EvolDir

May 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

Barcelona Sequencing2009 Oct1-3 2

Dear all, just a quick reminder with updated info on the meeting we are organizing on next generation sequencing in october Barcelona, Spain, to let you know that only 150 places are available and 80 have been filled already so if you are thinking of registering do so soon. Best regards

NEXT GENERATION SEQUENCING: CHALLENGES AND OPPORTUNITIES 1-3 october 2009, Casa Convalescencia, Barcelona, Spain http://ngs2009.uab.es REGISTRATION IS LIMITED TO 150 PEOPLE

COMMUNICATIONS: Abstracts should be submitted before July 2, some will be selected for oral presentation.

REGISTRATION: The cost is 300 and includes admission, abstract book, meals (noon), coffee breaks and farewell cocktail on saturday. The meeting will be held in Casa Convalescencia (http://www.uab-casaconvalescencia.org/).

INAUGURAL SPEAKER: Richard K. Wilson, Director of the Genome Sequencing Center, Washington University MO, USA: Sequencing the Cancer Genome

PLENARY SPEAKERS, in alphabetical order, and provisional title: - Michael Brudno, Canada Research Chair in Computational Biology, ON, Canada. Discovering INDEL and Copy Number genomic variation from short reads - Carlos Bustamante, Cornell University, NY, USA - Andrew Clark Cornell University, NY, USA. Using short-read sequencing to dissect allele-specific expression - Frank Oliver Gloeckner, Max Planck Institute for Marine Microbiology, Germany. Binning and phylogenetic classification in microbial metagenomic communities - Philip Green, University of Washington, WA, USA. Increasing throughput and data yield for the Illumina Genome Analyzer - Martin Groenen, Wageningen Agricultural University, Holland. SNP discovery and analysis of selective sweeps using massive parallel short-read sequencing - Roderic Guigó, Center for Genomic Regulation (CRG) Barcelona. Spain. The transcriptional complexity of the human genome:

Insights from Next Generation Technologies - Heinz Himmelbauer, Center for Genomic Regulation (CRG) Barcelona Spain. Plant genomics in the era of high-throughput sequencing: the case of the sugar beet - Michael Lynch, Indiana University IN, USA. Inferences on population- genetic parameters derived from likelihood analysis of high-throughput sequencing data - Gabor Marth, Boston College, MA, USA. Informatics tools for next- generation sequencing analysis - Gil McVean, Statistics Department, Oxford, UK. The 1000 Genomes Project - Douglas B. Rusch, Craig Venter Institute, MD, USA. Advances in Sequencing Technology and the Global Ocean Survey Expedition - Henk Stunnenberg, Nijmegen Center for Molecular Life Sciences, Holland. Aberrant DNA methylation in cancer: next generation sequencers provide genome wide views - Francisco M. De la Vega, Applied Biosystems, USA. Understanding human genetic variation at the personal and population level through massively-parallel whole-genome sequencing - Wang Jun, Beijing Genomics Institute at Shenzhen, China. Sequencing, sequencing and sequencing -

INSTITUTIONAL SPONSORS Fundación Genoma España: http://www.gen-es.org/ Ministerio de Ciencia e Innovación: http://www.micinn.org/ Universitat Autònoma de Barcelona: www.uab.cat MAIN PRIVATE SPONSORS Applied Biosystems: http://solid.appliedbiosystems.com Illumina: http://-www.illumina.com/ Roche: http://www.roche-applied-science.com/ REST OF SPONSORS Keygene: http://www.keygene.com Sistemas genomicos: http:/-/www.sistemasgenomicos.com/general_eng/index.php Miguel Perez-Enciso ICREA professor Dept. Ciencia Animal i dels Aliments Facultat de Veterinaria Universitat Autonoma de Barcelona 08193 Bellaterra, SPAIN Phone: +34 93 581 4225 Fax: +34 93 581 2106 miguel.perez@uab.es http://www.icrea.cat/-Web/ScientificForm.aspx?key=3D255 Come to the next generation meeting: http://ngs2009.uab.es Sebastian E. Ramos-Onsins, PhD Ramon y Cajal Research Position Consorci CSIC-IRTA-UAB (CRAG) Centre for Research in Agricultural Genomics

Dept. Ciencia Animal i dels Aliments Off. 208 Facultat de Veterinaria Universitat Autonoma de Barcelona 08193 Bellaterra, SPAIN

Phone: +34 93 581 4225 Fax: +34 93 581 2106

email: Sebastian.Ramos@uab.cat Skype: sebasramos

Join us to the Next Generation Meeting 2009 at Barcelona http://ngs2009.uab.es sebas@ramos.net

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Belgium Darwinism Apr28-30

Darwinism and the Specificity of Human Nature

INTERNATIONAL SYMPOSIUM 28-29-30 April 2009

Auditoire SOCRATE 10 Place du Cardinal Mercier 10-12 Louvain-la-Neuve Belgium

Darwinian theory displays a continuous scientific fecundity in fields such as neurobiology. The bicentenary of Charles Darwinâs birth is an occasion to assess the present state of knowledge. Political and religious dimensions are involved with Darwinism. Religious groups regularly dispute the freedom of education and research relating to the theory of evolution. The progress of the anti-evolution lobby in Europe is a matter of concern. Is the theory of evolution incompatible with faith in a divine dimension of creation? Why is this theory the target of religious fundamentalists? The aim of this colloquium is to put forward the issue of the specificity of the human nature at the crossroad of human and religious representations. Indeed, Darwinian theory inscribes mankind into the history of life and addresses the questions of origins and identity from a new point of view.

Participation is free, but registration is required. information: secretaire-teco@uclouvain.be or http://-www.uclouvain.be/darwin.html Tuesday, April 28th

20:00 Opening conference - Chair Marc Crommelinck

Christian de Duve Emeritus professor UCL and Rockefeller University, New York Nobel Prize in Medicine - 1974

Â« Ã lâÃ©coute du vivant Â»

Wednesday, April 29th

Morning : Darwinism : descent and avatars

Chair : Pierre-Joseph Laurent

09:00 Welcome speech Armand Spineux

09:05 Introduction BenoÃt Bourgine

09:20 Darwinism and ideology Dominique Lecourt

10:00 Darwinism and religion : theological considerations FranÃEuvÃ©

10:40 Coffee

11:00 Nature, culture in building social relationships of kinship Maurice Godelier

11:40 Roundtable 12:15 Lunchtime

Afternoon â“ Determinism vs. chance

Chair: Thierry Hance

14:30 Evolution, auto-organization and selection Stuart Kauffman

15:10 Science and religion John Haught

15:50 Coffee

16:10 Roundtable with the participation of Christian De Duve

17:30 Academic session chaired by professor Bernard Coulie Rector of UCL Conferment of Honoris Causa Ph.D.

By the Faculty of Medicine and the Faculty of Philosophical Sciences To professor Gerald Edelman Nobel prize in Medicine 1972

By the Faculty of Theology To professor John Haught

By the Faculty of Psychology and Sciences of Education to professor Marc Jeannerod

by the Faculty of Sciences and Faculty of Bioengineering to professor Stuart Kauffman

19:00 Reception

Thursday, April 30th

Morning- Humanization

Chair : Dominique Lambert

09:00 How did the brain become human ? Philippe van den Bosch Sanchez de Aguilar

09:40 Cognitive psychology and Darwinism

Xavier Seron and Marc Crommelinck

10:20 Coffee 10:40 The end of human exception

Jean-Marie Schaeffer

11:20 Roundtable

12:00 Lunchtime

Afternoon - Conscience

Chair : Xavier Seron

14:00 Neuronal darwinism Gerald Edelman 14:50

Sensorial and motor foundations of consciousness

Marc Jeannerod 15:30 Coffee 15:50 Neurosciences and philosophical anthropology

Bernard Feltz 16:30 Roundtable

17:30 Concluding speech AndrÃ© WÃ©nin

Prof. Thierry Hance UnitÃ© d'Ã©cologie et de biogÃ©ographie Centre de recherche sur la BiodiversitÃ© Place Croix du Sud, 5 1348, Louvain-la-Neuve, Belgique TÃ©l.: 32 10 47 34 93 Fax: 32 10 47 34 90 Attention: changement d'adresse mail! thierry.hance@uclouvain.be http://www.ecol.ucl.ac.be thierry.hance@uclouvain.be thierry.hance@uclouvain.be

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BrownU GenomicsEnvChange Jun8-11

The American Genetic Association 2009 Symposium on "The Genetics and Genomics of Environmental Change" will be held at Brown University in Providence, Rhode Island 8-11 June 2009

Providence is widely recognized as the Venice of southern New England and is very pleasant in June.

Abstract submission, registration and other details are available at the following website:

http://www.brown.edu/Departments/EEB/aga/ The program is open to everyone for poster presentations.

Invited Speakers include: Bill Bradshaw, University of Oregon John Colbourne, Indiana University George Gilchrist, College of William and Mary Elizabeth Hadly, Stanford University Ary Hoffmann, University of Melbourne/CEASAR Trudy Mackay, North Carolina State University Margie Oleksiak, University of Miami Outi Savolainen, University of Oulu Paul Schmidt, University of Pennsylvania Annie Schmitt, Brown University Jay Storz, University of Nevada Andrew Whitehead, Louisiana State University

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

Egypt DarwinLegacy Nov14-16

Darwin Now

Darwin Now Conference: Darwin's Living Legacy

Bibliotheca Alexandrina 14 - 16 November 2009

A conference organised by the British Council and the Bibliotheca Alexandrina, Egypt

The Darwin Now Conference will take place at the Bibliotheca Alexandrina, Egypt from 14 - 16 November 2009. The Programme Committee invites papers from a broad range of disciplines including: Science, History of Science, Philosophy of Science, Social Sciences, Education, The Arts and Media.

The conference will be arranged around three strands:

1. Cutting Edge Evolutionary Science Current research focusing on: Genetics; Genomics; Speciation; Origin of Adaptation; Epigenetics; Evolutionary Microbiology; Molecular Biology; Evolutionary Ecology; Biodiversity

2. Applications of Evolutionary Science Agriculture and Plant Sciences; Biomedicine; Engineering; Anthropology; Economic development.

3. Social and Cultural Impacts of Darwinism and Evolution Historical debates; Reception of Darwinism across cultures; Evolution and Education; Evolution and Ethics; Science, Religion and Society.

We would like to encourage papers from the following areas:

1. Evolution in the post-Genomic Era 2. Speciation and adaptation 3. Microbiological implications for evolutionary sciences 4. Issues in Biodiversity and evolutionary ecology 5. Epigenetics 6. Evolution at the molecular level 7. Evolutionary psychology 8. Agricultural applications of evolution 9. Biomedical applications of evolution 10. Evolution across the disciplines 11. History and reception of Darwinism 12. Evolution and religion 13. Ethics in light of evolutionary approaches 14. Debates in Science Education 15. What is science - evolutionary scientific method 16. Darwinism in the Arts (including literature) 17. Darwin and the Media - how should we communicate Darwinism and evolution Proposals for individual papers should include an abstract of no more than 250 words with no footnotes and be comprehensible to a non-specialist audience. Papers will be 15 - 20 minutes long. Paper submissions should be accompanied by biographies for all speakers. Poster Proposals should normally consist of an abstract of no more than 250 words with no footnotes and be comprehensible to a non-specialist audience.

All prospective participants should submit:

* An abstract of no more than 250 words with no footnotes and comprehensible to a non-specialist audience.

* Full contact details

* A short biography of no more than 250 words.

* Details of any specific audio visual requirements for your talk

Your proposal should be sent as a single electronic document.

In order that we can publicise the conference as effectively as possible, we will assume that in submitting an abstract, each participant is granting us the right to publish its content on the conference website and elsewhere: if you do not wish your abstract to be publicised, please advise us explicitly. Where appropriate, we may contact you seeking further information for use in conference press releases. The deadline for submitting a paper, session, or poster will be 1 June 2009. The conference programme will include parallel themed sessions, plenary lectures, education and outreach activities, and a conference dinner. Bursaries will be available to cover travel costs and accommodation. There will be a separate application procedure for bursaries once abstracts have been accepted. However, please indicate when submitting your abstract if you will be applying for a bursary. We would like to encourage paper and poster proposals from early career academics. Proposals should be sent electronically to: BAconfDarwin@britishcouncil.org Or by post to: Darwin's Living Legacy Conference (Darwin Now) British Council Bridgewater House 58 Whitworth Street Manchester, M1 6BB UK Please note that all conference participants must register for the conference in order to be included in the conference programme. Enquiries concerning this conference should be directed to: BAconfDarwin@britishcouncil.org For further information about the British Council Darwin Now project, please go to: www.britishcouncil.org/darwin Hayley.Foulkes@britishcouncil.org

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IowaCity SMBE 2009 Jun3-7 NextGenerationSeqSymposium

Dear all,

DEADLINE FOR ABSTRACT SUBMISSION TO THE SMBE CONFERENCE IN IOWA CITY HAS BEEN POSTPONED TO APRIL 5TH!

You are still in time to submit abstracts for posters and oral presentations to the Symposium on:

"Impact of Next Generation Sequencing on the Study of Evolution"

DESCRIPTION OF THE SYMPOSIUM: Over the past years DNA sequencing technology has undergone massive improvements. The introduction of the so-called next- and next-next generation sequencing technologies has finally allowed to process millions of DNA sequences in a massive, parallel and miniaturized fashion (for reviews see Shendure J et Ji H, Nat Biotechnol, 26(10):1135-45, 2008 and Mardis ER, Annu Rev Genomics Hum Genet, 9:387-402, 2008). Not only these methods represent technological innovations in terms of increased throughput and reduced costs, but, more importantly, they are dramatically changing the way of planning experiments, opening new areas of investigation. The resulting impact on evolutionary genomics is enormous: applications range from sequencing of ancient genomes to intra-population variability, from ecological diversity to mutational dynamics of cancer cells. For the innovation, the number and the variety of involved areas, we propose a symposium dedicated to unravel the impact of next-generation sequencing on evolutionary biology. The aim of the symposium will be twofold: from one side it will disclose the new perspectives offered by these approaches, while from the other it will face the experimental and computational challenges of correctly treating the data (including potential error sources, data handling and validation methods). Such a symposium will be intersecting and complementary to other already accepted symposia (e.g. Mutation accumulation in eukaryotic genomes and Population genomics, to name two), helping to expand the technological and applicative aspects.

CONFIRMED SPEAKERS:

- Mike Snyder, Yale University - Florian Kuchenbauer, Terry Fox Laboratory Canada

MEETING WEBSITE: http://smbe2009.org CONTACTS: - Francesca D. Ciccarelli, European Institute of Oncology Milan, Italy francesca.ciccarelli@ifom-ieo-campus.it - Anna De Grassi, European Institute of Oncology Milan, Italy anna.degrassi@ifom-ieo-campus.it

Hope to see you in Iowa City!

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

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IowaU SMBE2009 EpigeneticsEnvironmentEvolution Jun3-7

Hello all,

This is a renewed invitation for submission of abstracts for oral and poster presentations for the symposium on

"Epigenetics, Environment, and Evolution (EEE)"

during the annual meeting of the Society for Molecular Biology and Evolution at Iowa City, IA, USA (June 3-7, 2009).

6 15-minute slots will be available for contributed talks. Empirical studies on any system pertaining to the theme of the symposium are particularly encouraged for submission, so are some reviews with more theoretical components.

The deadline for abstract submission for consideration as a contributed talk has been changed to April 5th (all abstracts received after April 5th will be posters), but the deadline for early registration is still April 1st. For more general information about the meeting please go to http://ccg.biology.uiowa.edu/smbe/ . Again, I would also like to invite all the other evolutionary biologists to come to this symposium during the SMBE2009 meeting, particularly if you have had enough fun in the innumerable parties for Darwin this year and just want some fresh air.

Looking forward to seeing you at Iowa City!

"Epigenetics, Environment, and Evolution (EEE)" Symposium Description:

Traditionally, the molecular study of evolution has been focused on DNA sequence variation. This is convenient, and it is also based on the dogmatic belief that has developed since the discovery of the double-helix structure of DNA, which is, any evolutionary change must be based on mutation at DNA sequence level. This is a grossly simplified understanding of biology and a rather outdated view about life. In the last decade, increasingly more evidences have revealed that epigenetic changes, i.e., modifications of nucleotides (e.g., methylation of cytosine) and/or histones (acetylation, methylation, etc.) without any change at DNA sequence level, particularly under the influence of the environment, could dramatically alter important life traits and such alteration is heritable at least to some degree. Increasingly more evidences suggest epigenetic regulation may have played fundamental, rather than just supplemental, roles in development (e.g., cell differentiation), adaptation to environment, and diseases (like the occurrence of cancer). All these suggest possibly important roles played by epigenetics and the environment in biological evolution. A symposium about the relationship between epigenetics, environment, and evolution is due, particularly in this year of Darwin. In this symposium, the roles played by the environment and epigenetics in evolution will be addressed with respect to both molecular mechanisms and theoretical implications. Specific topics would include: (1) Can epigenetic changes alter important phenotypic traits? (2) How can the environment affect a genomes epigenetic state? (3) Are epigenetic alterations by the environment and subsequent phenotypic changes inheritable? (4) What does this mean for evolutionary theory?

Organizer:

Xianfa Xie Department of Biology, Brooklyn College, The City University of New York, Brooklyn, NY, USA

xianfaxie@brooklyn.cuny.edu

p.s. Please kindly forward this email to those who you know might be interested in this symposium but not on the evoldir email list (like some molecular biologists who have interests in mechanisms of evolution). Thanks!

Xianfa Xie <xiexianfa@gmail.com>

KansasCity ArthropodGenomics June11-14 Reducedregistration

Dear Colleagues, Print < http://www.k-state.edu/agc/symp2009/Update_ArthropodGenomicsSymposium.pdf > this e-mail from a PDF

In recognition of the current economic environment, we are lowering registration to attend the 3rd Annual Arthropod Genomics Symposium. Register by May 15, and pay only $345 ($175 for graduate and undergraduate students). Registration fees include a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and breakfast on Sunday. After May 15, the registration fee is $395 ($225 for students).

Other important deadlines: *Poster Abstract Submissions: Friday, May 15 *Hotel Reservations: Thursday, May 21, or until room block is filled

SYMPOSIUM WEBSITE: www.k-state.edu/agc/symp2009 Register at http://www.k-state.edu/agc/symp2009/register.html and attend Frontiers in Arthropod Genomics June 11 - 14, 2009, Kansas City, USA

WORKSHOPS and SEMINARS:

* Pre-symposium workshop on Chado Databases and Integration with GMOD Tools, Scott Cain, Ontario Institute for Cancer Research * Genomic Sequence Capture and Next-Gen Sequencing Seminar, sponsored by Roche NimbleGen * BeeSpace demonstrations

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

SYMPOSIUM PROGRAM: The symposium sessions will begin Thursday evening, June 11, and continue on Friday and Saturday, with additional events on Saturday evening and Sunday morning. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Workshops will be held Thursday prior to the Symposium and Friday evening. Activities will conclude by noon on Sunday, June 14.

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

KANSAS CITY JAZZ AND BBQ: Participants are invited to enjoy Kansas City's best BBQ - Fiorella's Jack Stack Barbecue and the Kerry Strayer Jazz Trio on Saturday night. The separate charge for this optional activity is $50 ($25 for students). Transportation will be provided.

KEYNOTE SPEAKER:

*William M. Gelbart, Harvard University,

"Opportunities & Challenges for Arthropod Genomics and

Informatics in the NextGen World."

FEATURED SPEAKERS:

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

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

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

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

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

* Kristin Michel, Kansas State University, "Mosquito salivary gland interactions with malaria parasites"

* Terence Murphy, National Center for Biotechnology Information/NIH, "Arthropod genome support at NCBI and the challenges of annotating genomes in the 21st century"

* Marcelo Ramalho-Ortigao, Kansas State University, "Sand fly functional genomics and beyond"

* Yoonseong Park, Kansas State University, "Evolutionary processes of the partnership between neuropeptides and their receptors"

* José Ribeiro, Laboratory of Malaria and Vector Research, NIH/NIAID, "An insight into the spitome of the blood sucking Nematocera"

* Denis Tagu, French Nat'l Inst. for Agricultural Research, Rennes, France, "Using the pea aphid genome to study phenotypic plasticity"

* Doreen Ware, Cold Spring Harbor Laboratory, "Annotation and comparative analysis of plant genomes"

* Stephen K. Wikel, University of Texas Medical Branch, Galveston, "Tick-host-pathogen research in the post-genomic era"

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

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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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Leiden FlowerSystematics Aug10-14

Symposium: Flowers on the tree of life as part of Systematics, a conference organized by the Federation of European Biological Systematic Societies.

Conveners: Livia Wanntorp, Louis Ronse De Craene Location: Leiden, The Netherlands, August 10-14th, 2009.

Visit www.biosyst.eu for submission of abstracts for posters and possibly talks.

Theme: Molecular studies during the latest decades, today we have a much clearer idea about the phylogenetic relationships of the flowering plants. This improved phylogenetic framework offers an increased opportunity to test phylogenetic hypotheses on the evolution of morphological characters of flowers. A detailed understanding of morphological characters provides the basis for evo-devo studies, particularly in the recognition of homologies of structures and their transformation series. This symposium welcomes contributions on floral ontogeny, morphology, and anatomy and their relationship to phylogenetics. The importance of floral character coding and the use of trees are highlighted.

The list of speakers is almost complete, but we encourage applications of preferably students for a talk or for a poster.

