.

Applications should include a covering letter describing your scientific background and interests and stating when you would be able to start, CV, publication list, and the names and contact details of three references who have agreed to provide a letter of reference. Please send your application by e-mail to Holger Jenke-Kodama at

esb_postdoc2009@oist.jp

Dr. Holger Jenke-Kodama Evolutionary Systems Biology Unit Okinawa Institute of Science and Technology

holger.jenke-kodama@oist.jp holger.jenke-kodama@oist.jp

Okinawa MetabolismEvolution

Evolution of secondary metabolism in bacteria

A postdoctoral researcher position is available in the Evolutionary Systems Biology Unit at the Okinawa Institute of Science and Technology (OIST). The unit's research focuses on the evolution of secondary metabolism in bacteria using computational biology as well as experimental approaches. The aim is to get a better understanding of evolutionary processes by generating and analysing data on the systems level. This will include genome analysis, sequencing, proteomics, comprehensive phylogenetics, metabolic and regulatory networks reconstruction, study of protein-protein interactions and modelling.

The successful applicant will be responsible for designing and carrying out experiments using bacteria, in particular cyanobacteria and myxobacteria. This will include construction of knockout mutants, metabolite analysis, sequencing and expression analysis both at the RNA and protein level. Further projects could comprise work with metagenomic libraries and single cell techniques. Candidates should hold a PhD in a relevant biological discipline. Knowledge in sequence analysis and computational methods related to molecular biology and "omics" methods would be an asset.

Initial contracts will be for two years and can be prolonged within the project period. Starting dates are negotiable.

OIST offers competitive salaries and additional allowances for relocation, housing and commuting.

Applications will be reviewed as they arrive, and will continue until the positions are filled.

Applications should include a covering letter describing your scientific background and interests and stating when you would be able to start, CV, publication list, and the names and contact details of three references who have agreed to provide a letter of reference. Please send your application by e-mail to Holger Jenke-Kodama at

esb_postdoc2009@oist.jp

Dr. Holger Jenke-Kodama Evolutionary Systems Biology Unit Okinawa Institute of Science and Technology

holger.jenke-kodama@oist.jp holger.jenke-kodama@oist.jp

RoyalBotanicGarden Edinburgh ConservGenetics

Conservation Geneticist - Post Doctoral Research Assistant

Starting Salary - £23,828 (Pay Band D)

Applications are invited for a 3 year fixed term postdoctoral position at the Royal Botanic Garden Edinburgh. The post is funded by the Natural Environment Research Council's 'Knowledge Exchange' scheme and the general remit of the post is to improve the integration of genetic information into conservation programmes. This will involve the synthesis and communication of existing research data. Specifically the post holder will be involved in (a) the development of a decision-making framework for integrating genetic information into conservation programmes, (b) trialing and refining this framework using a selection of UK Biodiversity Action Plan plant and animal species, (c) producing user-friendly handbooks that summarise and communicate key conservation genetics concepts and terminology for the benefit of conservation practitioners, and (d) providing online resources to support practical conservation management.

Applicants should have a PhD in the field of population genetics, molecular ecology or conservation genetics. Strong communication skills (written and oral) are also required.

The post holder will work with Pete Hollingsworth at RBGE, in collaboration with Raj Whitlock and Terry Burke (University of Sheffield) and Andrew Pullin (University of Bangor), and the post will involve extensive dialogue and interactions with conservation practitioners and policy makers in the UK.

This post attracts generous holiday entitlement and civil service pension benefits.

Informal enquires can be directed to p.hollingsworth@rbge.org.uk

A full job description and person specification can either be downloaded from http://www.rbge.org.uk/about-us/vacancies or can be obtained from Irene Morrice on 0131 248 2803 (i.morrice@rbge.org.uk). Applications should be made by way of CV and a covering letter and should be sent to Irene Morrice either by e-mail or by post to the Human Resources Department, 20a Inverleith Row, Edinburgh, EH3 5LR. CV's must be received no later than Wednesday, 28 October 2009.

Dr Pete Hollingsworth Royal Botanic Garden Inverleith Row Edinburgh, UK EH3 5LR Tel: +44 (0) 131 248 2883 Fax: +44 (0) 131 248 2901

p.hollingsworth@rbge.org.uk

RutgersU PopulationGenetics

Postdoc in Population Genetics in the Fonseca Lab, Rutgers University

A two-year USDA-funded postdoctoral position is available to investigate the population genetics of the invasive and medically important mosquito, Aedes albopictus, the Asian tiger mosquito (ATM). The position is inserted in a 5-year USDA-ARS funded cooperative agreement between USDA, Rutgers University, Brandeis University, and two Mosquito Control Programs in New Jersey, to develop strategies for the Area-wide management of the Asian tiger mosquito (ATM project). Dr. Fonseca is the PI at Rutgers. This position will involve both lab and field components, and there are multiple opportunities to develop independent lines of research related to molecular ecology, genetics of life-history traits, and population genetics of selection, especially regarding insecticide resistance. The ATM project involves large-scale surveillance and active mosquito control using standard and new control strategies. We are in Year 2 of this project and have just developed polymorphic genetic markers for the ATM. I seek a highly motivated individual with a PhD in Population Genetics or Evolutionary Ecology/Epidemiology. Experience with molecular biology and strong written and oral communication skills are critical. Salary is $39,800 per year plus benefits with a cost-of-living increase in the second year. This position opened unexpectedly (but for happy reasons) and I am looking to fill it as soon as possible. I will accept incomplete applications as a way of evaluating the level of interest. The Fonseca Lab is located within the Center for Vector Biology at Rutgers University, integrated in the Department of Entomology and the NJ Agriculture Experiment Station. Dr. Fonseca is also an active member of the graduate program in Ecology, Evolution and Natural Resources and the School of Public Health at the University of Medicine and Dentistry of NJ (UMDNJ). Please refer to http://rasp.rutgers.edu/-fonseca/ and to http://vectorbio.rutgers.edu/ for more info. Currently the lab has one postdoc, six graduate students, one part time technician, and a clerical aide. Applications should be sent to Dina Fonseca (dinafons@rci.rutgers.edu) and include the following: (1) a short cover letter describing research interests and qualifications, (2) a CV, (3) contact information for three references (please include phone#s), and (4) up to three representative publications. Review of applications will start immediately and continue until the position is filled. Informal inquiries are welcome.

Rutgers University is an Equal Opportunity/Affirmative Action Employer.

– Dina M. Fonseca, PhD Associate Professor

Center for Vector Biology Rutgers University 180 Jones Avenue New Brunswick, NJ 08901 Phone:(732) 932 3146 Fax: (732) 932 9257 email: dinafons@rci.rutgers.edu

"Dina M. Fonseca" <dinafons@rci.rutgers.edu>

SantaFeInst SocialSystemEvolution

SFI has openings for several "core-funded" postdoctoral positions this year. These are in the SFI Omidyar Fellows Program. In addition, David Krakauer and I have an opening for a postdoc on an NSF conflict dynamics grant, also at the Santa Fe Institute. This is a theory position. Position announcements are below.

Thanks so much Jessica Flack Santa Fe Institute http://www.santafe.edu/˜jflack POSTDOCTORAL POSITION ANNOUNCEMENTS

POSTDOC IN DYNAMICS OF CONFLICT IN BIOLOGICAL AND SOCIAL SYSTEMS The Santa Fe Institute has an opening for a postdoctoral fellowship in the dynamics of conflict. The position is funded through the National Science Foundation and is for two to three years.

The postdoctoral researcher will work closely with faculty Jessica Flack and David Krakauer analyzing large data sets and developing mathematical models. We expect the candidate to have a strong background and publication record in either dynamical systems, and or statistical physics, applied to biological or social systems. The work will be grounded in high resolution conflict time series, and involve the application of ideas from Bayesian statistics, information theory, game theory, dynamical systems, and the theory of collective phenomena. The postdoc will be required to spend approximately 80% of his/ her time on conflict related projects. For the remaining 20% of time, the postdoc is encouraged to collaborate with members of the larger SFI community.

The postdoc will be joining a research project that seeks to explain how complex social systems evolve, and how these systems minimize the dissipative effects of conflict through mechanisms of conflict management. In previous publications this group has made extensive use of non-parametric statistics, network methods, and information theory to study robustness in complex systems. Strong analytical skills and the ability to work with both large data sets and parsimonious models will be favored. The salary for the position will be 55K with standard SFI benefits, and funds are available to assist with travel and to bring collaborators to SFI.

To apply for this position, please send an email containing your CV and a two-page research statement to Drs. Jessica Flack and David Krakauer at jflack@santafe.edu. Please include names of three references and ask recommenders to send their letters to the above email address. The deadline for receipt of applications is December 15.

The Santa Fe Institute is an equal opportunity employer. For more information about the institute see http://www.santafe.edu . SFI OMIDYAR FELLOWS POSTDOCTORAL POSITION ANNOUNCEMENT

Jessica Flack <jflack@santafe.edu>

UArizona EvolutionInsectFlight

U of Arizona. Eco and Evo Physiology of Insect Flight

Postdoctoral Research position at the University of Arizona

A three-year position for a Postdoctoral Researcher is available in the laboratory of Dr. Goggy Davidowitz in the Department of Entomology at The University of Arizona (start date, January 2010). http://ag.arizona.edu/ento/faculty/davidowitz/index.html The research will examine the behavioral and physiological effects of humidity in foraging choice, flight physiology, flight metabolism and fitness in a natural population of a hawkmoth (Manduca sexta) from the scale of an individual flower up to an entire landscape. This project is in collaboration with Dr. Robert Raguso of Cornell University.

Goggy Davidowitz and his lab study ecological and evolutionary physiology, with an emphasis on the physiological regulation of body size, physiological tradeoffs, and plant-insect interactions.

The successful candidate will have experience in insect physiology, behavior and field research, with research experience in respirometry preferred.

To apply, please send a letter describing your research interests and qualifications, a CV, PDFs of three of your most significant papers, and contact information for three references to: Dr. Goggy Davidowitz (goggy@email.arizona.edu).

The University of Arizona is an Affirmative Action / Equal Opportunity Employer.