Preliminary list of speakers: Dennis Stevenson, Floral morphology and development in the age of phylogenetics and genomics. Sophie Nadot. Using a supertree to explore the evolution of androecium in palms. Dmitry Sokoloff, Patterns of diversity of polymerous gynoecia in eudicots and monocots. Paula Rudall, A new spin on flowers? The significance of centrifugal (basipetal) organ formation. Richard Bateman, Flowers of angiosperms and non-angiosperms. Peter Endress, Flowers: From alpha- to omega-morphology. Maria von Balthazar, Early diversity of lauralean flowers. Jim Doyle, Tracing the evolutionary diversification of the flower in basal angiosperms. Gerhard Prenner, Acacia celastrifolia: an enigmatic mimosoid legume with multiple carpels and more than 500 stamens per flower. Alexander Vrijdaghs, the homology concept and floral ontogeny.

More info from L.ronsedecraene@rbge.ac.uk or livia.wanntorp@nrm.se

– The Royal Botanic Garden Edinburgh is a Charity registered in Scotland (No SC007983)

Louis Ronse de Craene <L.RonsedeCraene@rbge.ac.uk>

London e-Biosphere09 June

A new Conference Update has been released for e-Biosphere 09. It announces the extension of the discounted early conference registration fee until 15 April 2009 and highlights several of the keynote speakers.

To view an online version of the Conference Update, please click the link below.

http://ukimages.images11.com/rwcode/-content.asp?SID=6&SiteID=9459&Sectio n368&EmailID450112&HitID=0 <http://-/ukimages.images11.com/rwcode/-content.asp?SID=6&SiteID=9459&Secti on368&EmailID450112&HitID=0>

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 <blocked::mailto:SchindelD@si.edu>

CBOL WEBSITE: http://www.barcoding.si.edu <blocked::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 20013-701

“Schindel, David” <schindeld@si.edu>

Marseilles 13thEBM acceptedabstracts

Dear all,

We are pleased to inform you that the first accepted abstracts of the 13th Evolutionary Biology Meeting at Marseilles are now available on our website: http:/-/sites.univ-provence.fr/evol-cgr/index.phpoption=-com_content&view=article&id=36&Itemid All the best,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

PortlandOregon SSB 2010 CallSymposia

Society of Systematic Biologists Call for 2010 Symposia

Evolution Meeting Portland State University Portland,Oregon 25-29 June, 2010.

The Society of Systematic Biologists invites proposals for symposia at the 2010 Evolution meeting to be held in Portland, Oregon, from 25-29 June 2010. The meeting will be held jointly with the American Society of Naturalists and the Society for the Study of Evolution, and our host is Portland State University.

Proposals should include (1) a descriptive title, (2) one or two paragraphs explaining the purpose of the symposium and its relevance to systematics, (3) a list of presentations including proposed speakers, their institutions or affiliations, and their presentation titles, (4) an indication of whether the speakers have been invited and whether they have agreed to participate, and (5) the proposed length of each talk. Symposia are restricted to half-day sessions. The society is particularly interested in symposia whose topics do not overlap with those from previous meetings (see SSB website for past symposia), that introduce new ideas or synthesize important concepts, or those that are particularly good examples of the analysis of empirical data. Proposals that unite systematics with other fields are also desirable. We encourage participation from young investigators and others typically under-represented in symposia.

Proposals will be evaluated at the SSB Council meeting during the 2009 annual meeting in Moscow, Idaho. Soon after, organizers will be notified of the status of their proposals. Selected symposia will receive funds to partially defer participant costs or honoraria.

Proposals should be submitted by email to the Program Chairperson: Kelly R. Zamudio Department of Ecology and Evolutionary Biology Cornell University Ithaca, NY 14853 Email: kelly.zamudio@cornell.edu

Phone: 607 254 4212

krz2@cornell.edu krz2@cornell.edu

Rennes France EvolutionaryBiol Jun8-12

The Departments of Environmental biology and Evolutionary Biology of the University of Rennes1 (UMR-CNRS ECOBIO), are organizing an international conference

"Evolutionary biology 2009: Phylogeny, speciation, co-evolution, development, genomes, life histories, plasticity& What is new?"

The conference will address major questions in evolutionary biology and will be held in Rennes, Britanny, France, from 8 June to 12 June 2009. The conference will address a wide variety of problems, including speciation, co-evolution, evolution of sex, constraints and Bauplan evolution, genome evolution, sexual selection, evo-devo and reconstruction of phylogenies .

Attached are the program and the registration form

Scientific and organizing committee:

Prof Jacques van Alphen- Marie Curie Chair, UMR ECOBIO, University of Rennes 1 and University of Leiden Dr Joan van Baaren- University of Rennes 1 Dr Malika Ainouche- University of Rennes 1 Dr Jean-Christophe Simon, INRA UMR BIO3P, Rennes Dr. Manuel Plantegenest, Agrocampus Ouest, UMR BIO3P Dr. Yannick Outreman, Agrocampus Ouest, UMR BIO3P Dr. Marie-Agn??s Coutellec, INRA Rennes, UMR ESE Dr. Christine Paillard, UMR CNRS 6539, Institut Europ??en de la Mer, Plouzan?? Dr Fr??d??ric Jean, MC, UMR CNRS 6539, Institut Europ??en de la Mer, Plouzan?? Prof Yves-Marie Paulet, UMR CNRS 6539, Institut Europ??en de la Mer, Plouzan?? Prof Jean Laroche, UMR CNRS 6539, Institut Europ??en de la Mer, Plouzan?? Dr Val??rie Stiger, LEBHAM, Institut Europ??en de la Mer, Plouzan??

M. L. AINOUCHE Evolution des Genomes et Speciation, Equipe MOB (Mecanismes ?? l'Origine de la Biodiversite) UMR CNRS 6553 Ecobio, Universite de Rennes 1 - CAREN Campus Scientifique de Beaulieu, Bat. 14A 35 042 Rennes Cedex France Ph. 33 (0)2 23 23 51 11 Fax 33 (0)2 23 23 50 47

Malika Ainouche <Malika.Ainouche@univ-rennes1.fr>

Richmond SystemsBiol Jun16-19

Abstract submission deadline: May 7, 2009

SUMMIT ON SYSTEMS BIOLOGY 2009: The Microbial World and Beyond June 16-19, 2009

The Third Annual Summit on Systems Biology will be held on June 16-19, 2009, in historic Richmond, Virginia located two hours south of Washington, DC. The Summit is comprised of five scientific sessions and two workshops to bring together computational and experimental scientists in the area of microbial systems. The third summit will discuss research directions and latest findings in the "omics" domain, as well as promote collaborations in microbial systems biology and related disciplines. Dr. Leroy Hood, Director of the Institute for Systems Biology, and Dr. Stuart Kauffman, of the University of Calgary, and a recipient of the MacArthur Foundation Award, and Albert-László Barabási, Director, Center for Complex Network Research, Northeastern University, all pioneers in Systems Biology, are members of the Summit Steering Committee.

The five scientific sessions are:

- Microbial Engineering - Metagenomics and Microbial Ecology - Host-Pathogen Interaction - Human Microbiome - Technological Advances in Systems Biology

The two workshops are:

- Tree of Life and Microbial Systems Biology - Gene Networks and Diseases

Program Design The three day program is divided into five (5) main sessions and two (2) workshops. The workshops will be held on the day preceding the formal opening of the conference. Web will also host two poster sessions, one for students and one for more senior researchers. There will be a New Technology Workshop as a pre-conference event, in concert with the student poster session on Tuesday evening, June 16. Instrument manufacturers will provide presentations and virtual demonstrations on the latest technology and applications.

Technical Symposia

Session I: Microbial Engineering The first session provides a broad overview of synthetic biology, systems biology and biological engineering and their applications to health, clean and renewable energy, and the environment. Specific topics include synthetic gene networks and the biosynthetic capacity of microbial systems. This session brings together a diverse group of participants from a variety of disciplines.

Session II: Metagenomics and Microbial Ecology The second session of the summit highlights the latest developments in our understanding of the emergence and evolution of pathogenic and non-pathogenic microbes with a particular emphasis on insights gained through genomic analyses of microbial communities.

Session III: Host-Pathogen Interactions The third session focuses on how innovative approaches and high-throughput techniques are used to study the complex interactions between bacterial pathogens and their eukaryotic hosts. Participants studying a range of pathogens using various host systems come together to discuss integrated systems approaches.

Session IV: Human Microbiome The fourth session provides the opportunity to discuss the latest advances in sequencing the human microbiome. The session underlines the importance of the metabolic function of microbiota and the role of symbiosis in health and disease.

Session V: Technological Advances in Systems Biology The final session focuses on how emerging technologies are driving advances in metagenomics, transcriptomics, proteomics and metabolomics at the microbial community level. The session features cutting-edge research on quantitative mass spectrometry and the latest advances in DNA sequencing.

Interactive Workshops

New Technology Workshop This event will involve presentations on the latest technology and applications by instrument manufacturers and active researchers on the opening evening of the conference, and will be held concurrently with the student poster session and reception.

Workshop I: Gene networks and disease The past decade has witnessed an exponential growth of biological data including genomic sequences, gene annotations, expression and regulation, and protein-protein interactions. We will include discussions on the relationship between oral pathogens and cardiovascular disease, with special interest in the virulence of Streptococcus sanguinis. This workshop focuses on the reconstruction and analysis of gene networks and pathways of human pathogens and their application to disease.

Workshop II: Assembling the Microbial Tree of Life During the 21st century, the advances on microbial systems biology will be closely tied to phylogenomics approaches to unravel the evolutionary relationships of the microbial world. By involving an interdisciplinary group of scientists and students from outside the tree of life community, including mathematicians, statisticians, clinicians, computer scientists, chemists, physicists, and engineers, the workshop will

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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

Rome Darwin2009 Emotions Apr27-29

In the occasion of the 200th anniversary of the birth of Charles Darwin and the 150th anniversary of the publication of his most important work, The origin of species, the Istituto Italiano di Antropologia in collaboration with the Università di Roma La Sapienza, organizes the Congress

Darwin 2009: emotions from an evolutionary perspective.

Our aim is to highlight the importance of the evolutionary processes of emotions and expressions, both for hominization (our yesterday) and communication (today). This issue is perfectly in line with the considerable development of neurosciences and connected areas in recent times (e.g. ethical and bio-ethical aspects) and which will continue to be the centre of attention also in the future. In order to reach this objective, various approaches and scientific theories (anthropological, biological, psychological and philosophical among others) will be presented, in order to encourage a synthetic and interdisciplinary vision. The Congress aims to involve not only researchers and university students, and the general academic world, but also the general public in the diffusion and sharing of knowledge.

The speakers list includes:

Bernardino Fantini (President of the Istituto Italiano di Antropologia, Université de Genève), Randolph M. Nesse (University of Michigan), Telmo Pievani (Università di Milano Bicocca), Alexander Rosenberg (Duke University), Michael Ruse (Florida State University), Klaus Scherrer (Université de Genève), Elliot Sober (University of Wisconsin).

The Congress Darwin 2009: emotions from an evolutionary perspective will take place on:

27 April Aula Magna, University of Roma La Sapienza

28 and 29 April Aula Gini, Faculty of Statistics of the University of Roma La Sapienza.

Attendance to the Congress is completely free. A certificate of attendance may be required during the Congress.

Please refer to our web site http://www.isita-org.com/Darwin2009/index.htm for further information and to info_darwin2009@isita-org.com for any queries.

"darwin2009@isita-org.com" <darwin2009@isita-org.com>

SanDiego ASM EvolutionaryMicrobiol May2010

*CALL FOR **SYMPOSIA* *PROPOSALS American Society for Microbiology Division R, Evolutionary & Genomic Microbiology 2010 General Meeting San Diego, CA May 23-27, 2010*

*ASM **Division R, Evolutionary and Genomic Microbiology*, is now soliciting suggestions for symposia to be presented at the 2010 ASM General Meeting to be held in San Diego in May, 2010.

To propose a symposium that represents a theme of broad interest within Division R, please provide the following:

1. A title for the session. 2. Convenor(s) 3. A description of the session in paragraph format. 4. Speakers with affiliations, titles and topics for the session. List five potential speakers and one or two alternative speakers. 5. Similar sessions in prior years if appropriate.

You may submit your ideas though the following link: http://gm.asm.org/index.php?option=com_content&task=view&id=164&Itemid=162 < http://mail.asmusa.org/t/585316/45181548/2933/0/ >.

There is a link on this page so you can check if candidate speakers have presented at a recent symposium. Although past speakers are not barred, the policy of Division R is to encourage alternative speakers where possible. In the interest of promoting the next generation of leaders in our field, organizers are also encouraged to include promising junior faculty in their program.

Note that this is a call for proposals only. Travel arrangements should NOT be made with potential speakers until you are notified that the proposal has been accepted by the ASM General Meeting Planning Committee. Proposals will be reviewed by divisional officers at the 2009 ASM General Meeting in Philadelphia; their recommendations will then be forwarded to the Planning Committee for final approval.

Proposals must be submitted by *May 11, 2009.*

Thanks very much. Sincerely, David Guttman

David S. Guttman Chair, ASM Division R, Evolutionary & Genomic Microbiology Professor Canada Research Chair in Comparative Genomics Director, Centre for the Analysis of Genome Evolution & Function Department of Cell & Systems Biology Department of Ecology & Evolutionary Biology University of Toronto

dsgutt@gmail.com

SantFeliu Spain DarwinEvolution Sep15-20

The European Science Foundation (ESF< http://www.esf.org/ >), in partnership with COST European Cooperation in Science and Technology< http://www.cost.esf.org/ >:

COMPLEX SYSTEMS AND CHANGES: DARWIN AND EVOLUTION - NATURE-CULTURE INTERFACE Hotel Eden Roc, Sant Feliu de Guixols, Spain 15-20 September 2009 Chaired by: Roland Pochet - UniversitÃ© Libre de Bruxelles, BE & Alain Peyraube - CNRS/EHESS, FR

Our closing date for application is the 3rd of July, 2009.

This conference is part of the 2009 ESF Research Conferences Programme and is accessible online from www.esf.org/conferences/09309< http://www.esf.org/conferences/09309 >.

Kind regards, Corinne Wininger Communications Officer - ESF Conferences

Please note that I am not in the Office on Wednesdays

European Science Foundation - Communications Unit 1 quai Lezay-MarnÃ©sia, BP 90015 67080 Strasbourg Cedex, France Phone: +33 (0)388 76 21 50 Fax: +33 (0)388 76 71 80 clemoal@esf.org<mailto:clemoal@esf.org> www.esf.org/conferences< http://www.esf.org/conferences >

Corinne Wininger - Le Moal <clemoal@esf.org>

Sheffield ComparativeGenomics Jul15-17

The Royal Entomological Society's Annual Meeting, Entomology09, includes a session on Comparative Genomics chaired by Casey Bergman (Manchester) with Jack Werren (Rochester) as invited speaker.

Abstracts for oral presentations or posters can be submitted at http://www.royensoc.co.uk/meetings.shtml, deadline 20 April.

Further details of the meeting are available via the web link. Evolutionary biologists will be particularly interested in the evening talk by Naomi Pierce (Harvard) and sessions on Chemical Ecology, Predation, Range Expansion and Insect Immunity.

Support for student attendance is available.

r.k.butlin@sheffield.ac.uk r.k.butlin@sheffield.ac.uk

UChicago DarwinAnniversary Oct29-31

The University of Chicago Celebrates the Darwin Anniversaries, October 29-31, 2009

Distinguished biologists, historians, and philosophers will gather in fall of next academic year to celebrate the Darwin anniversaries at University of Chicago. For the schedule of speakers and registration, please go to: < http://darwin-chicago.uchicago.edu. >http://darwin-chicago.uchicago.edu.

Jerry Coyne <j-coyne@uchicago.edu>

UConnecticut SequencingNonModelOrganisms Jun11-13

A conference and workshop at the University of Connecticut in Storrs to introduce participants to applications and strategies in the next generation of genome analysis in non-model organisms

Conference: June 11-13, 2009

Workshop*: June 14-15, 2009

*Limited space in the hands-on workshop is reserved for graduate students and post-doctoral trainees, by application and invitation only. Students and post-doctoral trainees do not have to attend the workshop and may register to attend the conference only.

Funds have been made available from the American Genetic Association to support attendance by graduate students and post-doctoral trainees. To learn more and to apply for AGA support, please contact: elaine.mirkin@uconn.edu

To learn more about the Conference program and to register, please visit the conference website at: http://www.regonline.com/Nextgeneration agajoh@oregonstate.edu

UIdaho SEE2009 Jun12-17 DeadlineExtended

The published deadline for talk/poster presentations at the upcoming Evolution meetings in June at U of Idaho (http:// evolutionmeetings09.org) is April 5. As several people have indicated that they need more time, we have decided to extend the deadline to April 17.

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

Olle Pellmyr Program chair, Evolution 2009

pellmyr@uidaho.edu pellmyr@uidaho.edu

UIdaho SSE2009 Deadline

Just a reminder that today is the deadline for submission of poster and talk titles for Evolution 2009, in Moscow, Idaho

On-line registration for the meetings will remain open to the day of the meetings, and walk-ins will be accepted.

For more info, see http://evolutionmeetings09.org Olle Pellmyr Program chair, Evolution 2009

pellmyr@uidaho.edu pellmyr@uidaho.edu

UIdaho SSE2009 Jun12-17 LateSubmissions

Evolution 2009 at University of Idaho is only a few weeks away, and regular submission of contributed talks and posters is now closed. Quite a few people missed the deadline, and for that reason we have arranged to reopen the registration for late submissions.

There is one change, in that we cannot promise that you will end up in the optimal session. All submissions received by the original deadline will have been sorted into sessions by topic. If there are still empty slots within an appropriate session, we will insert them. If not, we will compile talks into a session called “Late Breaking Evolution”.

To register, go the meeting website at http://www.uiweb.uidaho.edu/ evolution09/ and choose Registration on the menu.

Dr. Olle Pellmyr Program chair

Dept of Biological Sciences University of Idaho P.O. Box 443051 Moscow, ID 83844-3051 USA

phone 208.885.6807 (off) 885.8860 (lab) http://www.sci.uidaho.edu/biosci/faculty/pellmyr.html pellmyr@uidaho.edu pellmyr@uidaho.edu

UIdaho SSE2009 Jun12-17 Mentors

UNDERGRADUATE DIVERSITY AT SSE/SSB, CALL FOR MENTORS

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

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

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

Best regards, Rich Kliman

Rmkliman@cedarcrest.edu Rmkliman@cedarcrest.edu

UIdaho SSE UndergradDiversity 2

APPLICATION DEADLINE EXTENDED!

There are a few travel awards still available for the SSE Undergraduate Diversity Program, so the application deadline has been extended to 5 PM PST on Tuesday, April 7th. Travel awards cover all expenses, including airfare/transportation, lodging, food and conference registration. This is a great opportunity for undergraduates to attend and present their research at a national conference, so please forward this to any colleagues or students who might be interested.

Undergraduate Diversity at SSE/SSB 2009

For the seventh consecutive year, the Undergraduate Diversity at SSE/SSB program, funded by the Undergraduate Research and Mentoring in the Biological Sciences (URM) program at NSF, will take place at the 2009 meeting of the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB) in Moscow, ID. This year we have teamed up with staff at the National Evolutionary Synthesis Center (NESCent) to send up to 25 undergraduates to the meetings to present posters and receive mentoring from graduate students, postdocs and faculty in evolutionary biology. For full information and links to the application portal see:

http://www.oeb.harvard.edu/faculty/edwards/-community/application.html

The deadline for applications this year is April 1, 2009. However, proposals will be reviewed and accepted on a rolling basis, SO IT IS ADVANTAGEOUS TO APPLY EARLY. Applications can be made online through a special portal at the National Evolutionary Synthesis Center (NESCent) http://www.nescent.org/eog/-signup_evolution09diversity.php. Applications consist of a title, author line and abstract of the poster to be presented by the undergraduate; a one-page statement of academic interests and career goals; and a letter of recommendation. The personal statement should address how attending the Evolution meetings will help meet these goals, and should indicate whether or not the student plans to attend graduate school, if this is known. The letter of recommendation, ideally from the undergraduate's research advisor, should indicate how inclusion of the student will increase diversity of the group participants. All materials required for application can be found at the NESCent application portal. Details on selection criteria are available at the program headquarters at:

http://www.oeb.harvard.edu/faculty/edwards/-community/application.html

We can only accept applications from students who are US citizens or permanent residents. Applications will be accepted only from students registered or very recently graduated from U.S. institutions, including

Puerto Rico (i.e., no later than having finished classes during the winter or spring semesters before the meeting) and traveling to the meeting from within the US. Students demonstrating a need for funds to attend SSE/SSB will be given preference, and will be selected so that as a group, they will maximize cultural diversity among undergraduates at the meetings.

You can also contact one of the program organizers for more information:

Scott V. Edwards (sedwards@fas.harvard.edu) Richard Kliman (rmkliman@cedarcrest.edu)

at NESCent:

Jory Weintraub (jory@nescent.org)

UIowa SexRecombination May31-Jun3

UPDATE:

The deadline for abstract consideration for contributed talks has been extended to Monday April 20th, with decisions to be announced on the following week. All attendees who are not selected for a contributed talk will be automatically slated to present their work as a poster. Please note that registration fees need to be paid by April 24th to be considered for a contributed talk and/or travel award.

The above information may not be immediately reflected on the website.

"EVOLUTION OF SEX & RECOMBINATION: IN THEORY & IN PRACTICE"

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

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

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

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

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

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

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

Check the website for up-to-date information on confirmed speakers, details regarding registration, accommodation, etc.

Registration is $200 for grad students and postdocs and $300 for faculty. Registration includes the closing banquet (and keynote: Michael Lynch) to be held on the evening of June 2nd.

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

Facebook users: Join our official meeting group.

On behalf of the organizing committee,

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

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

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

UIowa SMBE 2009 AbstractDeadlineExtended

Another SMBE 2009 Deadline Extended!

We are extending the abstract submission deadline for contributed talks for four additional days (to April 5, 2009). All abstracts received by April 5th can be considered for contributed talks in both symposia-related and general-topic sessions. However, the April 1st deadline for early registration fees remains in place (see: http://ccg.biology.uiowa.edu/smbe/registration_fees.php).

The registration and abstract submission process for SMBE 2009 is a two-step procedure (see: http://ccg.biology.uiowa.edu/smbe/subform.php). Thus, you are welcome to register and pay for the meeting prior to submitting your abstract. All contributed abstracts received after April 5th will be automatically assigned to posters.

A few notes:

1. When submitting an abstract, please select the most appropriate symposium or general session for your work, as well as a second choice. See http://ccg.biology.uiowa.edu/smbe/symposia.php for up-to-date summaries of the SMBE 2009 symposia, including confirmed speakers. 2. If your work does not fit neatly into one of the symposia or general sessions, please apply for a contributed talk anyway. Selected talks will represent a wide diversity of topics. 3. A least three general (non-symposium-associated) contributed sessions will be held. However, depending on demand and available space, a few additional general sessions may be added to the program. 4. Some symposium-associated contributed sessions, if under- subscribed, will include talks on general topics. 5. We will consider adding a few additional topical sessions, as needed (e.g., transposable element evolution).

The above information may not be immediately reflected on the website.

General information on the meeting follows:

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

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

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

The SMBE 2009 scientific program will include 4 plenary talks and 23 symposia. The program will feature ˜215 talks; more than half will be contributed talks selected on a competitive basis from submitted abstracts. We anticipate that 300-400 poster contributions will be highlighted in two evening poster sessions.

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

* Biological networks from genes to populations * Epigenetics, environment & evolution * Evolution of networks * Genome evolution after polyploidy * Genomics of speciation & recent divergences * Historical roots of molecular evolution * Impacts of next generation sequencing on evolution * Insect evolutionary genomics * Molecular arms races * Molecular basis of speciation * Molecular evolution of biological complexity * Molecular evolution of functional noncoding sequences * Molecular evolution of plant:biotic interactions * Mutation accumulation in eukaryotic genomes * Origin & evolution of animal genomes * Population genomics: selection, demography & mutation * Population genomics: theory, computation & adaptation * Primate functional & comparative genomics * Reproductive protein function & evolution * Sex-specific demography us-

ing the X * Teaching molecular evolution * Types of molecular evolution * Vanishing genomes

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

–

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

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

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

UIowa SMBE2009 Xchromosome Jun3-7

This is an renewed invitation to participate in a symposium on the X chromosome at SMBE 2009 (Iowa City June 3-7):

"The X factor: analyses of sex-specific demography using the X chromosome"

We welcome talks about any research on the X chromosome, or research that compares how the X and the autosomes are differentially affected by natural selection, demographic history, or other population genetic factors.

SYMPOSIUM DESCRIPTION: In species with heterogametic males, the relative patterns of genetic variation on the X chromosome and the autosomes can reveal the signatures of sex-specific evolutionary processes related to demography and selection. With the continued development of DNA-sequencing technology, the X chromosome has become an increasingly important data source in population genetics. The X chromosome is particularly interesting to study because it possesses both independent markers (as compared to the nonrecombining Y chromosome and mitochondrial genome) and accessible haplotypes (as compared to the autosomes). Due to its method of inheritance and the prevalence of processes like polygyny, different generation time in females compared to males, bottlenecks, background selection, and hitchhiking in the histories of different species, making inferences from X-chromosomal data requires detailed modeling and careful data analysis. In the last few years, the number of papers using X chromosomal sequence data to study sex-specific demographic genomic signatures has vastly increased, making this year a timely one to hold a symposium on this topic. This symposium will provide a centralized venue to discuss results and future directions of inquiry to allow us to leverage X-chromosomal data and better understand differences in the evolutionary histories of male and female organisms.

Invited speakers include Nadia Singh, Molecular Biology and Genetics, Cornell University; and Jeff Wall, Institute for Human Genetics, University of California, San Francisco.

There will be six 15 min slots available for contributed talks. The deadline for abstract submission for contributed talks is April 5th. Poster presentations are also welcome!

Visit the meeting website (http://smbe2009.org) for further information about the conference.

Looking forward!

Sohini Ramachandran Organismic and Evolutionary Biology Harvard University

Jeff Wall Institute for Human Genetics University of California, San Francisco

Sohini Ramachandran <sramach@fas.harvard.edu>

UOxford DescentOfMan Sep2-4

The Association for the Study of Animal Behaviour: Summer Conference

The Descent of Man and Selection in Relation to Sex

2-4 September 2009

St. John's College, University of Oxford, UK

http://www.zoo.ox.ac.uk/events/asab09/ Celebrating Darwin's theory of sexual selection on the bicentenary of his birth

The scope of this summer conference is to celebrate the bicentenary of Darwin's birth, by promoting discussion on sexual selection in humans and other organisms. The conference will do this in two ways.

First, we will cover major recent developments in this rapidly-growing field by hosting a combination of plenaries from leaders in the field and research talks presenting novel work.

Second, we will celebrate the cultural revolution catalysed by Darwinian theory with a special event at the Oxford University Natural History Museum. This museum witnessed the very first debate on Darwinian theory in which Huxley and Wilberforce famously crossed swords and represents an ideal venue to consider Darwin's legacies 200 years from his birth.

Plenary speakers include: - Suzanne Alonzo (Yale University) Mating systems and reproductive strategies - Clive Catchpole (Royal Holloway, University of London) Sexual selection and bird song - Dave Hosken (University of Exeter) Sexual selection and sexual conflict - Geoffrey Miller (University of New Mexico) Sexual selection in humans - Tristram Wyatt (University of Oxford) Sexual selection and pheromones

Special Event at the Oxford University Natural History Museum "A Modern Darwinian Debate" - Pat Monaghan (University of Glasgow) - Tim Birkhead (University of Sheffield)

Conference format: - 8 speaker sessions - 1 poster session - Special event at the Oxford University Natural History Museum - Conference banquet

Key dates - Deadline for abstract submission- 19 July 2009 - Deadline for full registration o Early birds: 15 March - 31 May 2009 o Late registrations: 1 June - 17 August 2009 - Conference dates - 2nd-4th September 2009.

Organisers: Tom Pizzari, Claire Harvey & Tobias Uller

– Dr Tobias Uller Edward Grey Institute, Department of Zoology University of Oxford, OX1 3PS Tel: (+44) 01865 281194

tobias.uller@zoo.ox.ac.uk tobias.uller@zoo.ox.ac.uk

UProvidence Genomics Jun8-11

The American Genetic Association Symposium on the Genetics and Genomics of Environmental Change is fast approaching.

The dates are 8-11 June 2009, at Brown university in Providence, Rhode Island.

Details can be found on the web site:

http://www.brown.edu/Departments/EEB/aga/ Application deadline for Student travel grants has passed, but registration for the meeting and poster Abstract submission will remain open for the next two weeks.

See you in Providence

David Rand

David_Rand@brown.edu David_Rand@brown.edu

USiena Evolution Dec10-13

Dear all, please check the following congress:

EVOLUTION: INTERSECTING NATURAL AND SOCIAL SCIENCES

web: http://www.darwin.unisi.it e-mail: darwin@unisi.it

an International Congress organized by the Santa Chiara Graduate School and Pro.M Chair in Bioeconomics of the University of Siena.

The Congress will be held on 10-13 December 2009 in Siena (Italy), and will focus on three major themes at the intersection between organic evolution and social sciences:

- Bioeconomics and evolutionary mechanisms in social and natural sciences - Behavioural evolution and comparative studies of animal societies - Human nature and human culture: crossroads of evolution

In the context of Darwin bicentenary celebrations, we wish to approach his groundbreaking works trying to investigate the relationships between natural evolution and human social systems, and their possible implications for society. Both methodological and data driven presentations are welcome. The congress will include multiple sessions, invited lectures by leading researchers in each field and oral presentations by participants.

Invited speakers: Edoardo Boncinelli, University Vita-Salute and Santa Chiara Graduate School; Samuel Bowles, University of Siena and Santa Fe Institute; Luigi Luca Cavalli-Sforza, Stanford University; Michael T. Ghiselin, California Academy of Sciences and Santa Chiara Chair in Bioeconomics.

Scientific Committee: Samuel Bowles, Santa Fe Institute and University of Siena; Francesco Frati, University of Siena; Michael Ghiselin, California Academy of Science and Santa Chiara Chair in Bioeconomics; Janet Landa, York University; Ugo Pagano, University of Siena; Robert Rowthorn, University of Cambridge and Santa Chiara Chair in Bioeconomics; Lucia Sarti, University of Siena.

Additional information, session schedule and a preliminary program can be found on the Congress website, or you can e-mail us for any inquiry or to be entered in the Congress' mailing list.

Please forward this announcement to whoever might be interested or through your favourite mailing lists.

Francesco Nardi, Dr.

Dept. of Evolutionary Biology University of Siena

Master in Bioinformatics University of Siena

via Aldo Moro 2 - 53100 Siena Italy

Ph.: +39.0577.234420 (lab. 4398) Fax.: +39.0577.234476 E-mail: nardifra@unisi.it

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Zurich NicheEvolution Jul3-4 2

SECOND CONFERENCE ANNOUNCEMENT, "NICHE EVOLUTION" Reply-To: "Peter B. Pearman" <pearman@wsl.ch> Resent-Message-Id: <200904140928.n3E9SC1I006231@Dura7.UTS.McMaster.CA> Resent-Date: Tue, 14 Apr 2009 05:28:12 -0400 User-Agent: Thunderbird 2.0.0.21 (Macintosh/20090302)

SECOND CONFERENCE ANNOUNCEMENT

NICHE EVOLUTION - A unifying concept for systematics, ecology, palaeontology and conservation biology

3-4 July, 2009. Excursion on 5 July. Zurich, Switzerland

www.systbot.uzh.ch/niche < http://www.systbot.uzh.ch/niche >

MOTIVATION Evolution of ecological niches, in their various guises, has become a central theme in several research fields of biology. We argue that niches, how they evolve, and the consequences of their evolution, affect a wide range of disciplines in organismal and evolutionary biology, and as such could be seen as a unifying thread.

In this meeting we will explore the interdisciplinary impact of evolving niches, and so bring together systematists, invasion biologists, biodiversity specialists, ecologists, and palaeontologists. We want to explore the commonality of evolving niches. The focus is more on concepts than methods (although, of course, the methods used will impact massively on the concepts). The emphasis is more on how to understand the evolution of a niche, rather than the definition of the niche. There will be some talks on the basics of niches to set the stage for the topics of niche evolution. The idea is to bring people together working in this field and to provide a forum to discuss developments, prospects and needs with various users and specialists. Therefore, the program is structured to provide ample time for discussions between and after the sessions.

PLACE The meeting will take place at the Institute of Systematic Botany of the University of Zurich, situated in the botanical garden of the University of Zurich, within easy reach of public transport.

TALKS Only invited talks will be given, and contributions as posters are welcome. There will be an evening poster session.

Invited speakers include William Bond, Jeannine Cavender-Bares, Alastair Culham, Catherine Graham, Antoine Guisan, Sabine Jakob, Jennifer Lau, Peter Linder, Signe Normand, Peter Pearman, Townsend Peterson, Bob Ricklefs, Nicolas Salamin, Walter Salzburger, Harald Schneider, Jonathan Silvertown, Wilfried Thuillier and Niklaus Zimmermann.

POST-CONFERENCE ONE-DAY EXCURSION There will be an excursion for Sunday, 5 July, into the Alps. We will cross the Susten Pass (2'250 m). On Susten Pass we will visit the Steingletscher glacier, which has shown a dramatic reduction in the past decades, thus exposing much new habitat. We will be able to see the plant successions into these newly exposed habitats. This shows very dramatically the effect of climate change, and the potential new habitats exposed.

ORGANISERS Peter Linder, Alexandre Antonelli, Rafael Wüest (Systematic Botany, University of Zurich), Niklaus Zimmermann and Peter Pearman (Institute of Forest, Snow and Landscape Research, WSL, Zurich), Harald Schneider (Natural History Museum, London), Frank Blattner (IPK Gatersleben) and Nicolas Salamin (Computational Phylogenetics, University of Lausanne)

REGISTRATION IS OPEN, at _www.systbot.uzh.ch/niche_ < http://www.systbot.uzh.ch/niche >

Please distribute this information to all researchers and students potentially interested!

"Peter B. Pearman" <pearman@wsl.ch>

GradStudentPositions

Austria ExperimentalEvolution

PhD position in Experimental Evolutionary Biology

Application deadline: 25.April 2009

Project description: Most organisms reproduce sexually, despite high costs associated with this reproductive mode. In the last decades several theories have been proposed to resolve this "paradox of sex". A particularly tough challenge to such theories are organisms that give rise to obligate asexual lineages, because such organisms should face the constant danger of being replaced by their asexual descendants. This project focuses on obligate asexual lineages within monogonont rotifers.

The PhD project aims at analysing the population level consequences of obligate asexuality in the rotifer Brachionus calyciflorus. It is mainly concerned with the speed of adaptation in sexual vs. obligate asexual populations. The project relies on lab experiments at the individual and population level. Further techniques used/learned during this project include: microsatellite analysis, cryopreservation, as well as several technical skills involved in our automated culture systems, including computer programming.

The PhD project is embedded into complementary research themes of the working group, e.g. determining the genetic mechanism of obligate asexuality, or establishing the prevalence of OA in field populations. Further information on the lab can be found at http://www.oeaw.ac.at/limno/personnel/stelzer/stelzer.htm The project is supervised by Dr. Claus-Peter Stelzer at the Institute for Limnology in Mondsee (near Salzburg, Austria) and funded by the FWF for 3 years (Project P20735-B17). Salary is according to the FWF pay scale (http://www.fwf.ac.at/de/projects/personalkostensaetze_2008.html).

Applicants should be highly motivated and have a Master's or diploma degree in biology, or in a related field. A solid background in evolutionary biology is essential for this position, and this should be recognizable by the Masters thesis and/or documented by several courses during the studies. Experiences in experimental design, statistics and PCR-based molecular genetic methods are also advantageous, but not absolutely required.

The Institute for Limnology is located in Mondsee, a small town in the Salzkammergut lake area. Mondsee is 30 km east of the City of Salzburg, which is also the location of the nearest university. The Institute has a staff complement of approximately 25, including 10 research scientists, who work on various areas in ecophysiology and evolutionary ecology of aquatic organisms.

Applicants should send a cover letter summarizing their research background and interest in the position, a CV, and contact information for two referees (everything as one PDF document) to claus-peter.stelzer<at>oeaw.ac.at, by 25. April 2009. The ideal starting date is 1. June 2009.

Dr. Claus-Peter Stelzer Institute for Limnology Mondseestrasse 9 A-5310 Mondsee Austria

claus-peter.stelzer@oeaw.ac.at claus-peter.stelzer@oeaw.ac.at

Berne PopulationGenomics

PhD position

Population genomics of adaptation using next-generation sequencing

The CMPG lab is looking for a PhD candidate to study patterns of selection in the common vole (Microtus arvalis) using $B!H(Bnext-generation$B!I(B sequencing technology. Based on detailed information resulting from a first generation AFLP genome scan, particular genome regions and populations living in different environments will be subject to extensive DNA sequencing to determine the patterns of selection acting at different evolutionary levels.

We are seeking a highly-motivated, independent candidate with excellent organizational skills. The ideal candidate has a background in population genetics and/or bioinformatics, specific programming skills (C/C++, R, Perl), and some experience with molecular lab work. A degree equivalent to a diploma or M.Sc in Biology or Bioinformatics is required. Good knowledge of written and spoken English is essential. The working language in our group is English. Some knowledge of German or French would be beneficial for living in Switzerland but are not necessary.

The student will be supervised by Dr. Gerald Heckel and Prof. Laurent Excoffier. The CMPG lab is also part of the Swiss Institute of Bioinformatics (SIB, http://www.isb-sib.ch/), and offers a stimulating research environment with excellent facilities for computational and laboratory analyses. Information on our research group, the University of Bern and its magnificent surroundings can be obtained from http://cmpg.unibe.ch/ and http://bern.ch/.

The position is funded for three years, and the salary follows the Swiss NSF scale. The starting date is June 1st 2009 and cannot be really negociated due to the nature of the funding. For informal inquiries, please contact gerald.heckel@iee.unibe.ch.

Please send your application including a CV, a list of publications, a letter outlining your past research and particular motivation for this position (max. 2 pages), as well as contact details of 2-3 referees in a single pdf file to gerald.heckel@iee.unibe.ch.

Deadline for application is May 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>

CNRS France ReproductiveInvestment

Reproductive investment and mate choice when facing a pathogen

Duration: 01.09.2010 - 31.08.2013 (slight shifts of the dates are possible)

Type: PhD

Supervisor: Dirk S. Schmeller, Adeline Loyau

General Framework: Individual decisions about how much to invest in reproduction with whom to mate and can have tremendous consequences on population dynamics and therefore on population persistence. Costs of mounting an immune response against pathogens are known to be very high. Life history trade-offs teach us that an individuals energy is limited. Therefore, when an individual is facing, or has just been facing, a pathogen, this individual will invest less energy in reproduction. Low reproductive investment can be expressed both in males and females by lower display frequency, coloured signals of bad quality, poor quality sperm, poor quality eggs etc. Sexual selection theories about honest signalling predict that female mating preferences evolved to provide females with both direct and indirect benefits. Indeed, by preferring males of high phenotypic quality, females would mate with males of high health status. Therefore, females would avoid contracting a disease during mating, and they would gather genes for attractiveness and genes for resistance against pathogens for their offspring. When given the choice, individuals should avoid infected individuals as potential partners. In a population infected by a disease, mate choice should thus help resisting the infection at the population level. Female mate choice and female condition are known to affect maternal allocation in reproduction. Female in good health and females mated with attractive healthy males are indeed expected to produce better quality eggs. Parental effects can be strong and can even last over several generations, especially in amphibians for which carry-over effects were described. A low parental investment can therefore have major fitness consequences on offspring and even on several of the following generations.

Amphibians are currently facing a decline worldwide due to a pathogen, the chytrid fungus (Bd). The candidate will be part of the Biodiversa-project RACE (Risk Assessment of Chytridiomycosis to European amphibians), an international project aiming to develop a threat abatement plan for European amphibians. The PhD student will be supported by at least one master student every year and several internships (duration between 2 to 6 month).

The aims of the PhD project are: * to investigate the costs imposed by the Bd pathogen on reproduction of Lisotriton helveticus in terms of expression of secondary sexual traits and display, and maternal investment, * to examine whether mating decisions avoid spreading the disease

Profile: Knowledge of R, Matlab or SAS Knowledge or willingness to learn at least two of the following languages: French, Spanish, English Knowledge in behavioural ecology and population dynamics, interest in conservation biology Knowledge of genetic methods The successful candidate is required to hold a Master diploma or equivalent experience in biology. The salary will be in the range of around 1400EUR net/month.

Place of work: The Station dEcologie Experimentale in Moulis (SEEM) is a recently founded research and service unit of the Centre Nationale de la Recherche Scientifique (CNRS). SEEM, where the candidate will be working, is an interdisciplinary research group that combines the skills of population ecologists, behavioural ecologists, evolutionary biologists, and geneticists to study animal ecology. SEEM has a strong international flavour due its international staff and cooperation with institutes in the US and several European countries. SEEM is located in the foothills of the Pyrenean region Ariege (France). The station is currently undergoing extensive renovation and will soon host well equipped laboratories, comprising physiologic, genetic, and ecologic lab facilities as well as experimental sites. See our webpage at http://www.ecoex-moulis.cnrs.fr for more details.

Application: Applicants should submit a letter of application describing their experience and interests in the position, curriculum vitae, list of publications, and copies of certificates. Applicants may be called for an interview. We accept applications in pdf format sent to the addresses below. The closing date for applications will be 15th of June 2009. Interviews are foreseen during June 2009.

Contact details: Dirk S. Schmeller Adeline Loyau Station d'Ecologie Expérimentale du CNRS à Moulis 09200 Saint Girons, France phone: +33 5 61 04 03 73 / 64 fax: +33 5 61 96 08 51 dirk.schmeller@ecoex-moulis.cnrs.fr al@adeline-loyau.net www.ecoex-moulis.cnrs.fr "Dirk S. Schmeller" <dirk.schmeller@EcoEx-Moulis.cnrs.fr> "Dirk S. Schmeller" <dirk.schmeller@EcoEx-Moulis.cnrs.fr>

ConcordiaU ConservationBiol

Two positions (one PhD, one MSc) are now available to examine the evolutionary consequences of small population size for conservation biology (Location: Concordia University, Montreal, QC, Canada). Students will study interactions between population size, genetic diversity, adaptation, and phenotypic plasticity, using several populations of a salmonid fish in eastern Canada as a model system. The research will involve a combination of fieldwork, fish husbandry, common-garden experimentation and molecular genetic studies; previous experience in any of these areas is an asset.