– Goggy Davidowitz Assistant Professor Dept. of Entomology University of Arizona Email: goggy@email.arizona.edu Voice: (520) 626-8455 FAX: (520) 621-9190 http://ag.arizona.edu/ento/faculty/davidowitz/index.html Goggy Davidowitz <goggy@email.arizona.edu>

UArizona VertebrateEvolution

George Gaylord Simpson Postdoctoral Fellowship in Vertebrate Evolution - University of Arizona

The Department of Ecology and Evolutionary Biology announces one postdoctoral fellowship position for Fall 2010, named in honor of G. G. Simpson's long tenure at the University of Arizona. Simpson Fellows are expected to conduct an active research program in evolutionary biology, especially projects that are facilitated and complemented by the Department's extensive natural history collections in ichthyology, herpetology, ornithology, and mammalogy. The positions are part of a renewed commitment to natural history collections on the University of Arizona campus and an initiative in biodiversity informatics (http://loco.biosci.arizona.edu/bdii/). Postdoctoral Fellows are encouraged to establish research collaborations with faculty in the Department of Ecology and Evolutionary Biology and are expected to teach or contribute to one course per year in the Fellow's research specialty. Salary is $37,500 plus benefits (nine-month appointment). A research stipend of $5000 will also be included. The positions are renewable for at least a second year contingent on satisfactory performance.

Applicants should submit application materials online at the University of Arizona Human Resources website (https://www.uacareertrack.com; look for job #44102), including C.V., statement of research and teaching interests and experience, and two letters of reference. Reference letters should be emailed directly to sanderm@email.arizona.edu. Position is open until filled, but we anticipate reviewing applications beginning on Jan. 15, 2010. Contact Dr. Peter Reinthal (pnr@email.arizona.edu), Dr. Renee Duckworth (rad3@email.arizona.edu), or Dr. Michael Sanderson (sanderm@email.arizona.edu) for further information.

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Michael J. Sanderson

Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

Office: BSW 412 Phone:520-626-6848

lab web site: http://loco.biosci.arizona.edu UA Biodiversity Informatics Initiative: http://loco.biosci.arizona.edu/bdii PhyLoTA Browser: http://loco.biosci.arizona.edu/pb r8s software: http://loco.biosci.arizona.edu/r8s sanderm@email.arizona.edu sanderm@email.arizona.edu

UBarcelona Genomics bioinformatics evolution

RESEARCH POSITIONS IN GENOMICS, BIOINFORMATICS, AND EVOLUTION

Several openings are available to work on the project entitled "Evolutionary and functional analysis of polymorphic inversions in the human genome", selected for 5-year funding through an ERC Starting Grant from the European Research Council. This project aims to improve our understanding on the impact of inversions in the human genome at multiple levels by combining methods of different disciplines, such as next-generation genomic techniques, bioinformatics, population genetics, and molecular evolution. Successful candidates will form part of a young, highly dynamic, and interdisciplinary research team located at the Institute of Biotechnology and Biomedicine of the Universitat Autònoma de Barcelona (http://ibb.uab.es/).

Available positions:

We are seeking very motivated individuals with a doctorate or university degree and research experience in the following relevant fields:

1. Postdoc expert in high-throughput genomics and molecular biology techniques.

2. Postdoc with strong background in bioinformatic analysis of DNA sequences.

3. Postdoc with good knowledge in population genetics and molecular evolution.

4. PhD student in functional genomics and gene-expression analysis.

5. Research technician/Lab manager with basic training in molecular biology.

Conditions:

Salaries will be competitive according to profile and experience of candidates. Duration of contracts will depend on the specific position, ranging from 1 to 5 years.

Starting date:

All positions are available from January 2010.

Application:

Send a CV and a one-paragraph summary of previous research experience to Mario Cáceres (mcaceres@icrea.cat).

Application deadline:

Please send application as soon as possible, preferably before October 31 2009.

mario.caceres@crg.es

UChicago EvolutionaryGenetics

POSTDOC IN POPULATION GENETICS, UNIVERSITY OF CHICAGO

A postdoctoral position in population genetics is available in Molly Przeworski's group at the University of Chicago. The specific project is flexible. Current work in the group focuses on a wide range of topics, from the study of natural selection in humans and other primates to understanding patterns and processes of recombination. For more information, see http://przeworski.uchicago.edu/. Our group shares space and weekly lab meetings with those of Jonathan Pritchard and Matthew Stephens and enjoys close ties with other members of the Human Genetics and Ecology & Evolution departments, notably Anna Di Rienzo, Dick Hudson and Carole Ober. Moreover, it benefits from the large and outstanding community of researchers in population genetics, statistics and genomics at the University of Chicago.Applicants for the position must have either a background in theoretical population genetics, with experience in data analysis, or come from a quantitative field (such as statistics or computer science) and have a strong interest in genetics and evolution. Programming and bioinformatics skills are essential. Informal inquiries as well as applications (including a CV, copies of relevant publications and two letters of recommendation) should be emailed to Molly Przeworski at <mfp@uchicago.edu>. The starting date is Spring-Summer 2010.

Molly Przeworski Howard Hughes Medical Institute Dept. of Human Genetics Dept. of Ecology and Evolution University of Chicago http://przeworski.uchicago.edu mfp@uchicago.edu mfp@uchicago.edu

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UCLondon SexualAntagonismQTL

Dear all,

I am seeking to hire a postdoctoral associate to work on the genetic basis of sexual antagonism in Drosophila melanogaster. The post is funded by a grant from the Natural Environment Research Council to myself (PI) and Kevin Fowler (Co-I). The position is available for 3 years, starting in January 2010 (negotiable).

The official advert is pasted below. For more information and to apply, please visit http://tinyurl.com/-reuter-pdra. The application deadline is Friday 6th November 2009. Interviews will take place in the second half of November.

Best regards, Max

POSTDOCTORAL RESEARCH ASSOCIATE

Analysing quantitative trait loci of sexual antagonism in fruitflies

A position is open for a postdoctoral research associate at University College London to work with Max Reuter and Kevin Fowler on the genetic basis of sexual antagonism in fruitflies. The post is part of a project funded by the Natural Environment Research Council, the aim of which is to identify and characterise quantitative trait loci of sexual antagonism in Drosophila melanogaster. The project combines evolutionary and molecular genetic approaches to fine-map QTL of sex-specific fitness and identify candidate genes underlying sexual antagonism. Assisted by a full-time technician, the post-holder will conduct phenotypic and molecular analyses, including fitness assays, genotyping via SNP genomic markers, deficiency complementation tests, resequencing of genomic regions of interest, statistical analysis (in particular QTL mapping) and bioinformatics. The project will be based in a thriving research group within UCL's GEE. For further information on this project and the group, see http:/-/www.homepages.ucl.ac.uk/˜ucbtmre/Labsite . This position is an opportunity for a highly motivated, ambitious and independent individual who enjoys working in a team. The candidate will have (or be about to obtain) a PhD in a relevant discipline, a strong interest in evolutionary genetics, proven research skills (as evident in publication record and prior research findings), experience in advanced statistics and excellent verbal and written communication skills. Experience in the application of molecular biology techniques is desired, experience with high-throughput methods advantageous. Familiarity with Drosophila would be helpful but is not required. The post is available from 1st January 2010 (flexible) for 36 months, with a starting salary between £31,620 (£28,839 plus £2,781 London Allowance) and £35,239 (£32,458 plus £2,781 London Allowance), depending on experience.

Application Process: For more information and to apply using the online application process please vitis the post's page on the UCL HR website, accessible through http://tinyurl.com/reuter-pdra. It is essential that candidates ensure that their skills and experience meet the post's criteria outlined before applying. In case you have difficulties with the online system, plase email ian.evans@ucl.ac.uk, Ian Evans, Divisional Staffing Officer, Faculty of Life Sciences, University College London, Room 122, Darwin Building, Gower Street, London, WC1E 6BT. Telephone: 020 7679 4486. The closing date for applications is Friday November 6, 2009, 4:30pm. Interviews will take place during the second half of November.

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London 4 Stephenson Way London NW1 2HE, UK

Phone: +44-20-76795095 Fax: +44-20-76795052

http://www.homepages.ucl.ac.uk/˜ucbtmre/Labsite/ m.reuter@ucl.ac.uk m.reuter@ucl.ac.uk

UEdinburgh Coevolution

Dear Evoldir member, there is a 2-year post-doctoral position to study host-parasite coevolution available at the Institute of Evolutionary Biology, University of Edinburgh. The ad is framed in terms of Daphnia, but we are interested in other systems as well. The more formal description is below, and can be found at

http://www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=vacancies.detail&vacancy_ref=3011819&go=GO Where you will also find instructions on how to apply.

Informal enquiries to tom.little@ed.ac.uk

My lab web page is

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

This is a Wellcome Trust funded post on host-parasite co-evolution. The project is focused on a model host parasite system (host is the crustacean Daphnia) and seeks to gain insight into evolutionary dynamics and the genetic basis of disease resistance. The project will, depending on the interests of the successful candidate, involve culturing Daphnia, field sampling, experimental infections or molecular work. With respect to the latter. experience with molecular work (e.g. PCR, qPCR, transcriptomics) will be helpful and preferred.

Fixed Term: 2 years

Vacancy details Vacancy Reference: 3011819 Department: Biological Sciences Job Title: Post-Doctoral Researcher Job Function: Academic Job Type: Full Time Live Date: 15-Oct-2009 Expiry Date: 05-Nov-2009 Salary Scale: £29,704 - £35,469 Internal job: No. Anybody can apply for this position. Further Information: Further Information Conditions Of Employment: View Conditions of Employment

– The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

tom little <tom.little@ed.ac.uk>

UFlorida PathogenMolecularEvolution

Molecular Evolution of Pathogens

The Department of Pathology, University of Florida is recruiting for a Postdoctoral Associate position in the laboratory of Dr. Marco Salemi. Dr. Salemi's lab is strongly oriented towards computational and molecular biology, and it is involved in basic as well as clinically relevant research in the area of viral evolution, neuropathogenesis and molecular epidemiology of RNA and DNA viruses, with major focus on HIV and HCV. The lab will consist of DNA/RNA extraction/cloning, as well as a computational core with a large computer cluster, viral databasing tools and state-of-the-art phylogenetic and population genetic analysis software. Two major research areas are pursued: (1) the study of intra-host viral evolution and the correlation between viral evolution and pathogenesis; (2) the study of inter-host viral evolution, focused in particular on the molecular epidemiology of emerging pathogens, such as HIV, HCV and influenza.

Candidates must have a PhD in Bioinformatics, Biostatistics, Applied Mathematics, Molecular Evolution or related subject from an appropriately accredited academic, institution. Minimum requirements include object-oriented programming skills, and experience with DNA/protein sequence analysis. Experience with Phylogenetic analysis, coalescence, Bayesian MCMC methods and GIS programming is a plus. The successful candidate will be expected to work at the development and implementation of algorithms to investigate the molecular epidemiology and intra-host evolution of human and animal pathogens, with an emphasis on HIV and SIV.

The salary is negotiable based on qualifications and experience. The position will be filled as soon as possible.

Please send detailed CV and three letters of recommendation to:

Marco Salemi, Ph.D. Department of Pathology, Immunology and Laboratory Medicine PO Box 100275, University of Florida, Gainesville, FL 32610-0275. salemi@pathology.ufl.edu

sellung@pathology.ufl.edu sellung@pathology.ufl.edu

UFribourg PlantEvolutionaryGenomics

Postdoctoral position in plant evolutionary genomics

Project: Ecological & evolutionary genomics of a porous species boundary in European Populus

Supervision: Christian Lexer, University of Fribourg, Switzerland

A postdoctoral position is available in the newly established lab of Christian Lexer. I am looking for a highly motivated candidate with a keen interest in evolutionary genomics and speciation genetics and prior experience with/exposure to key methodologies relevant to these fields of research. The post is funded by a 3-year project grant from the Swiss National Science Foundation and involves several collaborating labs in Europe and the USA.

The research project will address key questions related to the ecological & evolutionary genomics of a porous' species boundary between Populus alba and P. tremula, two ecologically divergent European tree species related to Populus trichocarpa, the first completely sequenced forest tree. Within a team consisting of 1 other Postdoc, 2 PhD students, and a lab technician, the chosen candidate will take the lead role in laboratory and in silico research to address the role of functionally important genes in species isolation and adaptive introgression, and the size of genomic islands' of divergence between these hybridizing forest trees. In collaboration with other team members, he/she may also be involved in related research topics in Populus speciation genomics. Participation in fieldwork is possible, depending on interests. The chosen candidate will participate in the supervision of one PhD student active on the same project, and he/she will interact closely with collaborating labs in Europe and the USA. Prior experience with the use of DNA-based molecular genetic markers to answer evolutionary questions is essential for this project. Experience with (ultra-) high throughput DNA sequencing and the design of high-throughput SNP detection assays would be particularly desirable.

The starting date is negotiable (from February 2010 onwards). Funding is for three years (annual starting salary is ca. CHF 73'000). Knowledge of French or German is helpful in every day life, but the working language in the group is English. A doctoral degree in biology or related subject is required. Fribourg is a lively town with pleasant surroundings and an excellent quality of life. It is located ca. 30 minutes from the Alps, close to other cities such as Berne and Lausanne and just a little over an hour from Geneva.

To apply, please send an e-mail with the application materials in a single pdf file to Christian Lexer (christian.lexer@unifr.ch). Application materials should include a CV, a list of publications, and a short (less than one page) statement of research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 15 November will be given full consideration. Interviews will take place in December.

Further information and address for application: Dr. Christian Lexer, Associate Professor of Evolutionary Biology E-mail: christian.lexer@unifr.ch, Tel: +41 26 300 88 68 Web: http://www.unifr.ch/biol/ecology/-lexer/index.html For more information about Ecology & Evolution in Fribourg see http://www.unifr.ch/biol/-ecology/ (all departmental pages currently undergoing construction)

— Christian Lexer Associate Professor of Evolutionary Biology University of Fribourg, Department of Biology Unit of Ecology & Evolution Chemin du Musée 10, CH-1700 Fribourg, Switzerland Tel (office) +41 (0)26 300 8868 Tel (lab): +41 (0)26 300 8895 Fax: +41 (0)26 300 9698 Mobile: +41-77-4720-789 Email: christian.lexer@unifr.ch Web: http://www.unifr.ch/-biol/ecology/lexer/index.html christian.lexer@unifr.ch christian.lexer@unifr.ch

UGroningen GeneRegulation Computational

Postdoc position in Molecular Genetics, University of Groningen, the Netherlands at the Groningen Biomolecular Sciences and Biotechnology Institute, the Netherlands

The Postdoc will take part in a large collaborative project (BetNet) of the GBB with the Institute of Environmental Sciences (CML, Leiden University), the Mathematical Institute (MI, Leiden University), and the Leiden institute of Advanced Computer Science (LIACS, Leiden University), funded by the Dutch Science Foundation (NWO), within the Computational Lif Sciences programme. The goal of this project is to resolve the dynamics of gene regulation networks, by using the quantitative demands on the shape of bacterial bet-hedging strategy distributions that are imposed by fluctuating selection environments. As a model system, we study the adaptation of the distribution of sporulation-initiation timing in B.subtilis to randomly changing environments and cue reliability.

The project at Molecular Genetics mainly focuses on the experimental part, involving the design and execution of specific selection experiments in B. subtilis, the characterization of evolved strains by transcriptome analysis, time lapse microscopy, FACS, and whole genome resequencing of selected strains. For the modeling, evolution biology and bioinformnatics we will closely collaborate with the partners in Leiden.

Requirements: PhD degree in Molecular Microbiology or related disciplines. Preferably experience in working with Bacillus subtilis.

Appointment We offer a temporary full time position for a period of 2.5 years. Monthly gross salary is from 2379,- to 3755,- a month depending on qualification and experience of the applicant. Appointment will be under the term of the Collective Labour Agreement of Dutch Universities (CAO Nederlandse Universiteiten).

Further information and a full project desciption can be obtained by mailing o.p.kuipers@rug.nl. Applications: send a CV + accompanying letter to o.p.kuipers@rug.nl before October 31. The positions are at the Molecular Genetics Dept., University of Groningen, Kerklaan 30, 9728 XG Haren, the Netherlands.

Patsy Haccou <haccou@math.leidenuniv.nl>

UKansas StatisticalGenetics

Quantitative Genetics of Gene Expression in Drosophila

A Postdoctoral Scholar position is available in Stuart Macdonald's lab at the University of Kansas to bioinformatically analyze genomewide expression data collected on a set of 1,500 8-way Recombinant Inbred Lines. The goal of our lab is to understand the genetic basis of complex trait variation using Drosophila as a model system, and we are dissecting a number of traits in addition to gene expression (e.g., stress- and drug resistance, male genitalia shape). Using the gene expression data we will map and characterize eQTL and construct gene expression networks. This position will also provide an opportunity to develop an independent line of research, and collaborate with our group on a range of problems in quantitative genetics.

This position requires a Ph.D in evolutionary/computational biology or population/quantitative/statistical genetics, and a record of published, peer-reviewed research in areas related to population or quantitative genetics, or genome biology. In addition, since projects will involve very large phenotype and genotype datasets, demonstrated competency in programming is required (e.g. Unix, Perl, MySQL, R). Preference will be given to those candidates with previous experience in the analysis of genomewide expression data.

The University of Kansas (www.ku.edu) has an active academic community in the life sciences. The Macdonald lab is affiliated with the Department of Molecular Biosciences (molecularbiosciences.ku.edu) and also works closely with members of the Department of Ecology and Evolutionary Biology (www2.ku.edu/~eeb). The range and number of active research groups presents many opportunities for fostering academic and social interactions. The University of Kansas is in the city of Lawrence (www.visitlawrence.com, www.ci.lawrence.ks.us, www.lawrence.com, en.wikipedia.org/wiki/Lawrence,_Kansas) situated 45 minutes West of Kansas City.

The position is open and review of applications will begin immediately and continue until the position is filled. Informal inquires are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at https://jobs.ku.edu (position number 00066120). Attach a cover letter (describing your interest in the position and any relevant expertise), a full CV, and complete contact information for 3 referees. EO/AA Employer.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 1030 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

tel: 785-864-5362 fax: 785-864-5321 email: sjmac@ku.edu web: http://web.ku.edu/sjmac/ sjmac@ku.edu sjmac@ku.edu

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UKonstanz MolecularEvolution

ONE POSTDOC POSITION V in molecular evolution, genomics or bioinformatics. University of Konstanz, Germany.

At the University of Konstanz in Germany we have one postdoc position available starting on January 1, 2009 at the Genomic-Proteomics Center http://-cms.uni-konstanz.de/genomics-center/ in the Department of Biology.

Through the funding of the University of Konstanz by the "excellence initiative" of the German government we are in the process of establishing a Genomics-Proteomics Center that will include second generation sequencing technologies (Roche GSFLX and Illumina GA IIX). Therefore, we are particularly interested in a Ph.D. biologist/ bioinformatics with expertise in molecular evolution, molecular phylogenetics and bioinformatics. We expect that a post for a "junior professorship" in bioinformatics will be filled shortly as well.

The postdoc projects we are interested in have to do with fish genomics and in particular comparative genomics of cichlid fish. Other projects deal with the evolution of gene families and comparative genomics of chordates and vertebrates. Candidates should have a strong interest in bioinformatics, developmental and evolutionary biology and should be experienced in molecular techniques and/or computational biology. The person we are looking for should have skills in the analysis of second generation sequencing technologies and should be willing to interact with other groups in the University of Konstanz that would be using the facilities of the Genomics-Proteomics Center.

The salary is according to the German TVL salary scale that includes extensive health and retirement benefits. The initial contract period would be for two years with the potential for additional years of funding.

Further information on our research can be obtained from our web page: www.evolutionsbiologie.uni-konstanz.de . For publications see http://www.evolutionsbiologie.uni- konstanz.de/index.php?section' . Applications should include a CV, statement of research interests and email addresses of two references. Review of applications will commence on 1. December 2009. The starting date is flexible. Applications should be sent as one pdf file to axel.meyer@uni- konstanz.de .