Expected start date is September 2009 or January of 2010. Each position is contingent upon acceptance to the Department of Biology graduate program at Concordia University. If interested, please send an application including: (i) a CV; (ii) a brief cover letter describing research interests and their relationship with this research; (iii) names and addresses of two references, and (iv) documentation of undergraduate grades. Please send applications electronically to: Dr. Dylan Fraser, Department of Biology, Dalhousie University, Halifax, Nova Scotia, B3H 4J1. Fax: 902-494-3736. Email: dylan.fraser@dal.ca. Webpage: www.dylanfraser.com Dr. Dylan J. Fraser Postdoctoral Research Fellow Department of Biology, Dalhousie University, Halifax, Nova Scotia Canada B3H 4J1 Tel: (902) 494-6279; Fax: (902) 494-3736 Email: dylan.fraser@dal.ca Webpage: www.dylanfraser.com Dylan.Fraser@Dal.Ca Dylan.Fraser@Dal.Ca

DalhousieU Conservation

PhD position in Conservation Genetics of northern fishes

Support for a PhD position is available in the laboratory of Daniel Ruzzante at Dalhousie University (Halifax, Nova Scotia, Canada) for research in conservation genetics of fish in the north. The successful candidate should have experience with molecular techniques and should have a strong interest in conservation and landscape genetics. The project will involve fieldwork in the Canadian north. The position is expected to start in the 2009/2010 academic year and is contingent upon acceptance to the Department of Biology graduate program.

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

Daniel Ruzzante, Associate Professor Canada Research Chair in Marine Conservation Genetics Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1 phone: (902) 494-1688 fax: (902) 494-3736 e-mail: daniel.ruzzante@dal.ca

http://myweb.dal.ca/ruzzante http://patagonia.byu.edu Canada Research Chairs http://www.chairs.gc.ca ruzzante <Daniel.Ruzzante@DAL.CA>

Dijon France InsectImmunoEvolution

Graduate position: Dijon_France Immuno-Evolution of insects

A 3 year PhD position on âevolutionary immunology of insectsâ supervised by Dr JÃ©rÃme Moreau and Dr Yannick Moret is opened in the group of Evolutionary Ecology of the BiogÃ©oscience Laboratory (UMR 5561 CNRS) of the University of Bourgogne, Dijon, France.

Candidates must be in the last year of their master degree (or equivalent Diploma). Candidates should have a joined interest in both Evolutionary Biology, Behavioural Ecology. Good statistical skills will be appreciated.

Applications should be sent before May 20th Yannick Moret (yannick.moret@u-bourgogne.fr) and should contain:

1) A detailed CV and a motivation letter explaining the interests of the applicant to the project and the match between the CV and the PhD project.

2) Two recommendation letters that should be sent directly by email to JÃ©rÃme Moreau or Yannick Moret, if possible provided by the supervisors of the Master research training period.

3) Grades obtained in Master.

Candidates short-listed on base of their application will be interviewed in June and a decision will be taken soon after.

Project:

Infected vertebrate females transfer specific antibodies to their offspring, providing them with a temporary protection against the parasite during the time required for their immune system to mature. Invertebrates lack antibodies and trans-generational transfer of immunity was believed to be missing. Cumulative data from the field of ecological immunology provide evidence that an equivalent phenomenon does exist in arthropods. In the mealworm beetle, Tenebrio molitor (Coleoptera), individuals subjected to a microbial challenge produce offspring with enhanced immunity. These results raised numerous questions about the mechanisms involved that are entirely unknown, and about the evolutionary ecology of this phenomenon.

From an ecological and evolutionary point of view, the occurrence of such a phenomenon in insects suggests that there is a selective advantage to facultatively enhance offspring immunity after being exposed to parasite infection. After experiencing a parasitic attack, a host or its progeny might be subsequently exposed to a higher probability of infection, since parasites that are now present in the environment are likely to increase in frequency because on their reliance on hosts for transmission. Therefore, hosts exposed to a parasite infection may increase their net reproductive success by adjusting offspring immunity to improve resistance to prevailing parasites. The facultative aspect of this phenomenon suggests it might also be costly and may constrain for adjustment of offspring immunity according to the actual risk of subsequent infection. The project aims to study trans-generational transfer of immunity in Tenebrio molitor through the investigation of its underlying mechanism(s) and its adaptive significance through the estimation of its associated costs and benefits.

Yannick Moret ChargÃ© de Recherche CNRS Ãquipe Ãcologie Ãvolutive UMR 5561 BiogÃ©osciences UniversitÃ© de Burgogne 6 Boulevard Gabriel 21000 Dijon - France Tel. +33 (0)3 80 39 90 30 Fax. +33 (0)3 80 39 62 31 http://www.u-bourgogne.fr/BIOGEOSCIENCE/index.php?option=com_content&task=view&idT&Itemid=1

Yannick Moret <yannick.moret@u-bourgogne.fr>

GoetheU PlantDiversification

Thanks for adding the following job advertisement:

The Biodiversity and Climate Research Centre (BiKF) has recently been founded by the Senckenberg Gesellschaft fuer Naturforschung, the Goethe University Frankfurt am Main, and additional partners. It is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The Project Area Evolution and Climate invites applications for a Research Assistant (or PhD) Position Plant diversification in the Indomalesian, Australasian and Pacific islands region PG A1 [Ref. #A22] BAT IIa/2 Essentials: We look for a highly motivated candidate holding a Diploma or Masters degree in a relevant subject with a sound background in molecular systematics techniques (incl. proven experience in successfully working on DNA of old/historical herbarium specimens) and plant morphology. You will demonstrate interest in plant systematics and plant biogeography studies. Good communication skills, the ability to work independently and the willingness to conduct fieldwork in the Asian tropics are essential. A good working knowledge of English is required. It is desired that the successful applicant will earn a PhD degree in this position.

Job duties: You will combine existing DNA sequence data with new data collected and produced during the project to reconstruct evolutionary relationships and the biogeographic history of different plant taxa occurring in the Indomalesian, Australasian and Pacific islands region. The multi-gene phylogenetic trees will be set in a temporal context by fossil constraints. You will be expected to contribute to teaching at undergraduate levels. The willingness to develop and submit research funding proposals is required.

Salary and benefits are according to a public service position in Germany (BAT IIa/2, approx. 29.400 gross per annum). The Research Centre BiK-F advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

The contract shall start as soon as possible and will initially be restricted to 18 months, with possible extension subject to the acquisition of additional external funding. The duty station will be Frankfurt am Main, Germany. Please send your application by email, including 1) a cover letter outlining relevant background and work experience, 2) a full curriculum vitae, including a list of publications, 3) copies of educational certificates/thesis, 4) names and addresses of two referees, before April 28th 2009 to Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D60325 Frankfurt am Main, Germany, recruiting@senckenberg.de(Service and Finances), with Cc to alexandra.muellner@senckenberg.de (mailto:Klussmann-Kolb@bio.uni-frankfurt.de). For enquiries about the position and the contract conditions please write to Prof. Dr. B. Stribrny (Email: bernhard.stribrny@senckenberg.de) and for scientific enquiries to Dr. Alexandra Nora Muellner (Email: alexandra.muellner@senckenberg.de (mailto:Klussmann-Kolb@bio.uni-frankfurt.de)).

Ursula Maurer <Ursula.Maurer@senckenberg.de>

Halle Germany VirulenceEvolution

*** PhD POSITION: EVOLUTION OF VIRULENCE***

A PhD position is available in the Molecular Ecology Research Group of the Insitute for Biology at the Martin-Luther-University Halle-Wittenberg, in Halle (Saale), Germany (http://www.mol-ecol.uni-halle.de/-).

The project focuses on the evolution of virulence in a host-parasite system of bumblebees and their trypanosome parasites Crithidia. Using a combination of population genetics and an experimental evolution approach we will study how the hosts population structure shapes the virulence of a parasite.

We are looking for a highly motivated student having a Masters degree or equivalent in the relevant field. He/she should work well both as a member of the group and independently. Prior laboratory experience is required, and skills in handling and maintaining social insect colonies as well as knowledge of statistical analyses are preferred. Applicants should have a broad biological background, with special emphasis in the fields of evolution, ecology and genetics. Good English skills are required because working and teaching language is English.

To apply, please send letter of application including research interests, a C.V., and contact details for two or three references by e-mail (lattorff@zoologie.uni-halle.de). The position is open until filled, but for full consideration, apply by April 30, 2009. The position is fix term for three years (~1,000 EUR/month (approximately US$ 1,300). The preferred starting date is August, 1st 2009.

Halle hosts many excellent scientific institutions such as Helmholtz Centre for Environmental Research (UFZ), 3 Max-Planck Institutes and the Leibnitz Institute for Plant Biochemistry (IPB). Halle is the largest city of Sachsen-Anhalt with a good infrastructure, hosting 2 universities. Due to the high number of students Halle has a rich choice of social, cultural and sporting facilities (see www.halle.de).

For further information regarding the group and/or the project please contact Dr. Michael Lattorff Institute of Biology, Molecular Ecology Martin-Luther-University Halle-Wittenberg Hoher Weg 4 06099 Halle (Saale) Germany phone. +49-345-5526389 fax. +49-345-5527264 email. lattorff@zoologie.uni-halle.de www. http://www.biologie.uni-halle.de/zool/mol_ecol/ lattorff@zoologie.uni-halle.de lattorff@zoologie.uni-halle.de

ImperialCollege BacteriaRotifers

PhD studentship

Department of Life Sciences, Imperial College London

Supervisor: Dr T Barraclough

Project title: Community genomics of complex microscopic communities

The project will explore genomic interactions among species living in complex communities, specifically the importance of lateral gene transfer in adaptive responses and species interactions. The focus of the system will be bdelloid rotifers and bacteria. Bacteria have long been known to exchange genes widely with one another, genes that can provide important ecological functions such as virulence or antibiotic resistance. Recent work has shown that bdelloid rotifers have a unique capacity among animals to take up genes from a wide range of organisms and to domesticate those genes for their own use. This project will use natural and laboratory communities of bdelloids and bacteria to quantify ecological interactions within the system, and to test for the frequency of gene exchange among members V in part through phylogenetic approaches and in part through laboratory experiments. The project lies at the interface of evolutionary and ecological systems biology.

Were looking for a student with a good first degree and Masters degree. NERC funding is open to UK residents and EU nationals who have spent the last three years in the UK for education or employment (www.nerc.ac.uk/funding/available/-postgrad/eligibility.asp) .

To apply, please reply by 30th April, sending a CV and a brief letter explaining why you are interested in this PhD to Tim Barraclough at t.barraclough@imperial.ac.uk .

Funding Notes NERC funded 3 year studentship. Applicants must ensure they meet NERC's eligibility criteria (European/UK students only).

Timothy Barraclough <t.barraclough@imperial.ac.uk>

INRA Toulouse PopulationGenetics

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

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

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

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

KentStateU 2 PlantEvolEcol

Two Graduate Student Positions in Plant Evolutionary Ecology

Funding is available for two graduate students to work with Andrea Case (Kent State University, Ohio, USA) and Christina Caruso (University of Guelph, Ontario, Canada) on an NSF-funded research project. We are investigating the causes of population sex ratio variation in a gynodioecious plant (Lobelia siphilitica) across eastern North America. This project combines field experiments, controlled crosses in the greenhouse, and genotyping using microsatellite markers to determine how different mechanisms of evolution, as well as any differences in population history, contribute to variation in population sex ratio across L. siphilitica's range. There is ample opportunity for students to develop independent research associated with the project.

One Ph.D position is available in the Department of Biological Sciences at Kent State University. The student would participate in lab work as well as fieldwork in Ohio and Indiana. Familiarity with basic molecular techniques (DNA extraction, PCR, sequencing) and using genetic markers will be helpful. Stipends cover 12-mo salary, tuition and fees. Students have the option, but are not required, to teach. Details of how to apply to the program are available at http://bioweb.biology.kent.edu/GraduateProgram/-How_to_apply.html Prior to submitting a formal application for the Kent State position, candidates should send a brief statement of interest and CV to acase@kent.edu.

One Ph.D or M.Sc. position is available in the Department of Integrative Biology at the University of Guelph. The student will be responsible for overseeing controlled crosses in the greenhouse and conducting fieldwork in Ontario and Iowa. Applicants should have academic background and research experience in ecology and/or evolutionary biology. Experience working with plants in the greenhouse and field would be helpful. Information on the graduate program in Integrative Biology is available at http://www.uoguelph.ca/-ib/grad/graduate.shtml Prior to submitting a formal application for the Guelph position, interested candidates should send an unofficial transcript, CV (including references), and a brief statement of interest to carusoc@uoguelph.ca.

We strongly encourage applicants from underrepresented groups.

– Dr. Andrea Case Asst. Professor of Biological Sciences Kent State University Box 5190 Kent OH 44242-0001 USA Office: 245 Cunningham Hall Phone: 330-672-3699 acase@kent.edu http://bioweb.biology.kent.edu/FacultyPages/Case/
– Christina M. (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 Canada 519-824-4120 x52030 carusoc@uoguelph.ca http:/-/www.uoguelph.ca/ib/people/faculty/caruso.shtml
"CASE, ANDREA" <acase@kent.edu>

Leuven InsectEvolutionaryEcol

PhD studentship in Insect Evolutionary Ecology

GENERAL THEME: Evolutionary ecology of phenotypic syndromes (integrated patterns of behavioural, physiological and performance traits) in damselflies. The PhD project will concentrate on two questions: (1) Do larval phenotypic syndromes bridge metamorphosis and shape dispersal and mating success? (2) Do population characteristics (natal habitat effects) shape phenotypic syndromes and the resulting population differentiation in patterns of dispersal and sexual selection (geographic selection mosaics)? Special attention will be given to the comparison of new versus old populations which likely differ in traits related to dispersal.

PRACTICAL WORK will be a combination of (1) monitoring natural field populations, and (2) common garden experiments in semi-natural populations (mesocosms / insectaries) and in the laboratory. We have excellent research facilities with an outdoor research area, several temperature-controlled rooms, incubators, and a well-equipped laboratory for quantification of behavioural, physiological and performance traits like swimming speed and flight ability.

PROFILE: EU citizen with a master degree in Biology (also people finishing this degree are encouraged to apply) and with a strong interest in both field and laboratory work. Preference will go to candidates with experience in scoring behavioural, physiological and performance traits, or at least a strong motivation to learn relevant techniques. The candidate should combine research independence with a good team spirit. It is expected that the candidate applies for national funding opportunities. A car driving license is required.

OFFER: A full time job initially for a period of one year, but extendable to a total of four years pending good evaluation. Leuven (http://www.leuven.be) is a pretty historical university city with a very high and pleasant standard of living. The historic university, founded in 1425 (http://www.kuleuven.be/english), has a top research and teaching standard. Within our research group we have ample expertise working with damselflies (http://bio.kuleuven.be/de/dea/people_detail.php?pass_id=u0034380).

INTERESTED? Please send your CV, a letter of motivation including relevant experience, and contact details of two referents to

Dr. Robby Stoks University of Leuven Laboratory of Aquatic Ecology and Evolutionary Biology Deberiotstraat 32 B-3000 Leuven, Belgium E-mail: robby.stoks@bio.kuleuven.be <mailto:robby.stoks@bio.kuleuven.be>

Applications will be reviewed starting May 15 until the position is filled. The start date is spring or summer 2009, preferentially as soon as possible.

robby.stoks@bio.kuleuven.be

LMU Munich EvolutionaryBiol

Master Program in Evolution, Ecology and Systematics

The University of Munich (LMU) offers a 2-year, international master program for highly motivated students from Germany and abroad with a background in biology or a related subject. All courses are offered in English. Application deadlines in 2009: 30th of April (for non-EU students) and 30th of June (for EU-students and others who don't need a visa to study in Germany).

The EES Master program contains many innovative elements such as a mentoring program, integrated skills courses and individual research training. We also apply a feedback and revision system instead of simple grading. Classes are small and students have a lot of contact to the teachers. Thanks to funding by the Volkswagen Foundation, students can apply for their own research and travel money and for money to invite international speakers. Unfortunately, we cannot provide grants to cover costs of living. Students pay appr. 500 Euro tuition fees per semester.

For more information, please have a look at our website (http://www.eeslmu.de) or contact the program coordinator Elisabeth Brunner (brunner@bio.lmu.de).

Elisabeth Brunner

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

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

Tel: 0049 89 2180 74 208 http://www.eeslmu.de/eeswiki brunner@bio.lmu.de

brunner@biologie.uni-muenchen.de

MichiganStateU EvoDevo

PhD Studentship in Evolutionary/Ecological Developmental Biology, Michigan State University, USA.

A graduate student position in Evolutionary/Ecological Developmental Biology is available in the laboratory of Dr. Alex Shingleton, in the Department of Zoology at Michigan State University. The position is funded as part of a 5-year NSF grant exploring the developmental regulation of 'allometry' - the scaling relationship between organ size and body size. Variation in allometry dominates morphological diversity and the goal of the lab is to uncover the developmental mechanisms upon which selection has acted to create this diversity. The lab uses fruit fly as a model organism and employs molecular, genetic, physiological and behavioral methods to address our research questions. More details of the research being conducted in the laboratory are available at www.msu.edu/˜shingle9 The specific project concerns the role the insulin-signaling pathway plays in regulating scaling relationships in fruit fly. Previous research in the lab has identified this 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. The expectation is that this project will serve as a springboard to a more independent line of thesis research.

The project will suit students with an interest in Evo/Eco-Devo and integrative developmental biology. The ideal candidate should have good general laboratory skills, with a firm grasp of basic statistical methods. While the studentship need not involve formal teaching, the successful candidate will be involved in mentoring undergraduate students.

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. The ideal starting date is September 2, 2009, although applicants who wish to start January 2010 are also welcome.

Alexander W. Shingleton Assistant Professor Ecology, Evolutionary Biology & Behavior Program Genetics Program

Department of Zoology Natural Sciences Building Michigan State University East Lansing, MI 48824 Tel: 517-353-2253 www.msu.edu/ ˜ shingle9 shingle9@msu.edu shingle9@msu.edu

Netherlands LanguageEvolution

A PhD Position is available in the Max Planck Research Group: “Evolutionary Processes in Language and Culture” at the Max Planck Institute for Psycholinguistics in Nijmegen, The Netherlands. The research group “Evolutionary Processes in Language and Culture” is a small, independent group funded by the Max Planck Society to investigate structural variation in language and culture from an evolutionary perspective. We seek a talented and motivated student to carry out a mutually agreed research project in an area complementary to the interests of the group.

The PhD project will involve investigation of the determinants of variation in one or more large language families, e.g. Austronesian, Bantu and/or Indo-European (other families/regions can be considered on the basis of data access). The precise nature of the project will be agreed in collaboration with the successful candidate, but we envisage that it will be interdisciplinary in orientation, encompassing some of the following areas.

- Linguistic typology - Social anthropology - Evolutionary anthropology - Historical linguistics - Phylogenetics

The successful candidate will have access to the research group databases, and will have the opportunity to participate in group projects. Technical skills in computing (esp. sql, python, R) and statistics would be advantageous.

The Max Planck Institute for Psycholinguistics is a vibrant research environment in a charming university town. Nijmegen is situated 1.5 hours from Amsterdam, and has easy access to Belgium and Germany.

The PhD position is funded for 3 years (2 year initial contract with a 1 year extension). The research group provides fully equipped research facilities, technical support and research assistance, as well as a generous conference and travel budget, and support for possible fieldwork.

Closing date for application: May 15th, 2009.

The Max Planck Society is an equal opportunity employer. The business of the institute is conducted in English.

Applicants should send their CV, a short statement of research interests, a sample of their writing, and the names and e-mail addresses of at least two potential referees to:

Dr Michael Dunn Research Group Evolutionary Processes in Language and Culture Max Planck Institute for Psycholinguistics Postbus 310, 6500AH Nijmegen The Netherlands

and an electronic version (pdf preferred) to Michael Dunn <michael.dunn@mpi.nl>. Further enquiries may be sent by email.

– Michael Dunn, Max Planck Research Group Leader: Evolutionary Processes in Language and Culture Max Planck Institute for Psycholinguistics PB310, 6500AH Nijmegen, The Netherlands +31 (0)24 3521181 (wk) +31 (0)24 3521300 (fax) http://www.mpi.nl/-Members/MichaelDunn (until 20-04-2009) http://-www.mpi.nl/people/dunn-michael (thereafter)

Michael Dunn <michael.dunn@mpi.nl>

Paris Regensburg InsectParasiteDefence

[Paris-Regensburg] 3 year Phd position with joint supervision at the University Pierre et Marie Curie, Paris, France and the University of Regensburg, Germany on 'Division of labor and anti-parasite defences in social insects'. Application deadline: 11 May 2009

Long version:

We offer a 3 year PhD grant on 'Division of labor and anti-parasite defences in social insects' provided by the French doctoral school 'Diversité du vivant' (< http:/-/eddv.snv.jussieu.fr > http://eddv.snv.jussieu.fr), with joint supervision by:

Paris: Dr. Claudie Doums : Laboratoire d'Ecologie et Evolution, UMR 7625, Université Pierre et Marie Curie, 7 quai St Bernard, 75005 Paris. Tel : 01 44 27 38 09,

Email : cdoums@snv.jussieu.fr

Regensburg: Prof. Juergen Heinze and Dr. Sylvia Cremer : Evolution, Behavior and Genetics, Biology I, University of Regensburg, 93040 Regensburg, Germany

Email: juergen.heinze@biologie.uni-regensburg.de;

sylvia.cremer@ biologie.uni-regensburg.de

Preconditions:

Candidates must be in the last year of their master degree (or equivalent diploma) and come from the European Union or other European countries affiliated to the European area for higher education. Candidates should have an interest in Evolutionary Biology and be highly motivated to pursue their studies in the two host laboratories (work place will be the University Pierre et Marie Curie in Paris with regular visits to the University of Regensburg). Fluency in English is required.