This position is affiliated with the new graduate school in Chemical Biology V and the new International Max-Planck Research School for Organismal Biology. For more information visit http:// www.chembiol .uni-konstanz. de/ and http://cms.uni-konstanz.de/-organismal-biology/ . For these new programs we invite applications of qualified Masters students as well as Ph.D. candidates.

This search will remain open until the postdoc position is filled.

Informal inquiries should be addressed to Prof. Axel Meyer, Ph.D. (axel.meyer@uni-konstanz.de).

Prof. Axel Meyer, Ph.D. Chair in Zoology and Evolutionary Biology, Department of Biology, University of Konstanz 78457 Konstanz Germany - fon + 49 7531 88 4163 fax + 49 7531 88 3018 secretary: Ingrid.Bader@ uni-konstanz. de tel. + 49 7531 88 3069

Axel Meyer <axel.meyer@uni-konstanz.de>

ULeiden LifeHistoryEvolution

Post Doc into life history regulation m/f in Leiden (the Netherlands)

Vacancy number : B.09.JS.06

Position As a post doc you are responsible for carrying forward our research activities on the regulation of human life histories under adverse conditions. To this end we have initiated a cohort study in the North-East of Ghana. This study is part of a greater endeavor identifying cues that are relevant for early survival and determine the rate of ageing. Genetics play a key role but only within the peculiar environmental conditions to which the participants are exposed. It is a team effort in which several junior and senior researchers from (inter)national laboratories are involved. You will be positioned within the 'LifeSpan' project, a EU-funded Network of Excellence that is coordinated in Leiden. As a member of the management team, you will spend part of your time on coordinating and running the Network.

The department

You will be positioned within the Department of Gerontology and Geriatrics. The focus of this department is on scientific research on ageing and longevity, elderly people in means of patient care for elderly as well as participation in the medical and biomedical curriculum of Leiden University and hosting the training for geriatricians.

Your profile You have a background and PhD that enables you to study the genetic regulation of human life histories. You are able to work independently and in a team, and possess excellent communication skills, including fluent written and spoken English. You like to take initiatives and are driven by scientific interests. You are enthusiastic and inquisitive and possess the creative skills to find solutions though with a critical eye for your work. A flexible work approach and ability to cope with stress is essential and you will be expected to present and publish your findings. Experience in and affinity with scientific programming is an advantage. We encourage persons to apply who are enthusiastic about the LifeSpan initiative and who can contribute expertise relevant to the network, and are willing to work in a large multi disciplinary consortium.

We offer You will be employed on the basis of a 36-hour week and appointment is for two years, until 1 January 2012. Your salary will be a maximum of EUR 4,416 gross per month based on a full time position (according to the Collective Labour Agreement for University Hospitals).

The terms of employment offered by the LUMC are highly favourable. For example, you will receive an 8% holiday remuneration, a year-end bonus, a pension arrangement with the National Civil Pension Fund, and, if applicable, a bonus for unsocial hours. Also, as employee of one of the University Hospitals in the Netherlands, you may join our collective health insurance policy.

Moreover, the LUMC offers excellent facilities in the area of education, child-care centres, and career advice. In addition, you may enjoy various leave arrangements and other extras.

More information If you have any questions, or if you want more information about this position, please contact Prof Dr R.G.J. Westendorp, head of the Department of Gerontology and Geriatrics, telephone +31 (0)71 526 66 40 or r.g.j.westendorp@lumc.nl

Apply If you are interested in this job and your satisfy the requirements in the job profile, we encourage you to apply. You can do so by letter, by e-mail or by using the application form. You may rest assured that your details will be treated with strict confidentiality. After selecting a number of letters and CVs, one or two interviews will be conducted. An internal application procedure is being held for this job. If an internal and external candidate have matching abilities, our preference goes to an internal candidate.

Applying by e-mail Send an e-mail, stating your reasons for applying and including your CV, to Div2peno@lumc.nl. Clearly state the job number of the job you are applying for. You can include annexes with your e-mail (for example, your CV), provided they are in MS Word format.

Applying by letter Send your letter of application, stating your reasons for applying and including your CV, to:

LUMC Attn. Personnel and Organisation Department Bureau Bedrijfsvoering divisie 2 (K5-S) PO Box 9600 2300 RC Leiden The Netherlands

Please state the vacancy number on both the letter and the envelope

C.N.van_Beuzekom@lumc.nl

UMelbourne EvolutionaryBiol

Dear Evoldir,

I thought I'd alert evoldir readers to the following postdoc fellowship scheme at the University of Melbourne. Applicants may be drawn from any field in which the University of Melbourne has research strength, one of which is evolutionary biology and population genetics.

McKenzie Fellowships The University of Melbourne is building an ambitious program of research activity and aims to attract outstanding postdoctoral researchers to be part of that and to begin to build the next generation of research activity. The University offers a leading and lively research environment located in an environment that is internationally engaged, public-spirited, and with many outstanding areas of research strength. The McKenzie Postdoctoral Fellowship Scheme has been established to attract outstanding recent doctoral graduates to the university in areas of research priority for the university and its faculties, and in particular to recruit new researchers who have the potential to build and lead cross-disciplinary collaborative research activities inside and across faculties.

McKenzie Fellowships are open to applicants across all fields. Intending applicants should consult the guidelines of the program <http://www.research.unimelb.edu.au/__data/assets/word_doc/0005/167549/Guide lines.doc> and discuss their interest with the Faculty in which they would be located prior to submitting the application <http://www.research.unimelb.edu.au/__data/assets/word_doc/0011/167591/Appli cation_Form.doc> . In addition to this scheme, many faculty-based postdoctoral opportunities are available; and faculties, research strengths and projects actively encourage talented applicants to work with them to win support through the nationally competitive NHMRC and ARC schemes. University research priorities in terms of its future programs of research have been nominated both within faculties < http://www.unimelb.edu.au/-

az/faculties.html > and in an emerging program of major cross-university research institutes < http://www.researchinstitutes.melbourne.edu/home/ > .

The McKenzie Postdoctoral Fellowships are intended for: * Applicants who are not currently studying or employed at the University of Melbourne * Applicants may be drawn from any field in which the University of Melbourne has research strength, but must have an ability to contribute to new emerging research collaborations and programs across faculties or disciplines * Applicants will require a supporting statement from an existing faculty in which they would be located if successful, but the criteria for selection will be university-based and judged on demonstrated talent and achievement and the ability to make a substantial contribution to an already nominated or an emerging program of university research priority Two categories of award will be made. The Program is primarily intended for applicants who have recently completed or are about to complete their PhD, and the bulk of awards will be for fellows in this category. A small number of awards will be made to outstanding applicants who have completed already a first period of post-doctoral experience. Assessment in both cases will take account of achievement relative to opportunity.

Applications close Sunday 15 November, 2009. Please send your application via email to sdureau@unimelb.edu.au marked 'Application for McKenzie Post-Doctoral Fellowship'

see:

http://www.research.unimelb.edu.au/rgc/grants/find/schemes/uom/mckenzie_fell owships

Charles Robin email: crobin@unimelb.edu.au FAX: (61) 3 8344 5139 ph: (61) 3 8344 2349 http://www.genetics.unimelb.edu.au/research/robin/index.html map: http://www.genetics.unimelb.edu.au/images/map_bio21.jpg Charlie Robin <crobin@unimelb.edu.au>

UNebraska-Lincoln Bioinfo MolEvol

POSTDOCTORAL POSITION in Bioinformatics and Molecular Evolution at University of Nebraska-Lincoln

A postdoctoral position is available immediately in the Etsuko Moriyama lab at the University of Nebraska-Lincoln (http://bioinfolab.unl.edu/emlab/index.html). This is one year position supported by NIH stimulus grant. Extension beyond the first year depends on funding situation.

The research project emphasizes developing methods for protein classification and applying them against wide ranges of genomes. See 7TMRmine website for more details: http://bioinfolab.unl.edu/emlab/7tmr/index.php The target protein families and the research scope may be expanded.

Our lab has very interdisciplinary research environment. We regularly collaborate with researchers in many different fields. The postdoc will have opportunities to collaborate with researchers with diverse backgrounds, from computer science, bioinformatics, structural biology, molecular evolution, population genetics, to genomics and molecular biology.

Preference will be given to applicants who have experience in any combination of the following fields: computer science (especially machine learning), multivariate statistical analysis, bioinformatics (especially protein classification and structural analysis), comparative genomics, and molecular evolution (especially for protein functions). Strong background in biology is highly desired. Proficiency in programming (using any language) is required. Experience in MySQL database development/management will be appreciated.

Please send a cover letter and CV to emoriyama2@unl.edu. Applications will be reviewed as they arrive. Please feel free to contact me with any questions.

The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work- life balance, and dual careers.

Etsuko Moriyama, PhD Associate Professor School of Biological Sciences & Center for Plant Science Innovation University of Nebraska-Lincoln 403 Manter Hall Lincoln, NE 68588-0118

Email: emoriyama2@unl.edu Phone: 402-472-4979, Fax: 402-472-2083 (SBS business office)

Moriyama Lab web page: http://bioinfolab.unl.edu/emlab/index.html SBS faculty page: http://www.biosci.unl.edu/faculty/moriyama/index.shtml emoriyama2@unlnotes.unl.edu emoriyama2@unlnotes.unl.edu

UNevadaLasVegas AvianEvolution

POST-DOCTORAL POSITION: Neotropical Ornithology –A two-year postdoctoral position is available in the Klicka lab in UNLV's Barrick Museum of Natural History. Here we use molecular methods, combined with fieldwork, to study the evolution of neotropical birds in Middle America. One current focus of this research is comparative phylogeography involving a diverse array of avian taxa. Experienced researchers (Ph.D. or exceptional Masters students) with an interest in this area of research are encouraged to apply. The successful candidate will take a lead role in completing (data analysis and writing) several ongoing phylogeography studies while initiating others. Independent research that complements central objectives is encouraged, and additional research opportunities related to the evolution of Middle american birds exist within the lab. Preference will be given to candidates with experience in molecular laboratory methods and data analysis and to those who have demonstrated proficiency in scientific writing. Curatorial skills and the ability to converse in Spanish are desirable. A start date of Jan 2010 is preferred. Initial appointment will be for one year, with continuation for an additional year dependent upon performance. Salary will be commensurate with experience and qualifications but will likely be in the range of $40,000 - $45,000 per year. Please send via email attachment a letter of application, curriculum vitae, statement of research interests, and names and addresses of three references to DR. JOHN KLICKA (EM: klicka@UNLV.nevada.edu). UNLV is an Affirmative Action/Equal Employment Opportunity/ADA Employer. Women and minorities are encouraged to apply.

John Klicka Curator of Birds Barrick Museum of Natural History Box 454012, University of Nevada Las Vegas Las Vegas, NV 89154

e-mail: klicka@unlv.nevada.edu phone:(702)895-2749 fax:(702)895-3094

John Klicka <klicka@unlv.nevada.edu>

UOklahoma Daphnia evolution

Postdoctoral Fellowship position available: A Postdoctoral Fellowship position is available in my laboratory to work on a new 3-year NSF-funded project entitled, "Organism-environment interactions - impact of cultural eutrophication on Daphnia tracked by genomics, physiology, and resurrection ecology".

In a planned 36-month project in collaboration with colleagues at Oklahoma State University and Indiana University, the PIs will use an integrated approach involving genetic/genomic, physiological, and "resurrection ecology" methods to examine how cultural eutrophication (i.e., enrichment of freshwater systems with nutrients such as phosphorus) influences evolutionary changes in organisms. The waterflea, Daphnia pulex, which plays a major role in freshwater food webs (i.e. it eats algae/bacteria and in turn is fed upon by fish), will serve as the model organism. Daphnia are ideal for such studies because they produce resting eggs that can lay dormant in lake sediments for long periods of time. Decades-old eggs can be induced to hatch (i.e. "resurrection ecology") and viable DNA can be extracted from eggs that are centuries old. Moreover, the D. pulex genome has been sequenced and genetic/genomic methods (i.e. gene expression) are in place to study how changes in eutrophica tion (phosphorus-level) patterns over the past century have influenced how an organism like a daphniid can respond to ecosystem/environmental change. Results from this cross-disciplinary study will provide an excellent example of how man-made environmental changes (via eutrophication) influence natural (freshwater) ecosystems.

Funding is guaranteed for 2 years. The position would start August 2010. We are looking specifically for individuals who have ample bioinformatics/genomics skills, including the use of a variety of modeling approaches to study microevolutionary dynamics using large data sets.

For more details and information, please contact:

Dr. Lawrence J. Weider, Professor of Zoology Director, The University of Oklahoma Biological Station (UOBS) University of Oklahoma Norman, OK 73019 Phone: 1-405-325-4766 or 325-7438 FAX: 1-405-325-0835 http://www.ou.edu/uobs/weider.html ljweider@ou.edu

UOxford PlantAdaptation

Postdoctoral Research Assistant DEPARTMENT OF PLANT SCIENCES Grade 7: Salary £28,839 - £35,469 p.a. Applications are invited for a three-year postdoctoral position on a NERC-funded project, Genomic basis of adaptation and speciation in Senecio, led by Dr Dmitry Filatov, Department of Plant Sciences, University of Oxford. This project is devoted to a genome-wide analysis of molecular bases of speciation and adaptation in plant genus Senecio. In collaboration with Prof. Hiscock lab in Bristol (UK) we will conduct functional and evolutionary genetic analyses of coding and regulatory regions in Senecio genome in order to study their evolution during adaptation to contrasting environments of high and low altitudes. The research will involve high throughput DNA pyrosequencing from three Senecio species and population genetic and evolutionary genomic analyses of these sequences. Further particulars of the post are available on http://www.plants.ox.ac.uk/. It is anticipated that the successful candidates will begin on 1 February 2010 or soon thereafter. For more details of the Filatov lab see: http://dps.plants.ox.ac.uk/plants/staff/-DmitryFilatov.aspx .Applications, including application form, full curriculum vitae, the names and contact details of two referees, and clearly quoting reference AP09014 should be sent to the Departmental Administrator, Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB or by email to recruit@plants.ox.ac.uk. The closing date for applications is noon on Thursday 19th November 2009.

[Further particulars] Postdoctoral Research Assistant Ref No.AP09014

Genomic basis of adaptation and speciation in Senecio

This is a 36 month project funded by NERC with ideally a start date of 1 February 2010. The grant holder is Dr Dmitry Filatov and the successful applicant will be under his immediate direction in his research lab.

The Plant Evolutionary Genetics Group is led by Dr Dmitry Filatov and currently comprises four postdoctoral researchers and one graduate student, all working on different aspects of plant molecular population genetics and evolutionary genomics.

Project Description Title: Genomic basis of adaptation and speciation in Senecio

This project is devoted to a genome-wide analysis of molecular bases of speciation and adaptation in plant genus Senecio. In collaboration with Prof. Hiscock lab in Bristol (UK) we will conduct functional and evolutionary genetic analyses of coding and regulatory regions in Senecio genome in order to study their evolution during adaptation to contrasting environments of high and low altitudes. The research will involve high throughput DNA pyrosequencing from three Senecio species and population genetic and evolutionary genomic analyses of these sequences.

Selection Criteria

Candidates will be assessed in relation to the following selection criteria.

Strong interest in population genetics of speciation and adaptation.

Proven research skills and expertise in evolutionary genomic and population genetic analysis of DNA sequence data are essential.

Computer programming skills will be essential for processing and analysis of massive DNA sequencing data generated by modern high-throughput sequencing machines.

Familiarity with the high-throughput sequencing is desirable

A relevant publications record

Ability to work independently as well as a part of the team

Good writing and communication skills, including ability to write research articles and present research at international symposia.

The Department of Plant Sciences The Department of Plant Sciences is one of the leading science departments in the UK devoted to teaching and research in Plant Sciences, and is an internationally recognized centre for research directed towards improving our understanding of all aspects of plant biology at molecular, cellular, tissue, whole-organism and environmental levels. The Department is in the process of recruiting to a statutory professorship in addition to 26 university lecturers and senior fellows, some 45 postdoctoral research workers and some 35 graduate research students, and is responsible jointly with the Department of Zoology for teaching some 300 undergraduate students reading the Honour School of Biological Sciences. General conditions

The appointment will be on the postdoctoral Grade 7 scale for academic-related staff and the starting point will be within the range of £26,666 - £32,796 p.a. For a full-time appointment, the annual holiday entitlement will be 38 days (including 10 days to be taken on fixed dates at Christmas and Easter, and 8 public holidays). The appointment is subject to satisfactory completion of a six month probationary period, during which the notice period will be one month on either side. Once the appointment has

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UParisSud Orsay HumanSelection

Detection of multilocus selection in genes involved in alimentary processes in Humans.

We propose a postdoctoral position financed by the French Agence Nationale de la Recherche, project NUTGENEVOL. This project is a joint collaboration between the laboratories Ecologie, Systématique et Evolution located at the Université de Paris-Sud in Orsay near Paris (team of Frédéric Austerlitz) and Eco-Anthropology located at the National Museum of Natural History in Paris (team of Evelyne Heyer). This position is opened for two years, with a beginning before May 1st 2010 (the postdoc can potentially start later but will not in that case be funded for two full years). The NUTGENEVOL project consists in studying the selection pressures that occurred on genes involved in alimentary processes. The first aim of the postdoctoral position would be to focus on the multilocus analysis of selective pressure occurring on these genes. The other aspect of the project would be to analyse whether the genes under selection have specific functions in the gene networks involved in these processes.

These selective pressures are connected with the changes in alimentary diets in humans. Indeed, before the major Neolithic transition (~10,000 yBP), our hunter-gatherer ancestors had a meat-based diet, poor in carbohydrates and rich in protein. Therefore, genes favouring insulin resistance and gluconeogenesis were selected for, in order to constantly maintain sufficient level of glucose in the blood. These potentially thrifty genes may now be detrimental in urbanized societies, because under the present high carbohydrate diet, insulin resistance and gluconeogenesis may lead to metabolic disorders such as type II diabetes, obesity, and hypertension. To detect the selective pressures that occurred on these genes, we have obtained sequence polymorphism data for 11 candidate genes involved in these traits in two Central Asian populations: one pastoralist and one agriculturist population, for which differences in diet may have lead to different selective pressures on such genes. We are currently also obtaining data on polymorphism of DNA SNPs: 660,000 SNPs (Illumina, Human 660W Quad v1.0) in these two populations.

All the traits involved in this study are polygenic traits involved in gene networks, and a multilocus approach to detect selection would thus seem especially appropriate. Therefore, the postdoctoral position within this project would first consist in searching for selection that acts jointly on combination of SNPs in the same or different genes, using the data on candidate genes and SNPs. This will be performed for instance through the study of linkage disequilibrium between these loci. Other methodological developments may be considered. Similar studies could also be performed in public databases such as HAPMAP. For validation, the methods may be also applied to simulated data, using a program developed by other people from the group.

Another aspect of the postdoctoral position will consist for the genes under selection in analysing their position in the network, in order to test whether the position in the network could influence the level of selection occurring on these genes. A particular emphasis will be put on studying the level of pleiotropy of these genes, as selective pressures may differ for genes involved in one vs. several different functions. This research on gene networks will be mostly performed through searches in public databases.

Salary should be around 1900 euros per month. Interested candidates should send their application preferentially by email to Frédéric Austerlitz (see coordinates below). Please include a CV, a brief letter explaining your motivations and the coordinates of two or three potential references. Applications should be sent before November 15th. Please also do not hesitate to ask for further details at this address.