Application details: Applications should be sent to Claudie Doums and Sylvia Cremer/Juergen Heinze containing: 1) A detailed CV and a motivation letter explaining the interests of the applicant to the project and the match between the CV and the PhD project. 2) Two recommendation letters that should be sent directly by email to Claudie Doums or Sylvia Cremer/Juergen Heinze, if possible provided by the supervisors of the Master research stages. 3) Grades obtained in the Masters Project. Application deadline: 11.5.2009

Detailed project information: Living in social groups can increase the risk of pathogen infection owed to the strong genetic and geographic proximity of social group members. Parasites are therefore expected to exert a strong selective pressure. A large panel of social and individual defenses, based on immunological and behavioral responses, have evolved in social groups and provide a global resistance of the group to pathogens. Few studies have investigated how individual and collective defenses are integrated to acquire a group level immunity. Our research PhD project aim at analysing how the group members invest into these different mechanisms of defenses and how these investments vary with intrinsic factors (group size, genetic diversity, demography) and extrinsic (parasitism pressure). These questions will be addressed by considering the conceptual framework of division of labor in social insects, which is characterized by a non equitable distribution and a specialization of the different tasks between the colony members. Two ant species, which are largely studied in the two laboratories (Platythyrea punctata and Cataglyphis cursor), are interesting biological models for the project as they offer extreme variation in genetic diversity among workers by being able to reproduce by thelytokous parthenogenesis but also to use sexual reproduction. This project will require the use of microsatellite for genetic analysis, of different immunological techniques and involve behavioral observations.

'Sylvia Cremer' <Sylvia.Cremer@biologie.uni-regensburg.de>

Poitiers France EvolutionaryBiolWolbachia

A 3 year PhD position on Adaptative success of Wolbachia in arthropods supervised by Pr Didier Bouchon and Dr Mathieu Sicard is opened in the Ecology, Evolution, Symbioses Lab (UMR 6556 CNRS) of the University of Poitiers, France

Candidates must be in the last year of their master degree (or equivalent Diploma). Candidates should have a joined interest in both Evolutionary Biology and Molecular Biology. Fluency in English and could statistical skills are required.

Details on project: To understand the importance of switching events for the adaptative success of Wolbachia through arthropods lineages, we will investigate the proximal (i.e. immediate) and distal (i.e. long term) consequences of host-switching on the parameters of Wolbachia-arthropod symbioses. We will transfect terrestrial isopods to compare two situations: (i) symbioses between native partners and (ii) newly formed associations resulting from experimental host-switching.

Proximal consequences of host-switching will be assessed upon transfection through: - The effect of Wolbachia on recipient host life history traits - Colonization dynamics: Assessment of Wolbachia load by q-PCR, invasion visualized with FISH at adult stages and through developmental stages of the progenies - Host immunocompetence: Number and type of haemocytes, level of phenoloxydase in haemolymph, susceptibility towards various parasites.

Distal evolutionary consequences will be assessed through generations: - Host fitness: Survival and reproduction - Wolbachia vertical transmission rate - Extended phenotype of the association: Manipulation of reproduction. Moreover, simulation will be performed to analyze the evolution of genotype frequencies for both host and Wolbachia over the time after horizontal transfer, along with variable bacterial effects and host responses.

Application details: Applications should be sent to Mathieu Sicard (mathieu.sicard@univ-poitiers.fr) containing: 1) A detailed CV and a motivation letter explaining the interests of the applicant to the project and the match between the CV and the PhD project. 2) Two recommendation letters that should be sent directly by email to Mathieu Sicard, if possible provided by the supervisors of the Master research stages. 3) Grades obtained in Master.

Application deadline: 30.5.2009

– Pr. D. Bouchon

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

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

RutgersU Phylogenetics

I am seeking a graduate student for an NSF funded project on the phylogenetics of Trichoptera (Insecta). A GA at Rutgers University, in Central New Jersey, is available. Interested applicants should contact Karl Kjer at <kjer@aesop.rutgers.edu> for details. I am very flexible in terms of the kind of experience I am looking for. Morphological or molecular, insects, or other organisms, it does not matter. But I am looking for some prior demonstration of an interest in evolutionary biology and/or systematics/phylogenetics. Karl Kjer

Work: Home: Rutgers University, Cook College 28 Lincoln Ave. Dept. Ecol., Evol, & Natural Res., Highland Park, NJ 08904-1701 14 College Farm Rd. New Brunswick, New Jersey 08901

Office phone: (732)932-9880 Lab phone: (732)932-4269 or (732)932-4238 Fax 732 932-7229

Karl Kjer <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: Genetic consequences of environmental change on the evolution and demography of arctic species.

Final date for applications: May 4, 2009

Project description: The overall objective of this PhD project is to investigate the impact of environmental change on the evolution and demography in arctic species. This will be done through genetic analyses on both modern samples and on DNA retrieved from fossils up to 50 000 years old. The resulting genetic data will be integrated with information on past distributions and climates, as well as back-casted species distribution models. Specific questions that will be examined in the project include i) the timing of extinctions and demographic change in relation to past climate fluctuations, ii) when and where populations diverged and species evolved, and iii) to what extent local populations tracked changes in habitat availability when faced with climate change. Potential model species include lemmings, arctic foxes, reindeer and ptarmigan. 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. Prof. Anders Angerbjörn at the Department of Zoology will be co-supervisor.

Qualifications: To be qualified for research studies in systematics and evolution the applicant must have completed a research degree (e.g. Master's), or have passed in at least 120 hp (2 years) of biological studies, including an approved independent project in systematics and evolution of at least 30 hp at advanced level ("examensarbete"). Applicants who have in principle acquired the corresponding competence in Sweden or abroad, are also qualified. That is, applicants who have a Master's degree ("examensarbete") in an equivalent subject that is considered appropriate for this project are also encouraged to apply.

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. 03/09 LD" must have arrived at the address below by May 4, 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

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SyracuseU SexualSelection

The lab of Dr. Scott Pitnick at Syracuse University is conducting an ongoing search for mature, motivated candidates for PhD dissertation research in a broad range of topics addressing sexual selection and its role in population and species divergence and reproductive isolation. Potential projects are many and varied, but there are several research avenues currently ongoing. These include documenting evolutionary patterns of sperm conjugation and heteromorphism in water beetles, elucidation of mechanisms of sperm competition and conspecific sperm precedence in *Drosophila*, the integrated evolution of sexually selected and life history traits, and fitness effects of alternative male mating tactics in the yellow dung fly. If interested, please send CV, summary of research interests and experience, and contact information for 3 references to sspitnic@syr.edu.

Dr. Scott Pitnick Dept. of Biology Syracuse University Syracuse, NY 13244 USA +1 (315) 443-5128 sspitnic@syr.edu http://biology.syr.edu/pitnick/ Mollie Manier <maniermk@gmail.com>

TexasAMIntlU 2 CichlidEvolution

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

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

Prospective students should contact me directly:

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

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

mckidd@earthlink.net

UAdelaide EvolutionaryBiol

INTERNATIONAL PH.D SCHOLARSHIPS - EVOLUTIONARY BIOLOGY

UNIVERSITY OF ADELAIDE (AUSTRALIA)

The University of Adelaide is offering numerous full scholarships (covering all fees and a generous living allowance) to international students, enrolled for Ph.D degrees in areas of University Research strengths (which includes Evolutionary Biology).

Full details of the scholarships are here: http://www.adelaide.edu.au/graduatecentre/scholarships/postgrad/international/ Possible supervisors and labs for Ph.D studies are here: http://www.adelaide.edu.au/acebb/staff/ In the past, demand has been very high and to be competitive, applicants generally need some papers in international journals, or some postgraduate qualifications (e.g. masters).

Please direct all scholarship enquiries directly to the University Scholarships office and the leader of the research group you would like to work with.

Regards,

Mike

Michael Lee Associate Professor School of Earth and Environmental Sciences, University of Adelaide, North Terrace Campus, Adelaide 5005 Australia

Ph. 61-8-8207-7568 or 0407 685 921 Email Michael.S.Lee@Adelaide.Edu.Au or Lee.Mike@saugov.sa.gov.au www.adelaide.edu.au/directory/michael.s.lee Michael Lee <michael.s.lee@adelaide.edu.au>

UEdinburgh DiversityGeneMapping

Ph.D. Studentship at The Roslin Institute (University of Edinburgh)

We are currently recruiting a Ph.D. student (UK resident) to evaluate and apply novel statistical techniques for diversity-based gene mapping in livestock species. This four-year studentship is funded by a Genesis Faraday CASE BBSRC award with an enhanced stipend and other benefits provided by Genesis Faraday and the CASE partner, Aviagen Ltd.

The rationale for this gene-mapping approach is that variation will be reduced in regions of the genome subject to positive selection. Patterns of genome-wide diversity may reveal regions that have been under strong selection and contain genes with large phenotypic effects. This project will focus on the development, evaluation and application of methods of testing for selection using both simulated and genomic poultry data. This studentship will thus provide training in population and quantitative genetics, statistical methods, scientific computing and bioinformatics.

The student will be based at The Roslin Institute and the Institute of Evolutionary Biology (IEB) at the University of Edinburgh. The Edinburgh genetics research community is thriving, with strong expertise in population and quantitative genetics, making it an exciting place to study. The student will also spend time at Aviagen Ltd (Edinburgh), one of the major poultry breeders in the world with a strong commitment to research.

We are seeking an enthusiastic individual with an interest in population and evolutionary biology or animal genetics and aptitude with computer-based numerical analyses. The UK-based candidate should possess a good quality first degree in a relevant subject. Enthusiasm, dedication and aptitude are the most important characteristics; additional training in genetics and genome analysis are available at IEB.

The project involves a collaboration between Pam Wiener (Roslin), Chris Haley (MRC Human Genetics Unit), Brian Charlesworth (IEB) and Kellie Watson (Aviagen). For further information, please contact pam.wiener@roslin.ed.ac.uk. Applications including a full CV with names and addresses (including email addresses) of two academic referees, should be sent to: Human Resources, Roslin Institute (Edinburgh), Roslin, Midlothian, EH25 9PS. Email: roslin.hr@roslin.ed.ac.uk.

Pam Wiener The Roslin Institute University of Edinburgh Roslin Midlothian EH25 9PS phone: 44 (0) 131 527 4464 fax: 44 (0) 131 440 0434 new email: pam.wiener@roslin.ed.ac.uk

“The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336

Pam.Wiener@bbsrc.ac.uk Pam.Wiener@bbsrc.ac.uk

UGeneva ComparativeGenomics

PhD position Exploring Conserved Non-Coding sequences using comparative genomics

We are looking for a highly motivated and innovative PhD candidate to explore the evolution and patterns of selection acting on Conserved Non-Coding sequences (CNCs) in vertebrates using computational comparative genomics. It is estimated that about 4-7% of the human genome is under functional selection, yet only 2% encodes proteins. This implies that there is a repertoire of functionally important elements at least as large as the repertoire of protein-coding genes, whose functions remain largely unknown. The project will develop our lead findings and will benefit from established collaborations.

The ideal candidate should have a strong background in bioinformatics, including programming skills, and a good understanding of molecular biology and 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, heading the Computational Evolutionary Genomics group at the Department of Genetic Medicine and Development of 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: 31 May 2009.

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

Prof. Evgeny Zdobnov University of Geneva CMU / Dpt GEDEV Rue Michel-Servet 1 1211 Genève 4 Switzerland

Stefan.Wyder@unige.ch Stefan.Wyder@unige.ch

UGeneva EukaryotePhylogenomics

PhD position in Phylogenomics of Eukaryotes

We are looking for a highly motivated PhD student to work on phylogenomics of single-cell eukaryotes. Phylogenomics is a new field of evolutionary studies using large dataset of multigene sequences to infer phylogenetic relationships. Our group is specialized in evolution of amoeboid protists and recently successfully applied phylogenomic tools to investigate the very deep history of eukaryotes (see references below).

The present project focuses on evolution of Foraminifera, one of the most abundant and diverse groups of marine protists with well documented fossil record. The Foraminifera constitute the major group of Rhizaria, one of the six supergroups of eukaryotes recently established. However, despite their ecological and evolutionary importance, the Foraminifera and Rhizaria are among the few large groups of eukaryotes, for which there is still very limited amount of genomic data available. The project proposes to fill this gap by large-scale phylogenomic study of Foraminifera and related Rhizaria. The EST-based phylogenomic approach will be used to investigate the phylogenetic position of Foraminifera among Rhizaria, and in particular to test the hypothesis claiming their close relation to Radiolaria. The higher level relationships will be examined in order to identify the major steps in evolution of foraminifera, in particular the evolutionary importance of the passage from single to multichamber test and the multiple origins of calcification. The transcriptomic data will also be used to understand the genomic bases of some fundamental cellular processes present in Foraminifera. We will attempt to gain more insight into the mechanisms of reticulopodial motility and the unusual features of foraminiferal motor proteins. We will search for genes involved in the process of calcification. Finally, we will test the bacterial origin of denitrification recently discovered in some foraminiferal species.

The project is supported by the Swiss National Science Foundation and some genomic data will be obtained in collaboration with Genoscope (France). The position is based in the Molecular Systematics Group, Department of Zoology and Animal Biology, University of Geneva, Switzerland.

Starting date is the 1st of September 2009.

The candidate should have a diploma/MSc degree in biology or bioinformatics. She/he should have a strong interest in evolutionary biology of unicellular eukaryotes and a basic knowledge of their systematics and phylogeny. A solid experience in using various bioinformatic tools is required. The working language of the group is English but the knowledge of French would be helpful.

To apply, please send an e-mail with the cover letter, CV, and contact details of two referees to Jan.Pawlowski@unige.ch. Deadline for applications is 1st June, 2009.

References: Burki, F. & Pawlowski, J. (2006) Monophyly of Rhizaria and multigene phylogeny of unicellular bikonts Mol. Biol. Evol., 23:1922-1930. Burki, F., Shalchian-Tabrizi, K., Minge, M., Skaeveland, A., Nikolaev, S.I., Jakobsen, K.S. & Pawlowski, J. (2007) Phylogenomics reshuffles the eukaryotic supergroups. PLoS ONE, 2:e790. Burki, F., Shalchian-Tabrizi, K., Pawlowski, J. (2008) Phylogenomics reveals a new “megagroup” including most photosynthetic eukaryotes. Biology Letters, 10,1098/rsbl.2008.0224 Nikolaev, S.I., Berney, C., Fahrni, J., Bolivar, I., Polet, S., Mylnikov, A.P., Aleshin, V.V., Petrov, N.B., Pawlowski, J. (2004) The twilight of Heliozoa and rise of Rhizaria: an emerging supergroup of amoeboid eukaryotes. Proc. Natl. Acad. Sci. USA 101:8066-8071. Pawlowski J. and Burki F. (2008) Untangling the phylogeny of amoeboid protists. J. Eukaryot Microbiol. 56:16-25.

Dr. Jan Pawlowski Dept of zoology and animal biology University of Geneva, Sciences III 30, Quai Ernest Ansermet CH 1211 Genève 4, Switzerland

Phone: 00 41 22 379 30 69 Fax: 00 41 22 379 33 40 E-mail: jan.pawlowski@zoo.unige.ch
http://www.unige.ch/sciences/biologie/biani/msg/
Jan.Pawlowski@unige.ch

UGoteborg EchinodermAdaptations

Hello,

In attach an announcement for a PhD position at the Marine Ecology Department of the University of Göteborg in Sweden.

This is a 4 years project related to the impact of climate change (both global warming and ocean acidification) on marine species with special focus on echinoderms. The successful applicant will have to investigate how historical and temporal variability in environmental parameters can explain local adaptability. The sea urchin Strongylocentrotus droebachiensis will be used as model and different populations compared using a common garden approach combining ecology, physiology and genomic.

Do not hesitate to contact Mike Thorndyke (see anoucement) or myself for further infomatio

Deadline for application: 24 April 2009

For more information on our work related to this position, see:

Dupont S & Thorndyke M (2009) Impact of CO2-driven ocean acidification on invertebrates early life-history - What we know, what we need to know and what we can do. Biogeosciences Discussion. 6, 3109-3131. PDF: http://tinyurl.com/cz4ku6 (http://tinyurl.com/cz4ku6)

Dupont S, Havenhand J, Thorndyke W, Peck L & Thorndyke MC. (2008) CO2-driven ocean acidification radically affect larval survival and development in the brittlestar Ophiothrix fragilis. Marine Ecology Progress Series 373: 285-294. PDF: http://tinyurl.com/8tbc2z (http://tinyurl.com/8tbc2z)

Dupont S, Obst M, Wilson K, Sköld H, Nakano H & Thorndyke MC (2007) Marine Ecological Genomics - When Genomics meet Marine Ecology, Marine Ecology Progress Series 332: 257-273. PDF: http://tinyurl.com/9jvwxl (http://tinyurl.com/9jvwxl)

Sam

sam.dupont@marecol.gu.se

UGroningen EvolutionaryBiol

PhD scholarships in Evolutionary Biology and Ecology at the University of Groningen (Netherlands)

The Groningen Graduate School of Science is offering 25 PhD scholarships. These scholarships provide an internationally competitive level of student support, including four years of funding (ca. 20,000 euros annually) and an individual training budget. Candidates will be selected on the basis of their motivation and academic potential, and will have considerable freedom to develop their own project. A list of suggested topics can be found on our website. Many of these topics are in the areas of evolutionary biology, ecology and behavioural biology.

Located in a lively student city in the northern Netherlands, the University of Groningen (www.rug.nl) is renowned for its longstanding tradition of academic excellence and international approach to graduate education. The Centre of Ecological and Evolutionary Studies (www.rug.nl/cees) encompasses eight groups, which study ecology and evolution in a broad and integrative way. The research extends from the individual level via the population level to the ecosystem level; from terrestrial systems to oceanography; from micro-organisms to plants and animals. Research methods are also highly diverse, ranging from molecular studies in the lab (ecological and evolutionary genomics) to long-term field studies and theoretical modelling. The centre provides a stimulating research environment, an excellent course programme and modern up-to-date facilities.

Information about the programme and how to apply can be found at: www.rug.nl/gradschoolscience . Application deadline: May 1, 2009

Franz J. Weissing Professor of Theoretical Biology Centre for Ecological and Evolutionary Studies University of Groningen Nijenborgh 9 9747 AG Groningen The Netherlands tel: +31-50-363-8669 [or: 2131] E-mail: f.j.weissing@rug.nl URL: www.rug.nl/biol/theobio f.j.weissing@rug.nl f.j.weissing@rug.nl

UHawaii ConservationBiol

Graduate Scholarship in the Tropical Conservation Biology and Environmental Science (TCBES)

M.S. Program at the University of Hawaii at Hilo

http://www2.hawaii.edu/~tcbes/

Application deadline for graduate scholarship is 15 May 2009. A Bachelor's degree in biology is preferred with courses or experience in ecology, evolutionary biology, behavior or genetics.

Join a team that examines the mechanisms of local adaptation and speciation of Hawaiian Picture-winged Drosophila. We are currently focusing on several species on Hawaii Island and related species on other Hawaiian Islands. The Hawaiian Drosophila are known for their spectacular adaptive radiation, divergence of behavioral and sexually selected traits, and speciation. This project includes molecular, field, and behavioral studies to contrast patterns of neutral and expressed genetic variation among locally adapted populations and to quantify the fitness and behavioral differences of populations along elevation gradients. In addition, the research will examine molecular differences among closely related species and relate these differences to behavioral, ecological and morphological variation. The graduate scholar will receive training in field, molecular and behavioral methods and will contribute to the overall project, while also conducting thesis research.

The successful applicant will receive $22,000 annual salary, will enroll in the TCBES Program in August 2009, and will join a vibrant research community in evolutionary genetics at UH Hilo, comprising faculty, postdocs, and graduate and undergraduate students.

Students of Native Hawaiian, Pacific Islander, or other under-represented ancestries are especially encouraged to apply. For information on the TCBES Program and application procedures, visit: http://www2.hawaii.edu/~tcbes/ . Please direct questions to Dr. Donald Price (donaldp@hawaii.edu)

Donald Price Associate Professor of Biology Chair of TCBES Graduate Program University of Hawai'i at Hilo 200 West Kawili Street Hilo, HI 96720 Phone: 808-974-7365 Fax: 808-974-7693

donaldp@hawaii.edu

Donald Price <donaldp@hawaii.edu>

ULiverpool SeaBirdPhysiologyEvolution

UNIVERSITY OF LIVERPOOL School of Biological Sciences

NERC funded Studentship Eligibility: UK citizens and UK-resident (3 years+) EU citizens ONLY

Exploring the links between metabolism and fitness using seabirds as models Dr. J.A. Green jonathan.green@liverpool.ac.uk <mailto:jonathan.green@liverpool.ac.uk> and Dr. M. Berenbrink michaelb@liverpool.ac.uk <mailto:michaelb@liverpool.ac.uk>

Energy is the currency of life and understanding how animals gain, use and store energy is essential in helping us to understand how they function in their environment. Quantification of energetics enables us to understand the shape of the functional response curve between resource availability and reproductive success. This is particularly important as animals face changing environments and competition for their food resources.