Frédéric Austerlitz Laboratoire Ecologie, Systématique et Evolution UMR CNRS/Université Paris Sud/AgroParisTech 8079 Université Paris-Sud, Bâtiment 360 F-91405 Orsay cedex, France Tel : +33 1 69 15 77 20 / Fax : +33 1 69 15 46 97 frederic.austerlitz@u-psud.fr

webpages : Fréderic Austerlitz: http://www.ese.u-psud.fr/pages_perso/spip.php?article26 Evelyne heyer: http://www.ecoanthropologie.cnrs.fr/spip.php?article300&langÊ – Frederic Austerlitz

Charge de Recherche CNRS / CNRS researcher Laboratoire Ecologie, Systematique et Evolution UMR CNRS/Universite Paris Sud/AgroParisTech 8079 Universite Paris-Sud, Batiment 360 F-91405 Orsay cedex FRANCE tel: + 33 1 69 15 77 20 / fax: + 33 1 69 15 46 97 webpage: http://www.ese.u-psud.fr/pages_perso/

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UtahStateU BeetleEvolutionaryGenomics

Position Description

Postdoctoral Researcher: Mountain Pine Beetle Transcriptome Variation

The mountain pine beetle (Dendroctonus ponderosae; MPB) is an emerging model system for studying the effects of climate change. Research in this system is occurring at the interface between applied ecology, evolutionary genomics, and climate-change modeling. Utah State University has long been a center for MPB-related field research, climate-based modeling efforts, and quantitative genetic experiments. USU has recently developed collaboration with the University of Notre Dame to assess transcriptional variance related to developmental rates in larvae, using next-generation sequencing technology (Roche/454). These developmental rates vary with latitude and temperature, and total development time underlies synchronous emergence and mass attacks characteristic of MPB.

We are seeking a creative and highly motivated postdoctoral researcher with an interest in the interface between Applied Ecology and Genomics to fill a unique position with involvement at two campuses: Utah State University (USU) and the University of Notre Dame (ND). The researcher will be based at USU (where tissues will be prepared), but will also spend time at ND (where transcriptome sequencing will be performed). The specific allocation of time and effort among campuses will be decided jointly by the researcher and faculty at both campuses. Specific responsibilities will include: 1) organizing and preparing tissues for analysis in collaboration with USU faculty and the USDA Rocky Mountain Research Station, 2) overseeing data generation at ND, 3) data processing and synthesis, and 4) publication. The researcher will also be responsible for leading a semimonthly discussion group at USU on applied genomics. Candidates for this position must have earned a PhD in molecular biology, evolutionary genetics, or related field by the time of appointment. Candidates must demonstrate organizational skills, independence, and communication skills (written and verbal). Preference will be given to candidates with experience in RNA extraction and the analysis of transcriptome data. The position is funded for one year, but the candidate will be encouraged to work collaboratively through USU and/or ND on grant proposals extending the position. The successful applicant will benefit from interactions with USU researchers in the Ecology Center (http://www.usu.edu/ecology), the Center for Integrated BioSystems (http://biosystems.usu.edu), and in the newly established Genomics and Bioinformatics Core Facilities in the Eck Institute of Global Health at ND (http://globalhealth.nd.edu).

Inquires should be directed to Karen Mock at USU (karen.mock@usu.edu) or Michael Pfrender at ND (Michael.Pfrender.1@ND.edu). To apply for this position go to http://jobs.usu.edu/applicants/Central?quickFind=3D54488 or http://jobs.usu.edu (Req ID # 051880). Applicants will be asked to submit a cover letter detailing their interest and qualifications for this position, contact information for three references, and up to 2 representative publications.

Salary will range from $45,000 to $60,000 per year, plus benefits, depending upon experience and qualifications.? Utah State University is an Affirmative Action/Equal Opportunity Employer, and seeks to attract and retain a highly qualified and diverse faculty and staff.

karen.mock@usu.edu

UTennessee ComparativeMethods

Postdoc in developing and applying comparative methods

PI: Brian O'Meara, U of Tennessee, Knoxville (http://www.brianomeara.info)

A 2-year postdoctoral position is available for development, implementation, and application of methods for investigating trait evolution on trees. The postdoc will be an active member of the trait evolution working group of the iPlant Collaborative (http://iplantcollaborative.org), which is developing approaches to understand trait evolution on plant phylogenies with hundreds of thousands of taxa as part of iPlant's broader mission to support cyberinfrastructure across the plant sciences (funding for this position comes from iPlant).

The candidate can anticipate working in a highly collaborative, multi- institutional context that entails the working groups on data set assembly (Doug Soltis (U Florida), Pam Soltis (U Florida), Michael Donoghue (Yale)), gene tree reconciliation (Todd Vision (UNC)), high performance computing and scalable tree construction (Alexandros Stamatakis (Technical University, Munich), Casey Dunn (Brown)), and tree visualization (Michael Sanderson (U Arizona)). The members of the trait evolution working group include Joe Felsenstein (U Washington), David Ackerly (UC Berkeley), Rod Page (U Glasgow), and Jeremy Beaulieu (Yale).

In addition to undertaking basic research in phylogenetic methods, the postdoc will be expected to provide advice to and work in collaboration with cyberinfastructure developers in the iPlant team. Qualifications include familiarity with the data, methods, and software of phylogenetic analysis, and programming experience at least at the level of R or Perl scripts. It is always good to know botany, but this is not expected for the position.

The position is located at the University of Tennessee, Knoxville. Attractions of Knoxville include an active and collaborative Ecology and Evolutionary Biology department (http://eeb.bio.utk.edu), a low cost of living, a rich natural environment, and the new National Institute for Mathematical and Biological Synthesis (http://www.NIMBioS.org).

The position is available immediately. For more information, please email bomeara@utk.edu or see http://www.brianomeara.info/lab .

Brian O'Meara http://www.brianomeara.info Assistant Professor Dept. Ecology and Evolutionary Biology University of Tennessee, Knoxville

bomeara@utk.edu bomeara@utk.edu

UUtah EvolutionaryGenetics EvoDevo

EVOLUTIONARY GENETICS AND DEVELOPMENT AT THE UNIVERSITY OF UTAH

Postdoctoral and graduate student positions are available in the laboratory of Mike Shapiro in the Department of Biology, University of Utah. We seek highly motivated colleagues to study the genetic and developmental basis of morphological and behavioral evolution in vertebrates. Our current research focuses on molecular genetics, population genetics, and development of stickleback fish and domesticated pigeons. Specific projects will be tailored to the strengths and interests of successful candidates. For more information about the lab, please visit our website: http://www.biology.utah.edu/shapiro .

POSTDOCTORAL CANDIDATES Requirements: 1. Ph.D. in genetics, developmental biology, evolutionary biology, bioinformatics, or a related field 2. High level of motivation 3. Demonstrated ability and willingness to work both independently and collaboratively 4. Excellent written and oral communication skills

A strong background in statistics, genomics, or analysis of high- throughput sequencing data is preferred, but not required.

To apply, postdoctoral candidates should submit the following materials: 1. CV, including a publication list 2. Statement of research experience and interests 3. Names of three referees who will be willing to submit letters of reference upon request

Support is guaranteed for a minimum of one year and may be extended pending satisfactory progress available funds. Priority will be given to candidates who show promise for securing external funding through postdoctoral fellowship programs from NIH, NSF, or private foundations.

The position will remain open until filled. For full consideration, please submit application materials by November 15, 2009. A start date of January 2010 or shortly thereafter is preferred.

Please email application materials in PDF format to Mike Shapiro: shapiro@biology.utah.edu

While email is preferred, hard-copy applications may also be sent to: Mike Shapiro Department of Biology University of Utah 257 South 1400 East Salt Lake City, UT 84112

GRADUATE STUDENT CANDIDATES Graduate student candidates should apply for admission through the Department of Biology (http://www.biology.utah.edu/grad_app.php) and/ or the campus-wide Molecular Biology Program (http://www.bioscience.utah.edu/mb/mbApplications/index.html). Deadlines for both programs are in early January 2010. Graduate students are funded for at least 5 years though a combination of research assistantships, fellowships, and teaching assistantships. The department pays graduate tuition.

Informal inquiries are welcomed from potential postdoc and graduate applicants, prior to formal application.

SCIENTIFIC AND CULTURAL ENVIRONMENT The Department of Biology comprises a highly diverse and vibrant group of laboratories, with research interests ranging from environmental biology to biochemistry. We count members of the National Academy of Sciences, HHMI, and a recent Nobel laureate among our ranks. The genetics and developmental biology communities are strong on the University of Utah main campus and medical school and offer numerous opportunities for collaboration. Campus-wide NIH training grants support graduate students in both disciplines.

The University of Utah is located in beautiful (and affordable) Salt Lake City, with easy access to world-class entertainment and recreation. Salt Lake City and nearby Park City are home to the annual Sundance Film Festival and a vibrant year-round cinema scene, as well as outstanding restaurants and brewpubs. Several national parks are located within a just few hours' drive, and the university is within a 40-minute drive of at least six major alpine skiing and snowboarding resorts, including venues of the 2002 Olympics. Hiking and mountain biking trails begin essentially on campus. Indeed, Outside Magazine recently called Salt Lake City "one of the nation's most underrated outdoor meccas." The city is also a major airline hub, with non-stop flights throughout the U.S. and Canada.

shapiro@biology.utah.edu shapiro@biology.utah.edu

UVermont EvolutionarySocioGenomics

Post-doctoral Research Associate

A post-doctoral position is available in the Helms Cahan lab at the University of Vermont to join a new NSF/ARRA-funded project on the genetic architecture of reproductive caste differentiation and development in Pogonomyrmex harvester ants. We will be using high-throughput transcriptome sequencing and association mapping to identify genomic regions underlying the secondary loss of caste flexibility in ant populations displaying Genetic Caste Determination (GCD), an exceedingly rare mode of caste differentiation in which workers and queens are derived from genetically distinct mating crosses. The genomic resources developed over the course of the project will also be used to address evolutionary questions concerning the origin and causes of transitions in caste regulatory mechanisms, with potential applications in phylogeography, ecological genetics, development, and functional genomics, among others. The research associate will work in collaboration with graduate and undergraduate students to collect field samples for molecular analyses and mating crosses, identify SNP markers from comparative transcriptome data, and conduct association and QTL mapping. There will be plenty of opportunities for additional self-designed projects in the candidate's area of interest.

Applicants for the position should have a strong interest in evolutionary sociogenomics and a PhD in a relevant discipline. Familiarity with genomics techniques and/or bioinformatics would be very helpful, though is not strictly required as long as the applicant is strongly motivated to learn. Salary starts at $36,000 per year. The position is available beginning January 1 for two years, with the possibility of renewal. To apply, please send a cover letter detailing your interest and qualifications for the position, a current CV, and the names and e-mail addresses of two potential references to Sara Helms Cahan (scahan@uvm.edu). I will begin reviewing applications November 20th and continue until the position is filled.