Models predict that animals which maximise their energy gain while minimising their energy intake are likely to have greater fitness. The proposed project will investigate the links between rates of energy expenditure and performance in natural populations of seabirds. This should allow repeatability and heritability of these traits to be investigated and the relative importance of genotypic and phenotypic effects assessed. Seabirds are an ideal model for studies of this type as they are long-lived, philopatric, and show considerable reproductive skew. As a result, multiple generations of successful individuals can be found breeding alongside less successful individuals. The student will measure basal metabolic rate (BMR) and possibly field metabolic rate and determine how these traits are related to breeding success at different scales, while accounting for confounding effects such as age and seasonality. Measuring these variables will allow a number of conflicting hypotheses to be tested. Do successful animals have a low BMR which allows them to consume less food and pass more to their chick? Will successful animals have a high BMR, indicative of a high capacity to work and gain resources from their environment?

Opportunities exist for study in a number of different populations of seabirds, both at home and abroad, and the student will be expected to undertake fieldwork on isolated islands. Within the broad framework of the proposed project, there may be chances to develop experimental/manipulative approaches to answer these key questions.

Training :

Skills which will be learned during this project will include: Planning and executing expeditions and fieldwork. Ornithological/fieldwork techniques such as animal handling, biometric measurements and monitoring of breeding. Ecophysiological techniques including respirometry, the heart rate method and overall dynamic body acceleration (ODBA). Complex data handling in a variety of disciplines. Parametric statistics. Calculation of repeatability and heritability. Energy budget modelling. Writing and submission of data for publication. The student will need to train and apply for a Home Office Licence and will become familiar with the issues surrounding the ethics of experimentation on wild animals. The project will involve liaison with the governing and licensing authorities of the field sites.

References: Blackmer, A.L., Mauck, R.A., Ackerman, J.T., Huntington, C.E., Nevitt, G.A. & Williams, J.B. (2005) Exploring individual quality: basal metabolic rate and reproductive performance in storm-petrels. Behavioral Ecology 16, 906-913.

Nespolo, R.F. & Franco, M. (2007) Whole-animal metabolic rate is a repeatable trait: a meta-analysis. Journal of Experimental Biology 210, 2000-2005.

Wendeln, H. & Becker, P.H. (1999) Effects of parental quality and effort on the reproduction of common terns. Journal of Animal Ecology 68, 205-214.

Applications are invited from students who either hold or expect to obtain, a First or Upper Second class Honours degree in a relevant subject. Application by email, indicating the project(s) of interest (and supervisors) in priority order, giving the reasons for this, together with a c.v. including the names and contact details of two academic referees, should be sent as soon as possible to: Mrs. Linda J. Marsh, Research Support Office, School of Biological Sciences, The Life Sciences Building, Crown Street, Liverpool L69 7ZB (email: biolres@liverpool.ac.uk <mailto:biolres@liverpool.ac.uk>, Fax: 0151 795 5122). Please indicate where you first saw the project(s) advertised.

Dr Jonathan A Green Lecturer in Marine Biology

School of Biological Sciences University of Liverpool Crown Street Liverpool L69 7ZB UK

Tel: +44 (0) 151 795 4385 Fax: +44 (0) 151 795 4400

www.liv.ac.uk/marinebiology
Jonathan.Green@liverpool.ac.uk
Jonathan.Green@liverpool.ac.uk

UNebraska HemoglobinEvolution

Graduate Position: Hemoglobin Evolution - Univ. Aarhus (Denmark) and Univ. Nebraska (USA)

A salaried 3-year PhD position is available in the Department of Zoophysiology, University of Aarhus (Denmark). The project is part of a collaboration between researchers at the University of Nebraska, USA (Dr. Jay F. Storz) and the University of Aarhus (Drs. Angela Fago and Roy E. Weber).

The project is funded by the NIH and focuses on identifying adaptive functional changes in the hemoglobins of high-altitude mammals, with a primary focus on deer mice (Peromyscus). Studies will include structural and functional characterizations of natural and recombinant hemoglobins to identify mechanisms underlying changes in blood oxygen affinity following high altitude adaptation in mammals. The project involves an integration of molecular evolution, molecular population genetics, structural biology, biochemistry, and physiology.

Please note that the deadline for applications is 15 April 2009!

Candidates should contact us before applying, by sending their CV and recommendation letters to Angela Fago (angela.fago@biology.au.dk) and Roy Weber (roy.weber@biology.au.dk).

Applications will be evaluated by the Ph.D.-board of the Faculty of Science and scholarships will be awarded based on qualifications. Detailed information on the Ph.D. programme at Aarhus University and guidance to application is available at:

http://science.au.dk/en/studies/phd-studies/
JayF.Storz SchoolofBiologicalSciences UniversityofNebraska Lincoln,NE68588 Phone:402/472-1114 E-mail:jstorz2@unl.edu

http://www.biosci.unl.edu/labs/storz/index.html Jay F Storz <jstorz2@unlnotes.unl.edu>

UNewBrunswick 2 PopulationGenetics

2 Graduate Positions: population genetics, phylogeography, speciation

I seek two highly motivated and enthusiastic candidates to fill full time graduate student positions (MSc or PhD) in molecular ecology in the Department of Biology at the University of New Brunswick (Fredericton). My research focuses on the comparative population genetics and phylogeography of north Atlantic marine invertebrates and freshwater insects, and the biogeography of speciation in strongylocentrotid sea urchins.

Successful candidates should have a strong background in ecology and evolution, interests in population genetics and statistics, and preferably some experience with molecular techniques (but not required).

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/ The anticipated start date of both positions is September 2009. For more detail, or to apply, email a CV or resume, a letter of interest, and contact information for 2 references to Jason Addison (jaddison@unb.ca).

http://www.unb.ca/fredericton/science/biology/-Faculty/addison/addison.html – Jason A. Addison Assistant Professor, Department of Biology, University of New Brunswick, PO Box 4400 Fredericton, NB CANADA E3B 5A3 (506) 452-6210

jaddison@unb.ca

UPierreMarieCurie EvolutionaryTheory

PHD in evolutionary/theoretical ecology

We offer a funded PhD project focused on the influence of spatial structure on the ecological and evolutionary components of nutrient recycling. Applications are opened to master's students with a background in ecology that includes theoretical ecology and to master's students in mathematics or computing who have an interest in applying their skills to ecological issues. Candidates must be in the last year of their master degree (or equivalent diploma) and come from the European Union or other European countries affiliated to the European area for higher education. Please find below an abstract of the project. If interested, feel free to contact us for more details.

"Acquisition and recycling of nutrient: spatial, ecological and evolutionary components"

This project tackles the links between different phenotypic traits constraining the exploitation of resources by plants. Models will include explicitly ecological and evolutionary components of these traits, in a spatial context. This approach aims at provinding a better link between functional and evolutionary ecology, with important implications for community and metacommunity ecology. Some of the expected results, related to the storage capacity of nutrient by the community or to the effect of changes of traits on primary production may provide important insights for the management of ecosystems and agricultural systems.

The project will use metacommunity/metacosystem models as well as adaptive dynamics technics (or other types of evolutionary models), so that it is necessary that the candidate has good skills in theoretical ecology or applied mathematics.

For more information:

Nicolas Loeuille (nicolas.loeuille@gmail.com <mailto:nicolas.loeuille@gmail.com>, 01 44 27 36 10) Laboratoire Fonctionnement et évolution des systèmes écologiques (UMR7625, CNRS), Université Pierre et Marie Curie (Paris 6), 7 quai Saint Bernard, Bât. A, 7ème étage, case 237, 75252 Paris cedex 05 France

ou Sébastien Barot (Sebastien.Barot@bondy.ird.fr <mailto:Sebastien.Barot@bondy.ird.fr>, 01 44 32 37 03) RD-Laboratoire Bioemco (UMR 7618) Ecole Normale Supérieure 46 rue d'Ulm 75230 Paris cedex 05 France

Please apply before the 10th of may, with: -a detailled CV and motivation letter that details how you match the desired profile -grades of master degree -two recommendation letters or emails, to be sent directly to us

–

Sébastien Barot IRD-Laboratoire Bioemco (UMR 7618) Ecole Normale Supérieure 46 rue d'Ulm 75230 Paris cedex 05 Tél : (33) 1 44 32 37 03 sebastien.barot@ird.fr Site web : http://millsonia.free.fr/ Barot <Sebastien.Barot@bondy.ird.fr>

UppsalaU ComputationalGenetics

PhD student position available: Development and use of methods, algorithms and tools for functional evaluation of DNA variation related to growth in chicken

We are looking for a PhD-student to join our young and growing group. We provide a supportive environment and strongly believe in an interdisciplinary approach, so we encourage applicants with a non-standard background to apply. We are based in Uppsala, Sweden at the Swedish University of Agricultural Sciences and also have links with Uppsala University.

Empirical data from experimental chicken populations characterised phenotypically and genetically (e.g. genome resequencing and high-density genotyping) will be available for these PhD studies. Identification of mutations, pathways and genetic interactions underlying complex traits can improve our biochemical understanding and could be highly valuable for human medicine, agriculture and other areas of biology. This project aim to develop and use computational methods, algorithms and tools for functional evaluation of genetic variation located within identified quantitative trait loci. A good general understanding of molecular biology, programming skills and efficient utilisation of available bioinformatic resources are crucial components in this process.

Aside from work, you will have the chance to get to know Uppsala, which is a pretty university town, notable for its castle and cathedral. It is 40 minutes by train from Stockholm. We get some snow in winter and beautiful long summer days.

Qualifications A successful applicant should have relevant scientific education, be highly motivated for research and have an interest in molecular, quantitative and computational genetics. A strong mathematical / statistical background and programming experience are advantageous.

Forms for funding or employment Employment as PhD student 4 years

Further information This opportunity is also announced at http://www.slu.se/?id=3D1123&Granska=3D1&Utbildningsplatser_id=3D373 including information about SLU as an Equal Opportunity Employer as well as links and contacts for general information about PhD-studies at SLU.

If you have questions about us or our work, please contact Örjan Carlborg (Orjan.Carlborg@hgen.slu.se) or Stefan Marklund (Stefan.Marklund@hgen.slu.se). You can also find more information about our group at http://www.computationalgenetics.se and http://www.lcb.uu.se.

We are looking forward to hearing from you!

Applications Applications marked with ref no 251-861/09, must have arrived at the Registrar of SLU, P.O. Box 7070, S- 750 07 Uppsala or registrator@slu.se no later than 2009-05-29.

Selected recent publications: * Carlborg, Ö. and Haley, C. Epistasis: too often neglected in complex traits studies? Nature Reviews Genetics 2004 5: 618-625. * Carlborg, Ö., Jacobsson, L., Åhgren, P., Siegel, P., Andersson, L. Epistatsis and the release of genetic variation during long-term selection. Nature Genetics 2006 38:418-20. * Gjuvsland, A., Hayes, B., Plahte, E., Omholt, S., Carlborg, Ö. Statistical epistasis is a generic feature of gene regulatory networks. Genetics 2007 175:.411-420. * Le Rouzic, A., Siegel, P. and Carlborg, Ö. Phenotypic Evolution from Genetic Polymorphisms in Radial Network Architectures. BMC Biology 2007, 5:50. * Alvarez-Castro, J., le Rouzic, A. and Carlborg, Ö. How to perform meaningful estimates of genetic effects. PLOS Genetics 2008 May 2; 4(5):e1000062 * Le Rouzic, A., Alvarez-Castro, J. and Carlborg, Ö. Dissection of the genetic architecture of body weight in chicken reveals the impact of epistasis on domestication traits. Genetics 2008 179:1591-1599.

orjan.carlborg@lcb.uu.se orjan.carlborg@lcb.uu.se

USouthDakota Host ParasitePopGen

Graduate Student Position: Ph.D. student sought for host/parasite/conservation genetics study

Department of Biology, University of South Dakota, Vermillion, SD

I am seeking a doctoral student interested in the sylvatic plague/black-tailed prairie dog system. I recently received funding from the National Park Service for a three year study investigating the genetic concordance of black-tailed prairie dog (plague host) and flea (plague vector) populations in five western National Park units. We will use microsatellite and VNTR markers to investigate how plague is spread among black-tailed prairie dog colonies on the prairie landscape. The project will also involve plague detection using PCR in previously plagued and apparently naive colonies of prairie dogs. The results of this study may have important implications for the management of the black-footed ferrets and black-tailed prairie dogs in the study areas. A teaching assistantship is available to qualified applicants.

Minimum Qualifications: 1) MS in Biology or closely related field, 2) Desire and ability to carry out field work in remote areas with little supervision, 3) Experience with PCR and other molecular genetics lab techniques.

Preferred Start Date: August 15, 2009

Please contact: Hugh Britten, Ph.D., at hbritten@usd.edu for further details and visit www.usd.edu/biol/ < http://www.usd.edu/biol/ > for information about our graduate programs.

Hugh.Britten@usd.edu

UZurich ComputationalEvolutionaryBiol

WAGNER Andreas, Prof. aw@bioc.uzh.ch six digit code: 020000

PhD thesis in computational evolutionary biology

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

The successful candidate will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also necessary is a strong background in biology. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further

We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently. The working language in the laboratory is English. German skills, although helpful, are not essential.

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

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch <mailto:jobs_aw@bioc.uzh.ch>: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references. Please include the word $B!H(BEVO09$B!I(B in the subject line. The application deadline is May 22, 2009.

Christiane Gujan Administrative Assistant of Prof. A. Caflisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 (secretariat Prof. Caflisch) Fax 0041 (0)44 635 68 62 (secretariat Prof. Caflisch)

Tel. 0041 (0)44 635 61 42 (secretariat Prof. Wagner) Fax 0041 (0)44 635 61 44 (secretariat Prof. Wagner)

Christiane Gujan <gujan@bioc.uzh.ch>

Vienna PopulationGenetics

PhD Call 2009 at the University of Veterinary Medicine Vienna

Several PhD positions are available in the Institute of Population Genetics at the University of Veterinary Medicine in Vienna from autumn 2009. Through the analysis of natural variation the students will receive training in evolutionary theory and population genetics in an interdisciplinary research environment. Students will join a lively institute working at the interface between experimental and theoretical population genetics. Our institute represents a synthesis of theoretical and experimental expertise in population genetics (Christian Schloetterer), molecular evolution and bioinformatics (Carolin Kosiol), functional genetics (Alistair McGregor and Thomas Flatt) and conservation genetics (Franz Suchentrunk). We welcome applications from international students as the working language of the institute is English. Available projects include:

-Functional characterization of copy number variation in Drosophila (Schloetterer group)

-Probabilistic modeling of inter- and intraspecies sequence evolution (Kosiol group)

-Mechanisms and evolution of Drosophila life history and aging (Flatt group)

-Genetic basis of morphological variation in Drosophila (McGregor group)

-Measuring gene flow between hare species by massive parallel sequencing (Suchentrunk group)

See the following websites for more information on the projects and the application procedure:

http://i122server.vu-wien.ac.at/pop/index.html Application deadline is 15 May 2009

For questions and enquires, feel free to contact carolin.kosiol@vu-wien.ac.at

Carolin Kosiol Group Leader in Bioinformatics Institut für Populationsgenetik Veterinärmedizinische Universität Wien Veterinärplatz 1 A-1210 WIEN, Austria TEL +43(0)1-25077-4331 FAX +43(0)1-25077-4390 E-mail: Carolin.Kosiol@vu-wien.ac.at

http://i122server.vu-wien.ac.at/pop/lab_members/Carolin_Kosiol.html ckosiol@gmail.com

Jobs

AMNH NewYork LabResAssoc

Job: Laboratory Research Assistant Institution: American Museum of Natural History Location: New York City Start Date: May and on

The American Museum of Natural History's Sackler Institute for Comparative Genomics is looking for a skilled Laboratory Research Assistant to work with a group of researchers on projects across the taxonomic spectrum (viruses to mammals). Experience with DNA sequence and microsatellite data collection, as well as data management and analysis, are essential. Applicants must have demonstrated proficiency with up-to-date approaches, i.e. standard and alternative methods of DNA extraction including degraded tissues such as feces, bone and historical samples, standard skills for PCR and cloning, DNA sequencing and microsatellite optimization and analysis. Computer programs used in the lab for such analyses include Geneious, Sequencher, and GeneMapper, among others, so the applicants are expected to know how to process and edit trace files and score microsatellite genotypes. Knowledge of automated DNA sequencer (ABI 3730xl) usage and troubleshooting is essential. Knowledge of microsatellite library development is welcome. Applicants must hold a Bachelors or Masters degree in Biology, Genetics, Molecular Biology, Biochemistry, Evolutionary Biology or related fields. Preference will be given to applicants with work experience of over one year, data management skills, and proficiency with analysis software programs.

Interested applicants should send a cover letter detailing their experience and interests and a CV in PDF, along with the names and contact information of 3 references to Dr. Sergios-Orestis Kolokotronis at koloko@amnh.org. Applicants must put (and ONLY put) the following term (as-is) in the email subject line for applications to be considered: LabResAssistant.

The position is open as of May.

Sergios-Orestis Kolokotronis, PhD Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024 -USA- tel +1 212 313 7654 koloko@amnh.org http://genomics.amnh.org http://koloko.net koloko@amnh.org

AMNH NewYork LabSupervisor

Job: Laboratory Supervisor Institution: American Museum of Natural History Location: New York City Start Date: Immediately

Laboratory Supervisor American Museum of Natural History New York City

The American Museum of Natural History is looking for a Laboratory Supervisor to work with a group of researchers on a broad variety of systematic problems.

Responsibilities and Duties: Extract and Sequence DNA. Sequence editing (maintaining database) responsible for ensuring lab supplies are on hand, maintain lab equipment, training other laboratory users such as graduate students and postdoctoral fellows.

Qualifications: BS required, familiar with lab procedures for DNA extraction, PCR amplification, cloning, and sequencing. A plus if experienced in DNA analyzing equipment (3730 DNA analyzer and BIO Mech robot), High-throughput, Basic computer skills, experience with Lab related software (sequence editing software), and sequence databases.

Interested applicants should send a cover letter detailing their experience and interests and a CV in PDF, along with the names and contact information of 3 references to Ward Wheeler at wheeler@amnh.org. Subject line MUST include reference to Lab Supervisor Position.

The position is open now.

crowley@amnh.org

Berlin Bioinformatics MolecularBiology Biodiversity

Tenure-track Bioinformatics/Molecular Biology (3 positions) Next-Generation sequencing in Biodiversity Research

The Berlin Center for Genomics in Biodiversity Research (GenDiv) seeks to fill three tenure-track positions in support of a next-generation sequencing facility. The Center is jointly operated by the Berlin Botanical Garden - Botanical Museum (BGBM), the Freie Universitaet Berlin (FU), the Leibniz-Institute for Freshwater Ecology and Inland Fisheries (IGB), the Leibniz-Institute for Zoo & Wildlife Research (IZW), the Museum fuer Naturkunde Berlin (MfN), and the University of Potsdam. We are seeking highly motivated applicants for the following positions:

1 Bioinformatics Scientist 1 Molecular Biology / Genomics Scientist 1 Laboratory Research Technician

All positions are tenure-track, initially limited to two (technician) or three (scientists) years, and are available as of December 2009 (starting dates negotiable). Successful candidates must be willing to work closely with a diverse team of senior scientists, postdocs, and students. S/he will conduct research at one of three Leibniz-Institutes in Berlin (IZW, IGB, MfN), and at the core facility at BGBM. The working language of the laboratories is English and we value diversity in backgrounds and nationalities.

Bioinformatics Scientist (at IZW). The successful candidate will play a central role in linking experimentalists and evolutionary biologists studying gene expression. S/he will be in charge of bioinformatics data processing and analysis and will be heavily involved in interpretation of data. Requirements include a PhD in molecular biology, bioinformatics or related field, with a strong publication record and excellent skills in genomics and large-scale sequence analysis. The ideal candidate will have bioinformatic programming/scripting experience and a background in evolutionary biology.

Molecular Biology / Genomics Scientist (at IGB). The successful candidate will be responsible for exploiting next-generation sequencing for biodiversity research. S/he will be heavily involved in collection, analysis, and publication of data. Requirements include a PhD and strong publication record in genetics, genomics, or a related field. The ideal candidate will have experience with next-generation sequencing as applied to microbial genetics or environmental metagenomics.

Laboratory Research Technician (at MfN). The successful candidate will have completed an apprenticeship, preferably as a laboratory technician (BTA, MTA, CTA), or will have a Bachelors degree. Knowledge of molecular genetics in the field of genome sequencing is desirable. The ideal candidate will have experience with computers, the ability to work in a team, and demonstrated reliable performance.

Applications should be submitted by 30 May 2009, but will be considered until the positions are filled. Please submit your CV (including publications and funding), a cover letter indicating your research interests and experience, and the names and contact details of three referees to genomics_biodiv@fu-berlin.de. The Consortium is determined to increase the proportion of women in successful scientific careers and particularly encourages female scientists to apply.

For additional information and informal inquiries, please contact:

Bioinformatics Scientist: Dr. Simone Sommer (sommer@izw-berlin.de, Tel +49 (0) 30 5168 315)

Molecular Biology / Genomics Scientist: Dr Michael T. Monaghan (monaghan@igb-berlin.de, Tel +49 (0) 30 6418 1684)

Research Technician: Dr. Thomas von Rintelen (thomas.rintelen@mfn-berlin.de, Tel +49 (0) 30 2093 8404).

www.igb-berlin.de www.izw-berlin.de www.museum.hu-berlin.de www.wgl.de – monaghan@igb-berlin.de

BiK-F Germany ResAssist MolecularSystematics

The Biodiversity and Climate Research Centre (BiKF) has recently been founded by the Senckenberg Gesellschaft fuer Naturforschung, the Goethe University Frankfurt am Main, and additional partners. It is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The Project Area C (Adaption and Climate) invites applications for the position of a

Research Assistant (or PhD) position Project C2.4 [Ref. #C35] BAT IIa/2

The successful applicant will use molecular systematics techniques to investigate recent changes in the southern European ranges of lineages of the Hyles euphorbiae complex (Lepidoptera: Sphingidae). Extant populations will be sampled repeatedly to detect ongoing changes in haplotype composition. For comparison, methods of ancient DNA analyses will be used to sequence older museum specimens from areas of present hybrid zones. It is desired that the successful applicant earn a PhD degree in this position.

The applicant should hold an earned Diploma or Masters degree in biology, and have a sound background in population genetics and/or molecular phylogeography. Experience with RNA and qPCR is an asset for project prolongation. Fluent written and oral communication skills in English and willingness to develop and submit research funding proposals are required.

Salary and benefits are according to a public service position in Germany (BAT IIa/2). The Research Centre BiKF advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

The contract shall start as soon as possible and will be initially restricted to 19 months, with possible extension subject to the acquisition of additional external funding. The place of employment will be Dresden, Germany. The employer is the SENCKENBERG GESELLSCHAFT FUER NATURFORSCHUNG.

Please send your application by email attachment, mentioning the reference of this position (#C35) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2 referees and a copy of your diploma thesis and/or other exams before April 20th to: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. Email (to Service and Finances): recruiting@senckenberg.de with Cc. to anna.hundsdoerfer@senckenberg.de. For enquiries about the position and the contract conditions please write to Prof. Dr. B. Stribrny (email: bernhard.stribrny@senckenberg.de) and for scientific enquiries to Dr. A. Hundsdörfer (email: anna.hundsdoerfer@senckenberg.de).

Ursula Maurer M.A. Wissenschaftliches Koordinationsbüro LOEWE - Biodiversität und Klima Forschungszentrum BiK-F Besucheradresse: Georg-Voigt-Straße 16 Postadresse: Senckenberganlage 25 D-60325 Frankfurt am Main

Tel.: 069-7542-1819 Fax: 069-7542-7904 info-bik-f@senckenberg.de www.senckenberg.de/bik-f

Tiefsee- entdecken, erforschen, erleben

Sonderausstellung in der Wolfgang-Steubing-Halle des Senckenberg Naturmuseums: 19.12.08 â 30.6.09 www.tiefsee.senckenberg.de (http://www.tiefsee.senckenberg.de/)

Ursula Maurer <Ursula.Maurer@senckenberg.de>

CostaRica FieldAssist FrogVariation

Field assistant needed between 14th of May and 13th of July for an international research project on the granular poison frog, Oophaga granulifera, in Costa Rica.

This is a PhD project based at the Department of Zoology of the University of Veterinary Medicine (TiHo) in Hannover, Germany (supervisor Heike Proehl) and carried out in collaboration with Dr Nicholas Mundy, University of Cambridge, UK.

Aim of the project is to investigate the geographical variation in morphology, behaviour and genetic traits analysing different populations of Oophaga granulifera inhabiting pacific Costa Rica.

The field assistant will collaborate in collecting biometric measurements, males advertisement calls and tissue samples for genetic analysis.

There is a reimbursement of 100 Euros per week.

If you are interested please feel free to contact me for details.

Best wishes,

Oscar Brusa

Oscar Brusa <oscar.brusa@tele2.it>

Groningen ResearchTechnician MolEvolGenetics

Research Technician A research technician position is available at the Centre for Ecological and Evolutionary Studies (CEES) at the University of Groningen. The candidate will join a recently started research group that studies parasitoid-host interactions to unravel the evolutionary genomics of adaptations. The overall aim of the research group is to identify what genomic features (e.g., SNPs, transposons, epigenetic regulation) enable a rapid evolutionary response to adverse environmental conditions. The research technician will participate in various projects within the research group.

Requirements and duties The candidate will have a degree (BSc/HBO or equivalent) in a relevant subject (such as molecular biology or genetics), affinity with evolutionary biology, extended experience with molecular biology techniques and ideally will have worked with Drosophila previously. You will have excellent organisational and research skills, and a positive attitude to learn and troubleshoot new methods. The main duties include experimentation in molecular biology, genetics and insect biology, as well as meticulously carrying out routine fly work.

Additional conditions of employment Applications are invited for an experienced research technician, who will carry out research work and maintain fly and parasitoid stocks for Evolutionary Genomics research. The University of Groningen can offer you a salary dependent on qualifications and work experience from 1902,–(scale 7,number 0) up to a maximum of 2324,– (scale 7, number 4) gross per month for a full-time position. The position will be available for a period of 3 years, starting as soon as possible.

Additional information For more information you may contact Dr. Bregje Wertheim, e-mail address: b.wertheim@rug.nl. Or additional information can be obtained through one of the following links. About the organization: http://www.rug.nl About the Evolutionary Genetics group: http://www.rug.nl/biologie/-onderzoek/onderzoekGroepen/evolutionaryGenetics/-index Application Cover letters in English language, including a personal motivation (important!), a curriculum vitae, and the names and addresses of three referees (including telephone number and E-mail address), to be sent before 23 March 2009 to: vmp@rug.nl. Also send an electronic copy of your application to b.wertheim@rug.nl. When applying for this job always mentions the vacancy number 209077.

Bregje Wertheim Rosalind Franklin Research Fellow Evolutionary Genetics Biological Centre University of Groningen Postbus 14 9750 AA Haren The Netherlands

tel: +31 50 3639039 e-mail: b.wertheim@rug.nl

Kunming 2 ConservationBiol

Two PRINCIPAL INVESTIGATOR POSITIONS (Yan2 Jiu1 Yuan2) in ecology, conservation biology, and evolution, at the Chinese Academy of Sciences, based at the Kunming Institute of Zoology (KIZ), Kunming, China.

The Ecology, Conservation, and Environment Center

(ECEC) at KIZ (www.kiz.ac.cn) invites applications for two full-time PI positions in ecology and evolution, broadly defined. The rank is equivalent to an Assistant or Associate Professor in the US.

Senior applicants (those with faculty positions) will also be considered and are eligible for special recruitment packages from the national government.

The ECEC was recently established as a joint center between the Chinese Academy of Sciences and the University of East Anglia (UK). The ECEC's mission is to conduct international-quality research in ecology and conservation biology, to train Chinese and foreign Ph.D. and postdoctoral researchers, to lead the development of ecology and conservation science in China and Southeast Asia, and to provide information necessary for environmental policy-making. The KIZ is one of China's leading scientific research institutes for evolutionary biology, its faculty are internationally recognized, and the institute is building an ecology and conservation group on this foundation.

This is a superb opportunity to pursue an independent research program, backed by a large research team and ample funding. Highly qualified candidates conducting research on any taxa and in all areas of ecology, evolution, and conservation biology are encouraged to apply. We especially encourage applicants with research programs involving molecular ecology and bioinformatics, theory and modeling, conservation planning and economics, and/or climate change. Responsibilities include contributing to the ECEC's mission, obtaining external funding, and publication in top, international journals.

Considerable startup funding is available, generally at levels higher than those offered by European or US universities, and faculty will be members of the KIZ's State Key Laboratory of Genetic Resources and Evolution. Facilities at the KIZ include 454 next-gen sequencing, SNP, and gene-chip facilities in a new, national barcoding center to be installed this year, extensive internet journal access, a zoological museum with over 600,000 specimens, and access to CAS field stations, datasets, and facilities around the country. In addition to opportunities for collaboration within the ECEC and KIZ, there are ample local opportunities for collaboration with ecologists and evolutionary biologists at the Xishuangbanna Tropical Botanical Garden (xtbg.ac.cn &www.ecologicalevolution.org) and the Kunming Institute of Botany (www.kib.ac.cn), as well as local universities. In the near future, faculty from the three institutes, including the ECEC, will be combined to establish a new National Laboratory in biodiversity.

The working languages at the KIZ are Chinese and English. All nationalities are welcome to apply, and most faculty have had international research experience. It is possible to conduct research outside China with grant monies from China. Starting data is flexible.

Candidates with a strong record of accomplishment (a Ph.D., postdoctoral experience, and published papers in SCI journals) should submit a CV, a statement of research interests and plans, and pdfs of three publications. Please also include the names, addresses, and contact details of three individuals who can provide letters of recommendation. A single, combined PDF or zipped file is preferred and can be emailed to <ECEC.KIZ@gmail.com>. Informal enquiries can be made with the center's director, Dr. Douglas Yu <dougwyu@gmail.com>.

Applications will be reviewed starting 31 July 2009 until the positions are filled. This advert will be repeated over the next months.

Background information:

The Chinese Academy of Sciences (CAS) was established in 1949 and is China's national research organization, funding research and training in basic science and technology across a countrywide network of research institutes. CAS goal is by 2010 to make 30 of its research institutes internationally recognized and 3 to 5 of them world class.

KIZ: Established in 1959. Primary research areas have been evolutionary genetics and developmental biology, animal systematics, and animal and human disease models. There are about 200 staff, including 1 CAS member, and about 50 faculty, of which 7 PIs are supported by a CAS Excellent Young Scientists Program. There are about 100 MSc and 100 PhD students enrolled.

From 2005-8, the institute published 812 papers (505 in SCI-indexed journals), including articles in Science, Am. J. Human Genetics, PNAS

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Kunming EvolutionaryBiology

Two PRINCIPAL INVESTIGATOR POSITIONS (

Yan2 Jiu1 Yuan2) in ecology, conservation biology, and evolution, at the Chinese Academy of Sciences, based at the Kunming Institute of Zoology (KIZ), Kunming, China.

The Ecology, Conservation, and Environment Center (ECEC) at KIZ invites applications for two full-time PI positions in ecology and evolution, broadly defined. The rank is equivalent to an Assistant or Associate Professor in the US. The ECEC was recently established as a joint center between the Chinese Academy of Sciences and the University of East Anglia (UK). The ECEC's mission is to conduct international-quality research in ecology and conservation biology, to train Chinese and foreign Ph.D. and postdoctoral researchers, to lead the development of ecology and conservation science in China and Southeast Asia, and to provide information necessary for environmental policy-making. The KIZ is one of China's leading scientific research institutes for evolutionary biology, its faculty are internationally recognized, and the institute is building an ecology and conservation group on this foundation.

This is a superb opportunity to pursue an independent research program, backed by a large research team and ample funding. Highly qualified candidates conducting research in all areas of ecology, evolution, and conservation biology are encouraged to apply. We especially encourage applicants with research programs involving molecular ecology and bioinformatics, theory and modeling, conservation planning and economics, and/or climate change. Responsibilities include contributing to the ECEC's mission, obtaining external funding, and publication in top, international journals.

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Candidates with a strong record of accomplishment should submit a CV, a statement of research interests and plans, and pdfs of three publications. Please also include the names, addresses, and contact details of three individuals who can provide letters of recommendation. A single, combined PDF or zipped file is preferred and can be emailed to <ECEC.KIZ@gmail.com>. Informal enquiries can be made with the center's director, Dr. Douglas Yu <dougwyu@gmail.com>.

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KIZ (www.kiz.ac.cn): Established in 1959. Primary research areas have been evolutionary genetics and developmental biology, animal systematics, and animal and human disease models. There are about 200 staff, including 1 CAS member, and about 50 faculty, of which 7 PIs are supported by a CAS Excellent Young Scientists Program. There are about 100 MSc and 100 PhD students enrolled.

From 2005-8, the institute published 812 papers (505 in SCI-indexed journals), including articles in Science, Am. J. Human Genetics, PNAS USA, The Plant Cell, Genome Res., PLoS Medicine, and Human Molecular Genetics. 230 of these papers were published in journals ranked in the top 30% by the Thomson-Reuters Journal Citation Report. PIs have earned several patents and numerous awards from the Chinese Academy of Sciences and other national bodies, plus 3 awards from international organizations. Two PIs head CAS-Max Planck Junior Scientist groups.

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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

Munich EvolGradProgram Coordinator

The EES-LMU Graduate Program in Evolution, Ecology and Systematics at the University of Munich (LMU), currently funded by the Evolution Initiative of the Volkswagen Foundation, is looking for a *Coordinator (part time or full time)* for our Master and Ph.D. program, the summer school, and the seminar series. The position is initially for 6 months, with a possible extension for 33 months. The ideal candidate should have a degree (preferably a Ph.D.) in biology or a related field. He/she should be highly motivated and have good communication skills. Proficiency in English and German is required. Experience with teaching, administration or curriculum coordination is an advantage.

The novel, research-oriented Master program started in fall 2007, mainly with international students. The structured Ph.D. program started in February of this year with a cohort of 15 PhD students.

The EES-LMU Graduate Program is run by the Biology Department of the LMU. In addition, the LMU Department of Earth- and Environmental Sciences, the Max Planck Institute for Ornithology, the Bavarian Natural History Collections, and groups at the Munich Technical University are involved. The coordinator functions as an interface between university administration, teachers, and students, and he/she could be involved in teaching. The coordinator will also organize summer schools, conferences and a seminar series, and he/she will contribute to the website http://www.eeslmu.de/eeswiki . EES-LMU offers a great working environment for someone interested in science and teaching, and who enjoys interacting with students and professors to improve education in ecology, evolution and systematics.

The position is initially available at TVöD 13 according to the German salary scale. Application review will start May 15th and will continue until the position is filled. Interviews will be held in late May. Informal inquiries and applications including a letter of motivation, CV, and names and telephone numbers of two references, should be sent preferably by email (as a single pdf file) to

The Speaker of the EES-LMU Program Prof. Dr. Susanne Foitzik foitzik@biologie.uni-muenchen.de <mailto:foitzik@biologie.uni-muenchen.de> +49 89 2180 74 209

– Prof. Dr. Susanne Foitzik Department Biologie II Behavioral Ecology (Verhaltensökologie) Ludwig-Maximilians-Universität München Großhaderner Str. 2 D - 82152 Planegg / Martinsried Germany

Phone: + 49 89 / 2180 74 209 Fax: + 49 89 / 2180 74 221 e-mail: foitzik@biologie.uni-muenchen.de http://ecology.bio.lmu.de/etho_e/index.htm foitzik@zi.biologie.uni-muenchen.de foitzik@zi.biologie.uni-muenchen.de

OhioStateU Tech PlantEvolution

Laboratory technician position (research associate I) Mercer lab at Ohio State University Plant evolutionary ecology in agricultural systems Applications accepted April 4-12

I am seeking a highly motivated individual to fill a full-time lab technician (Research Associate I) position in a newly established lab at The Ohio State University, Columbus, Ohio. The successful candidate will work on projects related to the evolutionary ecology of agricultural plants – both weedy and cultivated.

In particular, my lab focuses on the evolutionary impacts of crop-wild hybridization in sunflower as it relates to risk assessment for transgenic crops and the effects of climate change on crop genetic resources in the US and Mexico. Both projects involve a combination of molecular and quantitative genetic approaches with lab, greenhouse, and field components. The successful candidate will assist in design of studies; coordinate and conduct experiments; collect and maintain data and records; execute data organization and relevant statistical analyses (including regression and analysis of variance) to prepare research manuscripts for publication; perform literature searches and assemble reviews of relevant topics for preparation of grant proposals or manuscripts; provide general supervision to undergraduate students and hourly student employees; and support research performed by graduate students and postdoctoral researchers.

The required characteristics of a successful candidate include an MS degree in Biology, Agronomy, or a related field; the ability to translate, adapt and apply academic and practical knowledge in the conduct of biological science research; experience working with plants in the field or greenhouse; ability to work independently on all aspects of research; experience performing statistical analysis; excellent written and oral communication skills; and considerable experience with Microsoft

Word and Excel. Desirable characteristics include prior experience as a laboratory technician in a biological research lab; experience running statistical analyses on SAS; experience with molecular genetic analysis; and willingness to travel in the US and Mexico. The position would start as soon as possible.

To apply, submit an on-line application through the Ohio State University jobs website (< http://-jobs.osu.edu/ >http://jobs.osu.edu/). The position will be posted from April 4 - April 12. During that period, you can search for the position on the website using requisition number 344324. In addition to the standard application form, please include a cover letter indicating why you are interested in the position, as well as a resume or CV.

Kristin Mercer Assistant Professor The Ohio State University Department of Horticulture and Crop Science 310D Kottman Hall 2021 Coffey Road Columbus, OH 43210

Office: (614) 247-6394 Lab: (614) 247-8626 (341 Kottman) Fax: (614) 292-7162

email: mercer.97@osu.edu

mercer.97@osu.edu

PeabodyMuseum TempAssistant

Museum Assistant I

FIXED DURATION. Three years from date of hire.

General Purpose This is a National Science Foundation funded project. The museum assistant will participate in the organization, physical care, and documentation of fluid-preserved vertebrate specimens, and be responsible for the effort to rehouse most of the specimen lots in new containers, update cataloging in the Peabody's electronic database, and print new specimen labels.

Essential Duties of the Position 1. Be responsible for the effort to rehouse the fluid-preserved vertebrate specimens into updated containers, verify specimen information using the museum's EMU database, and print updated labels for all specimen lots.

2. Organize a variety of identified vertebrates according to a specific system of taxonomic classification.

3. Sort and identify to species fluid-preserved fish specimens, and assist with the identification of fluid-preserved amphibian, reptile, bird, and mammal specimens.

4. Recognize unique accessions, collection events, and use taxonomic keys in cataloging specimens.

5. Under the direction of the Collection Manager and Museum Assistant III, electronically catalogue specimens using the museum's EMU database, and manage other aspects of data associated with specimens.

6. Perform general maintenance of fluid-preserved specimens.

Experience and Training 1. Required: Bachelor's degree in biology, or related filed with specific courses in organismal biology.

2. Work experience with natural history collections.

3. Knowledge of fish diversity demonstrated through coursework, fieldwork, or research.

4. Working knowledge of computer programs that include word processing, spreadsheets, and databases.

Skills and Abilities 1. Ability to work with various fluid preservative fixing agents, such as ethanol and formaldehyde.

2. Working knowledge of species diversity of North American freshwater fishes, deep-sea fishes, and Antarctic marine fishes.

3. Physical dexterity to manipulate organisms under a dissecting microscope.

4. Ability to lift heavy containers or specimens (50 lbs.).

5. Ability to work with a dermestid beetle colony for the preparation of osteological specimens.

Application and Salary Information

Persons should send a letter outlining interest in the position, a CV, and names to three references to Thomas J. Near (thomas.near@yale.edu).

The first year salary is $38,863 with a 4.5% raise in each of the two following years.

thomas.near@yale.edu thomas.near@yale.edu

PennStateU 6 InfectiousDisease

The following ad will shortly appear in Science. Informal enquiries to any of us. www.cidd.psu.edu< http:/-/www.cidd.psu.edu/ > .

Infectious Disease: Faculty Appointments in The Evolution & Dynamics of Pathogens

The Eberly College of Science, The College of Agricultural Sciences, The College of Earth and Mineral Sciences, The Huck Institutes of Life Sciences and The Penn State Institutes of Energy & the Environment are seeking to appoint a number of faculty positions in the fields of theoretical and empirical infectious disease biology. Specifically we are interested in exciting interdisciplinary candidates who are Mathematicians, Physicists, Climate Modelers or Biologists, to provide novel insights into parasite-host interactions that range from within-host interactions, between-host transmission events and population-level dynamics.

We seek interactive people who can work across disciplines and identify novel insights and solutions to managing the disease burden. We encourage candidates interested in dynamical issues relating to pathogen epidemiology and evolution, such as the evolutionary impact of drugs, vaccines and insecticides, and the role of ecological and evolutionary factors in the invasion and emergence of diseases. We also seek candidates with expertise in theoretical modeling and the interaction of climate and disease - specifically dynamical downscaling of global and regional climate to elucidate the biological processes of disease transmission. The candidates will become integral to one of our centers of excellence in infectious disease such as The Center for Infectious Disease Dynamics http://www.cidd.psu.edu/ , The Center for Molecular Immunology and Infectious Disease http://cmiid.psu.edu< http://cmiid.psu.edu/ > or The Earth Systems Science Center: http://www.essc.psu.edu/ . We are cluster hiring in this area and will consider appointment at any scale for Assistant, Associate or Full Professor. Penn State offers highly competitive salaries and startup package with institutional support for students. Please submit one electronic application consisting of a covering letter including future research plans, curriculum vitae and the names of three references to Judie Burns at jeb1@psu.edu<mailto:jeb1@psu.edu>. Review will start June 15th and continue until a number of positions have been filled.