To find out more about research in the Helms Cahan lab, go to: http://www.uvm.edu/~biology/Faculty/Helms/Helms.html To find out more about the Biology Department, go to: http://www.uvm.edu/~biology/ Dr. Sara Helms Cahan 307A Marsh Life Sciences Department of Biology University of Vermont Burlington, VT 05405 Tel: (802) 656-2962 Fax: (802) 656-2914 E-mail: scahan@uvm.edu

sara.cahan@uvm.edu sara.cahan@uvm.edu

UWashington HumanExomeAnalysis

A postdoctoral position is available immediately in the research group of Joshua Akey in the Department of Genome Sciences at the University of Washington. The position is supported by NIH stimulus funds to create the Northwest Genomics Center and is available for two years, with the possibility of extension beyond this time frame.

The Northwest Genomics Center, under the direction of Debbie Nickerson, Phil Green, Jay Shendure and Mark Rieder, will resequence the exomes of 5,000 genomic DNA samples derived from well-phenotyped NHLBI cohorts (http://www.nhlbi.nih.gov/recovery/media/stimulus.htm). This exciting data set will provide rich opportunities for the postdoctoral candidate to pursue questions related to human evolutionary history, natural selection, and genotype-phenotype relationships. The ideal candidate will have a strong background in population genetics or in relevant areas of mathematics and statistics, strong computational and programming skills, experience in analyzing large data sets, and be self-motivated and independent.

The Department of Genome Sciences offers an outstanding intellectual environmental for trainees. Research in the department addresses questions in biology and medicine by developing and applying genetic, genomic, and computational approaches that take advantage of genomic information. Departmental faculty are exceptionally distinguished and include eight members of the National Academy of Sciences and one Nobel laureate. In November 2006 the entire Department of Genome Sciences moved to the newly constructed, state of the art Foege Building (http://www.gs.washington.edu/ and http://www.gs.washington.edu/faculty/index.htm).

Joshua Akey University of Washington Department of Genome Sciences Foege Building S-303 / Box 355065 Seattle, WA. 98195-5065 Phone: (206) 543-7254 Fax: (206) 685-7301

akeyj@u.washington.edu akeyj@u.washington.edu

Vanderbilt BioinformaticsHost-MicrobeInteractions

VANDERBILT UNIVERSITY: POSTDOC IN BIOINFORMATICS AND HOST-MICROBE INTERACTIONS

The Bordenstein laboratory at Vanderbilt University seeks postdoctoral applicants to study patterns of genome evolution that shape invertebrate-microbe interactions. Efforts will include computational analyses of full-genome-sequences and fine-scale analyses of molecular evolution, as well as some molecular lab work. The primary project will examine evolutionary forces shaping genetic variation in the tripartite symbiosis of invertebrates, Wolbachia bacteria, and their bacteriophages. Sources of genomic data will span next generation sequencing, Sanger sequencing, and microarrays. Demonstrable computational skills preferred including Linux, Perl,database management, and molecular evolution analyses. The candidate will have strong publications, excellent verbal and written communication skills, and the ability and interest in mentoring junior scientists. Experience of working in multidisciplinary teams involving bioinformaticians and biologists is important.

If interested, please contact Seth Bordenstein immediately by email (s.bordenstein@vanderbilt.edu) with (i) a curriculum vitae noting at least three references and (ii) a statement of intent and experience noting when you can start. Vanderbilt is located in the cultural and educational center of Nashville, TN. The position will be filled as soon as possible.

Lab: http://bordensteinlab.vanderbilt.edu Department of Biological Sciences: http://www.vanderbilt.edu/biosci/ –

Seth Bordenstein Assistant Professor Department of Biological Sciences Vanderbilt University VU Station B, Box 35-1634 Nashville, TN 37235

email: s.bordenstein@vanderbilt.edu phone: 1.615.322.9087 fax: 1.615.343.6707 http://bordensteinlab.vanderbilt.edu Shipping Address for Packages: Seth Bordenstein Vanderbilt University U7215 BSB / MRB III 465 21st Ave South Nashville, TN 37232

Seth Bordenstein <s.bordenstein@vanderbilt.edu>

Vienna PopulationGenomics

Vienna, Austria: Career Track Postdoc Position In Population Genomics

A career track postdoctoral position in population genomics is available at the Institute of Population Genetics at the University of Veterinary Medicine in Vienna.

The deadline is approaching quickly: 30 October 2009.

Research profile: We are searching for an outstanding candidate with a strong background in population genetics, who is interested in using next generation sequencing (NGS) for population genetic inferences. We encourage experimentalists with a strong aptitude for NGS data analysis as well as theoreticians to apply for this position. Preference would be given to candidates with interest in population genetics of epigenetic programming.

Background about the position: The University of Veterinary Medicine in Vienna (Vetmeduni Vienna) offers a new funding scheme to attract outstanding postdocs to Vienna. The position has two funding phases. In the first phase the candidate is expected to carry out preparatory work for a full research grant application to be submitted to the FWF (Austria's major funding body for basic research). Based on a successful evaluation after two years, the postdoc will be promoted to a group leader with approx. 80k base funding for research/year. After 2-3 years the group leader will be reviewed and upon positive review s/ he could be offered a tenured faculty position at the university.

The post will be based at the Institute of Population Genetics (http://i122server.vu-wien.ac.at/pop/-index.html). The Institute hosts research groups in experimental population genetics (C. Schlötterer), functional population genetics/evodevo (A. McGregor), life history evolution and aging (T. Flatt), conservation genetics (P. Burger) and evolutionary modeling (C. Kosiol). The Vienna research area offers many additional possibilities for collaborations in population genetics: Nick Barton, Reinhard Bürger, Andreas Futschik, Ines Hellmann, Joachim Hermisson, Magnus Nordborg, and Claus Vogl.

Deadline for application: The closing date for applications is 30 October 2009. Please submit a cover letter, CV, statement of research interests, and the names and contact details of three academic references as a single pdf file by e-mail to Dr. Thomas Flatt: thomas.flatt@vu-wien.ac.at

Dr. Thomas Flatt Institut für Populationsgenetik Veterinärmedizinische Universität Wien Veterinärplatz 1 A-1210 Wien Austria/Europe

VOX +43-1-25077-4334 FAX +43-1-25077-4390 E-mail: Thomas.Flatt@vetmeduni.ac.at

http://i122server.vu-wien.ac.at/pop/Flatt_website/-flatt_home.html flatt.thomas@gmail.com

YaleU SexualSelection

Postdoctoral Position To Study Sexual Selection and Social Evolution

A NSF-funded postdoctoral position is currently available in the lab of Suzanne Alonzo (PI) at the Department of Ecology and Evolutionary Biology at Yale University to develop theory on how individual social or behavioral interactions affect evolutionary dynamics. The postdoctoral researcher will work independently and in collaboration with the PI to determine the precise questions to be addressed. A Ph.D. in evolution, ecology, or mathematical biology is required. A background in sexual selection, social evolution or evolutionary ecology is preferred. Applicants should have a background in evolutionary or ecological theory and have previous experience developing mathematical models. Individuals with experience using adaptive dynamics, game theory or quantitative genetics are especially encouraged to apply.

Application deadline is November 1, 2009. Position will remain open until filled. In the cover letter, applicants are asked to describe their theoretical background and experience with mathematical modeling explicitly. Please submit a curriculum vitae, brief statement of research interests, up to 3 relevant manuscripts and contact information for 3 references to Suzanne H. Alonzo by email(Suzanne.Alonzo@Yale.edu). Please put: "Sexual Selection and Social Evolution Postdoc" in the subject line.

Yale University is an Equal Opportunity/Affirmative Action Employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

"Suzanne H. Alonzo" <Suzanne.Alonzo@Yale.edu>

WorkshopsCourses

Lyon ComparativeGenomics Jan18-29

Dear all,

We are happy to announce that the registration for the 3rd edition of our European Course on Comparative Genomics in Lyon (France) is now open.

Our course will be held at ENS Lyon from January 18 to 29, 2010.

It will cover the following topics: Transposable elements and genome evolution, The origin of new genes, Comparative epigenomics, Evolutionary genomics of the origin of humans, Genome and phenotype, Recombination and genome evolution, Sex chromosomes and sex determination, From phylogenetics to phylogenomics, Microbial genomics

Confirmed speakers include D Charlesworth, M Schartl, L Duret, S Glemin, M Gouy, E Douzery, E Green, L Quintana Murci, M Joron, M Robinson-Rechavi, E Lerat, JN Volff, A McLysaght, E Rocha, G Fischer, G Yvert, V Colot.

All teaching is in English.

We will accept 30 students. Priority will be given to Master students. The course is open to students from all the European universities.

Registration is free but required and will close on November 27. Results will be released a couple of days later.

More details at http://lbbe-dmz.univ-lyon1.fr/spip_cg/ Best regards,

Gabriel Marais & Jean-Nicolas Volff

Dr Gabriel Marais

Bioinformatics and Evolutionary Genomics Biometry and Evolutionary Biology Dpt. (UMR 5558) University of Lyon 1 Mendel's building, 16 rue Raphael Dubois 69622 Villeurbanne cedex France

Tel: (+33) (0) 4 72 43 29 09 Fax: (+33) (0) 4 72 43 13 88

Email: marais@biomserv.univ-lyon1.fr Web site: http://lbbe.univ-lyon1.fr/ Gabriel Marais <gabmarais@gmail.com>

Nicaragua Biodiversity Jan1-10

Dear community,

a colleague asked me to distribute this:

Freshwater Tropical Biology: Field Techniques in Biodiversity Monitoring

1-10 January, 2010

FUNDECI/GAIA (www.gaianicaragua.org)

Topics covered:

1. What is important about wild plants and animals? 2. Vegetation monitoring - structure and composition 3. Biology of tropical freshwater fishes 4. Fish identification tools and techniques 5. Fish monitoring techniques-netting and in situ observation 6. Fish dietary analysis 7. Aquatic invertebrates 8. Biodiversity calculation methods and their interpretation 9. Conservation issues and actions

Field work, including netting and observations using SCUBA, will be conducted in Lake Apoyo and in Lake Xiloa, Nicaragua. We will also visit Lake Managua and Lake Nicaragua, important freshwater fisheries resources and habitats for dozens of endemic fish species. The course coordinator, Dr. Jeffrey McCrary, has published dozens of research papers on natural resources of Nicaragua, including discoveries of several fish species. For more information, contact us at apoyo@gaianicaragua.org or call 011-505-8882-3992. Updates on the course will be provided at www.gaianicaragua.org/course1-2010.html . Sincerely, Jeffrey McCrary

Matthias Felix Geiger <matthias.f.geiger@stud.uni-muenchen.de>

SanDiego ConservationGenomics Jan9-13

Plant and Animal Genome XVIII International Conference Population and Conservation Genomics Workshop http://www.intl-pag.org/18/18-pag.html January 9-13, 2010 Town and Country Convention Centre, San Diego, California

A workshop on Population and Conservation Genomics will be held at the Plant and Animal Genome XVIII International conference. You are invited to attend this Workshop and submit abstracts for oral presentations on any population and conservation genomics aspect of both plants and animals. The topics may include: population genomic diversity and structure; molecular evolution; adaptive molecular genetic variation; selection signatures; candidate-gene and genome-wide association studies; application of genomics in conservation and management of genetic resources; genomic effects of domestication, management practices, fragmentation, bottlenecks, climate and environment change, and transgenic deployment; and gene conservation; etc.

Six oral presentations will be selected from the submitted abstracts. Each of the first six speakers will receive a $100 discount in their registration fees. Please send your abstract of no more than 250 words by e-mail to Om Rajora (Om.Rajora@unb.ca) as an attached Word file no later than October 24, 2009. You will be notified by October 30th whether your abstract has been selected for an oral presentation. Authors whose abstracts are not selected for oral presentations are highly encouraged to present a poster at the conference.

Inquiries and Abstract Submission

For information and questions regarding the Population and Conservation Genomics workshop, please contact Om Rajora at the following coordinates. Dr. Om P. Rajora, Canada Research Chair in Forest and Conservation Genomics and Biotechnology, Faculty of Forestry and Environmental Management, University of New Brunswick, Fredericton, NB E3B 6C2, Canada. Tel: (506) 458-7477 or (506) 458-7475 Fax: (506) 453-3538 E-mail: Om.Rajora@unb.ca

Om Rajora <Om.Rajora@unb.ca>

SanDiego ConservationGenomics Jan9-13 CallAbstracts

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“Rajora, Om” <orajora@unb.ca>

SanDiego PopulationGenomics Jan9-13 FinalCallAbstracts

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Six oral presentations will be selected from the invited and submitted abstracts. Each of the first six speakers will receive a $100 discount in their registration fees. Please send your abstract of no more than 250 words by e-mail to Om Rajora (Om.Rajora@unb.ca) as an attached Word file no later than October 24, 2009. You will be notified by October 30th whether your abstract has been selected for an oral presentation. Authors whose abstracts are not selected for oral presentations are highly encouraged to present a poster at the conference.

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Om.Rajora@unb.ca

Santiago ConservationGenetics Jan12-22

*****VERSION EN CASTELLANO ABAJO*****

NOW ACCEPTING APPLICATIONS for the sixth intensive course offered by the Red de Genética de la Conservación (ReGeneC): “VI Taller de Genética para la Conservación: procesos microevolutivos en especies silvestres,” 12-22 January, 2010.

COURSE CONTENT: This unique 11-day intensive course in conservation genetics, offered in Spanish, is designed for Latin American graduate students and young professionals embarking on projects of their own applying genetic tools to conservation problems. Combining lectures, computer labs, hands-on data analysis, discussions, and student presentations, the course provides a survey of genetic, evolutionary, ecological, and statistical theory and applications, as well as the philosophical, ethical, practical, and legal issues relevant to conservation projects. Student evaluations from previous years consistently rate the high student-faculty ratio as a particular course asset, allowing in-depth formal and informal interactions that focus on individually-tailored improvement of student projects. Detailed content is available at http://regenec.ula.ve/taller/ene2010/ PARTICIPATING FACULTY: To offer a wide array of locally-relevant perspectives and examples in a unified course format, professors come from five Latin American countries (Argentina, Brazil, Chile, Mexico, and Venezuela), and have experience with a wide array of taxonomic groups. See http://regenec.ula.ve/taller/ene2010/invitados.html for this year’s faculties.

APPLICATIONS: All documents must be received by October 18, 2009. Please see “Preinscripciones,” http://regenec.ula.ve/taller/ene2010/preincripcion.html for details and scholarship availability.

COURSE HOST: This year’s course is hosted by Instituto de Ecología y Biodiversidad y la Universidad de Chile (Santiago, Chile) in collaboration with ReGeneC members. It is mainly supported by Ministerio de Planificación, from Chile, and ReGeneC.

For more information, please send an email to regenec@gmail.com or regenec@ula.ve.

VERSIÓN EN CASTELLANO

ABIERTO EL PERÍODO DE POSTULACIÓN para el sexto curso intensivo latinoamericano, ofrecido por la Red de Genética para la Conservación (ReGeneC): "*VI** **Taller** de Genética para la Conservación: **procesos microevolutivos en especies silvestres*," a celebrarse del 12-22 de enero 2010.

CARACTERÍSTICAS DEL CURSO: Es de tipo intensivo, con una duración de 11 días. Se dicta en español, con algunos elementos en portugués. Está diseñado para estudiantes de postgrado y profesionales jóvenes, que comienzan a desarrollarse en el área de la genética para la conservación y cuyos proyectos de investigación se centran en especies silvestres de América Latina. Su énfasis va dirigido a la aplicación de herramientas de genética y evolución para el entendimiento y apoyo a la solución de problemas en conservación.

Mediante la combinación de clases teóricas y prácticas (bioinformática y análisis de datos), discusiones y la presentación de proyectos por parte de los estudiantes, el curso proporciona una visión amplia sobre la teoría y práctica de genética, evolución, ecología y estadística, asícomo aspectos relevantes desde el punto de vista filosófico, ético, de manejo y legal para proyectos de conservación. La evaluación del curso, por parte de los estudiantes que han participado en ediciones previas, consistentemente resalta como un aspecto muy positivo la interacción estudiantes/profesores que tenemos en el curso, lo que permite profundizar en los diferentes aspectos tratados en el curso y en el análisis detallado de los proyectos de cada estudiante. Esto incide sustancialmente en la comprensión y mejoramiento de los proyectos postulados en el proceso de pre-inscripción. El contenido del curso está disponible en: http://regenec.ula.ve/taller /ene2010/programa.html

PROFESORES PARTICIPANTES: Para ofrecer una perspectiva amplia sobre los diferentes enfoques aplicados en genética para la conservación en América Latina, esta edición del curso cuenta con profesores, miembros de ReGeneC (http://regenec.ula.ve), provenientes de cinco países (Argentina, Brasil, Chile, México y Venezuela), con experiencia en diferentes grupos taxonómicos, tal como puede verse en: http://regenec.ula.ve/taller /ene2010/invitados.html< http://web1.ula.ve/portales/regenec/taller/ene2010/invitados.html >

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UColorado PlantEvoDevo Jan29-31

The Leaf: Integrating Evolution, Development, and Function The NSF Molecular and Organismic Research in Plant History (MORPH) Research Coordination Network is hosting the third in a series of evo- devo workshops. This intensive workshop will provide an opportunity for a select group of doctoral students and distinguished investigators in plant evolutionary developmental biology to interact. Each participant will outline critical issues associated with his/her evolutionary, developmental, and/or functional research program and there will be extensive discussion. MORPH will pay all travel, accommodation, meal expenses.

Application Deadline: November 6, 2009

Workshop dates: Jan 29th-31st, 2010

For more information, please see our website:

http://www.colorado.edu/eeb/MORPH/MORPH/Workshop_2010.html or contact William (Ned) Friedman: ned@colorado.edu

"Robert L. Baker" <Robert.Baker@Colorado.EDU>

USheffield GenomicsOfSpeciation Jan10-13

"Genetics and Genomics of Speciation" Workshop Sheffield, Great Britain 10-13 January 2010 A workshop funded by the EU Marie Curie Initial Training programme SPECIATION

Organisers: Roger Butlin, Rhonda Snook, Claudius Kerth and Allan Debelle, on behalf of the Marie Curie Initial Training Network: SPECIATION

With current large scale SNP genotyping and next generation sequencing technologies huge amounts of genetic variation can be scored accross the genome of non-model organisms. This offers new opportunities for powerful tests of evolutionary models and to find the genetic basis of population divergence, ecological adaptation and the origin of species. This workshop will mainly focus on the detection of genomic regions under selection and restricted gene flow between diverging populations using data of genomic variation. The invited speakers are some of the leading scientists in this field and include Wolfgang Stephan (University of Munich, Germany), Chris Wheat (University of Helsinki, Finland), Terry Burke (University of Sheffield), Jon Slate (University of Sheffield) and Stuart Baird (CBGP Montpellier).

15 free places for participation in the workshop are now open for application. Applications are invited from early career stage researchers and should include a CV and short statement indicating why you are interested in this workshop. 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. The application deadline is the 27th of November.

Please send applications and enquiries to Angela Wright: a.p.wright@sheffield.ac.uk

Venue: Losehill Hall, Derbyshire (between Sheffield and Manchester), we hope to provide transport from Manchester Airport and Sheffield train station to the conference centre.

More information on the workshop and updates can be found at http://speciation.group.shef.ac.uk/ The workshop follows this year's Population Genetics Group conference, Liverpool, 6-9 January, see: http://-sites.google.com/site/popgroup2010/Home .

Provisional workshop programme:

Monday, 11 January

Morning - Wolfgang Stephan (University of Munich, Germany): Genetic signatures of natural selection'

Afternoon - Chris Wheat (University of Helsinki, Finland): New generation sequencing approaches for finding genes under selection'

Evening - Terry Burke (University of Sheffield): What comes after "Next Generation Sequencing"?'

Tuesday 12 January

Morning - Jon Slate (University of Sheffield): Choosing and using SNPs'

Afternoon - Stuart Baird (CBGP Montpellier): Genes under selection in hybrid zones'

Evening - Tim Birkhead (University of Sheffield): Research ethics'

Wednesday 13 January

Morning - speaker to be announced: Experimental design'

Afternoon - outing into the Peak District National Park

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Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly 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.