Andrew Read, Centre for Infectious Disease Dynamics, Departments of Biology and Entomology, 208 Mueller Laboratory, The Pennsylvania State University, University Park, PA 16802, USA

www.thereadgroup.net< http://www.thereadgroup.net >

www.cidd.psu.edu< http://www.cidd.psu.edu >

www.bio.psu.edu< http://www.bio.psu.edu >

www.ento.psu.edu< http://www.ento.psu.edu >

+814 867-2396 (office, biology) +814 863-4444 (office, entomology) +814 867-2397 (lab)

+814 865-9131 (fax)

a.read@psu.edu a.read@psu.edu

PennStateU ResAssist MolEvol

Job: Research Assistant in Molecular Evolution Institution: Pennsylvania State University Location: University Park, PA, USA Start date: immediately (or negotiable)

An academic Research Assistant position is available immediately in a molecular evolution laboratory supervised by Dr. Blair Hedges in the Department of Biology at The Pennsylvania State University (http://evo.bio.psu.edu/hedgeslab/). The successful candidate for this position will assist with ongoing research projects, with primary responsibilities to include preparation of DNA to be sequenced, evolutionary analysis of DNA sequence data, and some laboratory management duties including occasional training and supervision of laboratory personnel. Requires a bachelor of science degree in the biological sciences (biology, biochemistry, molecular biology or related area) and a master of science degree (or equivalent experience) in the biological or computer sciences (or related fields). Must have laboratory skills in working with DNA and analytical skills in working with DNA sequence data. Computer programming skills are advantageous, but not required. Salary commensurate with experience. Screening of applicants to begin immediately and continue until position is filled. To apply, email a cover letter briefly describing your experience, interest in the job, and career goals, along with your resume, college transcripts (unofficial acceptable), and contact information for three references to Dr. Hedges at sbh1@psu.edu (place “Evolution position” in subject line). This is a non-tenure track, fixed-term appointment funded for one year from date of hire with an excellent possibility of re-funding. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

sbh1@psu.edu sbh1@psu.edu

SouthAfrica FieldAssist Meerkats

Field assistant for study on prospecting behaviour in meerkats, South Africa

A field assistant is required for a PhD student from the University of Cambridge conducting research on the variation in extraterritorial prospecting behaviour in meerkats, at the Kalahari Meerkat Project, Northern Cape, South Africa, from August 2009 to February 2010.

Daily work involves radio-tracking, behavioural and movement data collection of prospecting male meerkats, helping with field experiments, and many hours under the desert sun.

All living and transport expenses whilst in South Africa will be covered.

Previous field experience is preferred, but not essential. Applicants are required to have a driving licence and experience. Interested applicants should send a cover letter and CV to:

Raff Mares, crm53@cam.ac.uk

For position advert: http://www.zoo.cam.ac.uk/-zoostaff/larg/pages/Mares_Assistant.PDF For more information about the field site (Kuruman River Reserve): http://www.kalahari-meerkats.com raffmares@gmail.com

Stuttgart CropPopulationGenomics

Group leader / Research associate in Stuttgart/Germany

Quantitative genetics or population genomics of crop plants (2 x 3 Years)

A position as non-tenure track “Assistant Professor” (German government salary scale E13 or A13) is available immediately in the Institute of Plant Breeding, Seed science and Population Genetics at the University of Hohenheim, Germany in the newly established research group 'Crop plant biodiversity and breeding informatics' led by Karl Schmid.

We are looking for a commited scientist who works in one of the following areas: â Evolutionary genetics of environmental adaptation in model or crop plants â Population and evolutionary genomics of crop domestication â Development and application of population genetic methods for genetic mapping and plant breeding

We are particularly interested in candidates with a solid quantitative or evolutionary background and good bioinformatics skills who plan to incorporate modern genomic approaches into their research program. The position is ideally suited for a Ph.D. with previous postdoc experience who wants to start his or her own independent research and to acquire external funding from national and international sources.

The successful applicant will be initially appointed for three years with the possibility of extension for another three years. Some teaching is required, which will be conducted in English, and there is the possibility to obtain the Habilitation.

The University of Hohenheim is located on a beautiful campus in the South German city of Stuttgart and has recently been evaluated as one of the top agricultural universities in Germany. Further information on our group can be obtained from http://evoplant.uni-hohenheim.de or from the contact information below.

Please send your application (cover letter, CV, Publications, Research interests, addresses of at least two references) until 3 May 2009 as electronic documents (PDF) to the following address:

Prof. Dr. Karl Schmid Institute of Plant Breeding, Seed Science and Population Genetics Fruwirthstrasse 21 D-70599 Stuttgart Germany Phone: +49 711 459 23487 Email: karl.schmid@uni-hohenheim.de

Karl Schmid <karl@minzer-schmid.de>

TexasAMU NineMnth ComparativeAnatomy

The Department of Life Sciences invites applications for a non-tenure-track, instructor-level position in Anatomy & Physiology to begin in academic year 2009-10. This is a full-time, nine-month appointment. Minimal requirements for the positions are a Master's degree with eighteen graduate hours in the appropriate discipline, and prior experience in an academic setting.

More information is available at: http://sci.tamucc.edu/openpositions/ap.html .

Please do not email me about this position. I am not on the search committee. There is a contact for questions listed at the link above.

Deb Overath

R. Deborah Overath, Ph.D. Assistant Professor of Biology Local Program Director Hispanic Leaders in Agriculture and the Environment Department of Life Sciences (ST 312) 6300 Ocean Drive, Unit 5800 Texas A&M - Corpus Christi Corpus Christi, TX 78412

Phone: (361) 825-2467 Fax: (361) 825-2742

"Overath, Deborah" <Deborah.Overath@tamucc.edu>

Trondheim FieldAssist BirdBreedingEvolution

Field Assistant / Potential PhD Student Position

The Evolution of Cooperative Breeding in Birds

Detailed behavioural observations and life history data will be collected on an already tamed population of colour-banded apostlebird groups at UNSW Arid Zone Research Station at Fowlers Gap, Australia. This study is part of wider empirical and theoretical work involving collaborators in various countries, but specifically Prof. Jon Wright (NTNU, Norway), Dr Andrew Russell (Sheffield Univ., UK) and Dr Simon Griffith (Macquarie Univ., Australia). We are specifically interested in the evolution of helping-at-the-nest and the effects of individual 'state', and so observations will be accompanied by assessments of individual variation in body mass by getting habituated birds to stand electronic balances. This is an expenses paid field assistant position in the first instance, with the opportunity to apply for a funded PhD position. All nationalities eligible (masters degree preferred). Preferred start date Aug 2009.

– Prof. Jonathan Wright Institute of Biology, NTNU, Trondheim, N-7491 Norway.

E-mail: jonathan.wright@bio.ntnu.no Tel: +47 73 596070 Fax: +47 73 596100

Jonathan Wright <jonathan.wright@bio.ntnu.no>

UAberdeen PopulationBiology

We are seeking an enthusiastic researcher to join ECOCYCLES, a part of the FP7 ERA-NET program BiodivERsA funded by NERC and DEFRA, and based within a thriving group of ecologists at the University of Aberdeen http://www.abdn.ac.uk/ibes/research/ecology/ . We seek a research fellow in Quantitative Population Ecology with an interest in life histories, conservation and strong statistical skills. You will explore, using modelling and analytical approaches, the demographic response of avian and mammalian predators to changes in cyclic prey dynamics in four different ecosystems across Europe. You will be highly motivated, capable of independent work, have a relevant degree and proven track record in publishing papers in international journals. You will have expertise in ecological and population processes, experience of working with trophic prey interactions, experience of stochastic matrix projection models, and/or statistical analysis of time-series and/or capture-recapture data. You will have a sound knowledge of programming (with R or C++) and experience of working in teams.

Informal enquiries may be made to Professor Xavier Lambin (x.lambin@abdn.ac.uk<mailto:x.lambin@abdn.ac.uk>).

Details on http://www.abdn.ac.uk/jobs/display.php?recordid=3DYZY191R The University of Aberdeen is a charity registered in Scotland, No SC013683.

x.lambin@abdn.ac.uk x.lambin@abdn.ac.uk

UCDavis BioinformaticsForestGenomics

The following Bioinformatic Scientist position is available through the Department of Plant Sciences at the University of California at Davis

Candidate is responsible for scientific and systems programming, design and analysis, database administration, network administration, system administration, research and collaboration in support of projects related to conifer genomics.

Applicant should have the following qualifications:

Academic background in computer science, statistics and bioinformatics. Experience in applying and implementing bioinformatics analysis tools, algorithms, and databases. Programming experience with languages/tools, such as Perl, Java, C/C++, PostgreSQL, Oracle, and MySQL. Experince with multiple operating systems, modern programming languages, relational database management systems, and web technologies. Written, communication and presentation skills to participate in scholarly articles published in peer-reviewed journals. Supervisory skills to effectively participate in hiring, training and providing direction to undergraduate students, graduate students, and staff

To learn more about current research, please visit: http://dendrome.ucdavis.edu To learn more about this position and to apply, please follow the instructions @ http://www.employment.ucdavis.edu/applicants/-Central?quickFind=52079 jillylee@gmail.com

UGeneva ScientificProgrammer ComparativeGenomics

Scientific Programmer Bioinformatics infrastructure development and data mining.

We are looking for a highly motivated, innovative and independent person with a strong background in software engineering and hands-on experience in building and managing large-scale data analysis pipelines in Unix environment to support numerous bioinformatics research projects led by the members of the lab, and possibly being involved in practical data mining. We are working at the exciting interface of bioinformatics and genomics, and operate with Terabytes of data in a HPC Unix cluster environment.

Candidates must demonstrate clear evidence of successful work, and have at least 3 years experience in a multidisciplinary research environment. Practical programming experience in Unix environment, SQL databases, and fluency in English are required. Knowledge of Web technologies (Web 2.0, AJAX, CSS, PHP), statistical data analysis, and MATLAB is a plus.

The Computational Evolutionary Genomics group, headed by Prof. E. Zdobnov, is part of the Department of Genetic Medicine and Development of the University of Geneva Medical School. We are also part of the renowned Swiss Institute of Bioinformatics (SIB, http://www.isb-sib.ch/), 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.

Salaries: 68'000-94'000 CHF/y depending on experience.

Closing date for applications: 31 May 2009.

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

Prof. Evgeny Zdobnov University of Geneva CMU / Dpt GEDEV Rue Michel-Servet 1 1211 Genève 4 Switzerland

Stefan.Wyder@unige.ch Stefan.Wyder@unige.ch

UNorthCarolina ChapelHill ResAssist HybridFitness

Subject: Research Opportunity at University of North Carolina

Karin Pfennigs lab in the Department of Biology at the University of North Carolina, Chapel Hill seeks a research technician for a collaborative project studying gene expression and hybrid fitness in spadefoot toads. This project is in collaboration with Corbin Jones Lab, also at UNC. The position is a 1-year post and is therefore ideal for recent graduates seeking additional experience prior to graduate school.

The successful candidate will have a BA/BS degree and experience in a molecular lab. In particular, the candidate must have good organizational skills, be detailed oriented, and be comfortable with isolating DNA and RNA, as well as performing PCR and Western Blots. Although preference will be given to local (North Carolina) candidates, all applications will be considered. Some background in evolutionary biology is a plus, as is experience working with vertebrates. Salary will range from $25-30K depending on experience.

Please submit a letter of interest, resume/CV to Drs. Karin Pfennig (kpfennig@email.unc.edu) or Corbin Jones (cdjones@email.unc.edu). Please also arrange to have 3 letters of reference sent separately. Additional information about the project can be found at: http://www.bio.unc.edu/Faculty/kpfennig/ . 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

"Corbin D. Jones" <cdjones@email.unc.edu>

UTexasAustin ResAssoc EvolutionaryBiol

Position Title: Research Associate

Employer: Howard Hughes Medical Institute

Where: Section of Integrative Biology, University of Texas at Austin, Austin, TX

Classification: Full-time

Starting Salary: $28,000 to $35,000 annually depending on qualifications, plus benefits.

Start date: September 1, 2009

Duration: Renewable annually, with an expected duration of three years. Depending on performance, the Research Associate may have the option of extending for up to an additional three years (six years total).

Job summary:

The Bolnick lab in the Section of Integrative Biology at the University of Texas at Austin, is seeking a highly motivated research associate to assist with a study of how macroparasites drive immune system evolution in a fish host. The research associate will be an employee of the Howard Hughes Medical Institute.

Responsibilities will include:

Quantifying parasite incidence and identity in wild-caught fish specimens. DNA extraction, amplification, and sequencing/genotyping of hosts and parasites. Assisting in daily management of the laboratory, including purchasing, equipment maintenance, database management, and animal care. The technician will assist with periodic field work on Vancouver Island, Canada, to obtain specimens.

Minimum qualifications:

A Bachelor's degree in biology or equivalent field. A strong work ethic, an ability to work independently, and good organizational skills.

Preferred qualifications:

A Masters degree in an appropriate subfield of biology, including but not limited to evolution, ecology, immunology, parasitology, ichthyology, molecular genetics, or bioinformatics. Experience with parasite taxonomy, molecular genetics tools (DNA extraction, PCR, sequencing, SNP arrays, expression arrays, or pyrosequencing), and/or database management and bioinformatics would be useful.

To apply:

Mail a letter of application with a description of past research experience and education (degree, institution, GPA, courses taken), a curriculum vitae, and the names of three references to:

Dr. Daniel Bolnick Section of Integrative Biology One University Station C0930 University of Texas at Austin Austin TX 78712, USA

Alternatively, the application may also be sent as a single pdf file to: danbolnick@mail.utexas.edu

For more information on the Bolnick lab, visit: https://webspace.utexas.edu/dib73/Bolnicklab/-Bolnicklab.html The Howard Hughes Medical Institute is an Equal Opportunity Employer.

Dr. Daniel I. Bolnick Assistant Professor Section of Integrative Biology One University Station C0930 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@mail.utexas.edu

UWesternSydney Biodiversity

Academic positions in Plant Biochemistry, Ecological Systems/Biodiversity, Nutrient Cycling/Biogeochemistry

Exciting opportunities exist to join the Centre for Plant and Food Science at the University of Western Sydney (UWS), as Lecturer/Senior Lecturer (Academic Levels B/C). We are seeking three energetic scientists with a sound research track record and established or emerging international reputation in any of the three disciplines:

- Plant Biochemistry (reference 245/09) - Ecological Systems / Biodiversity (reference 246/09) - Nutrient Cycling / Biogeochemistry (reference 247/09)

The Centre for Plant and Food Science at UWS conducts fundamental and applied research in a range of areas that include climate change biology, plant-environment interactions, sustainable plant production, applied entomology, soil microbiology and ecological systems. The Centre boasts significant research facilities including state-of-the-art equipment and infrastructure. The successful applicants will be expected to conduct research within the Centre for Plant and Food Science and contribute to teaching in the School of Natural Sciences, UWS.

Position Enquiries: Professor John Cairney, +61 (02) 4570 1404, or j.cairney@uws.edu.au <mailto:j.cairney@uws.edu.au>

Closing Date: 20 May 2009

More detailed information and an application guide can be obtained from http://uws.nga.net.au/cp/. Scroll to the job reference numbers (above). Click on the reference number and follow the instructions at the bottom of the page on 'How To Apply'.

Dr Markus Riegler Centre for Plant and Food Science School of Natural Sciences University of Western Sydney Locked Bag 1797 Penrith South DC NSW 1797 Australia

office: +61-(0)2-4570 1229 fax: +61-(0)2-4570 1314

"be part of symbiosis research"

M.Riegler@uws.edu.au M.Riegler@uws.edu.au

UZurich EvolutionaryBiol

The Faculty of Science at the University of Zurich invites applications for a

Professorship in Ecology and Evolution

We seek outstanding, innovative applicants with a record of excellence in research, who have proven their ability to develop and apply novel or interdisciplinary concepts in ecology and evolution. Areas of interest include, but are not limited to, evolution of complex traits, speciation, evolution of development, population or quantitative genetics, ecophysiology, biodiversity, or species interactions.

The successful candidate is expected to develop a strong, indepen- dent research program, attract external funding, and contribute to graduate and undergraduate teaching. The position is open rank (tenure-track assistant professor to full professor).

Zurich offers a stimulating scientific and cultural environment, including a rich spectrum of research activities in life sciences and medicine, and provides extensive opportunities for collaborations with research groups at the Faculties of Science and of Medicine of the University of Zurich, as well as teams at the nearby ETH Zurich.

The University of Zurich provides generous research support, including earmarked funds for personnel and running expenses, and competitive start-up packages.

Applications should include a curriculum vitae, a publication list, a summary of present and future research interests, and a vision statement that outlines major unsolved problems in the field and how they could be tackled by the planned research. Documents should be sent, together with names and addresses of three potential referees, to Prof. Michael Hengartner, Dean of the Faculty of Science, University of Zurich, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland by June 15, 2009. The application material should be submitted as a single PDF file to jobs@mnf.uzh.ch.

For further information, please contact Prof.Lukas Keller at lukas.keller@zm.uzh.ch.

Lukas Keller <lukas.keller@zm.uzh.ch>

Other

ABIPrism377 DNASequencer to give away

Offering: ABI Prism 377 DNA Sequencer as is. The instrument is not working at the

moment and needs repair and we are unclear about the problem. It comes with the Power Mac G3 (incl. keyboard and mouse) and a spare laser unit, which was taken out of the instrument at another time of repair, but is still useful. Further included are all the accessories (glass plates, combs etc.).

Please not that recipient pays for crating and shipping.

If interested please contact:

Katrin Sommerfeld

for Dr. Andrew Roger

Dalhousie University Dept. of Biochemistry & Molecular Biology 5850 College Street Halifax, NS, B3H 1X5, Canada email: ksommerf@dal.ca Phone: (902) 494-3569

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

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

AFLP extraction answers

Dear all,

Many thanks to all the contributors, it really helps.

Many asked for the answers. They where quite varied, so I copied below the original messages, with slight editions.

Cheers,

Matthieu

——— 1. Rachel

I have been doing exactly this over the past year or so.... and so I have a few pointers. Hopefully they're useful.

1. I went the silver staining route initially but had a hard time extracting the band from the polyacrylamide and found the whole process rather messy and time consuming...

2. After ditching the silver staining method I began using MetaPhor agarose (I assume this is like Nusieve...),

and that's worked really well. I do isolate the band after whole amplification, and re-amplify, and then run them out again. I've been able to resolve bands of sizes from 75 to 400 bp with no trouble.

3. For the final extraction I ran a 100bp ladder next to 5uL of the PCR followed by an empty well and then the rest of my sample (~20uL). After running it overnight at about 34V I then cut out the ladder and 5uL PCR areas of the gel and stained them in EtBr - this then became my reference by which I could cut out the fragment of interest from the unstained 20uL lane. I did this so that I didn't have any EtBr knicks in my fragment of interest - maybe overly cautious, but I thought it was worth it.

——— 2. Erick (my summary + translation)

You could use the same fluorescent PCRs as the ones used on the automatic sequencer, but loaded into a classical vertical electrophoresis (denaturing, 0.4 cm thick), visualise the bands with a FMBIO II scanner, and cut them at this very moment. Labour intensive and boring but efficient.

——— 3. Bob

I can confidently tell you that separation on acrylamide followed by silver-staining is really not all that painful. I've done it hundreds of times (many hundreds of gels!) for microsatellites (though now I use fluor-labeled primers and run them on the 3730). Forget the silver-staining kits, by the way. They're complicated and expensive. If you're interested, I can send you the silver-staining technique we used that is cheap and fast and dependable. I still use a modified silver-staining method for SSCP analysis on tiny Bio-Rad Protean-3 minigels.

I used Bio-Rad's 38x30cm rig called the Sequin-Gen GT. Great for microsatellites, but not sure you'll get the separation you'll need for AFLPs, depending on how many AFLP bands you have, and where in the spread they occur. But Bio-Rad makes a variety of formats, and I found their setup for pouring, etc., to be really sweet. I did most of this work while at postdoc at Duke, and I had several undergrads trained in the procedure, from loading gels all the way to silver-staining. Lots more "fun" than agarose gels!

The nice thing about the 38x30 is that it's just less gel to handle, making the staining and handling much easier. We actually did quite a few AFLP runs on the 38x30, and got good enough results that we were able to score bands - and compare these to the results we were getting from the fragment analysis on the ABI instrument (this was a few years ago, pre-3730). I doubt Nusieve is going to work - but it might be worth a try - and I know nothing about spreadex.

——— 4. Phillip

My student has the attached paper currently in press, in which she describes using a Dark Reader(r) Transilluminator (Clare Chemical Research, Dolores, CO, USA) to extract AFLP bands from Spreadex gels.

[note: the paper is in Journal of Heredity: AFLP Fragment Isolation Technique as a Method to Produce Random Sequences for Single Nucleotide Polymorphism Discovery in the Green Turtle, Chelonia mydas, by Roden et al 2008/9]

——— 5. David

If you have some funds for equipment purchase, the combination of a Li-Cor DNA analyzer (a slab polyacrylamide gel-based sequencing/genotyping system using infrared dyes) and Li-Cor's Odyssey fluorescent imager would probably be an option to consider. (I'm assuming they still market the Odyssey system.) The Odyssey provides the opportunity to visualize the bands and locate the spot where the bands you want to excise are.

——— 6. Adam

You can easily do it on just agarose. We do it regularly.

1) Run the amplification again, adding one base to one of the primer sets. There are 4 reactions, and your band will show on one of them. You may need to do this using the regular ABI separation gel. 2) Do this again with one primer added to the other base. Unless you have a high band density, you can probably do this on agarose. 3) If necessary, add another base and do it again. 4) Your band will show up sufficiently separated from the others that you can get it out with a cut-off 1-ml micropipette tip, purify it and sequence it. 5) Then if necessary, make primers to get it out of the rest of your material using regular PCR.

— / —

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

Biological images

Hi all,

We are getting a new science building and one of the features will be beautiful floor to 3-story ceiling glass panels depicting various (somewhat abstract) images from science. I am looking for high resolution pictures of butterfly wing spots, close-ups of animal eyes, close-ups of feathers, or close-ups of color patterns on your favorite creature (we have plenty of plant images). If you can send me an image or a website address and PERMISSION to use these photos, I would be grateful!

Sincerely,

Amy McMillan, Ph.D, Buffalo State College (mcmillam@buffalostate.edu)

“McMillan, Amy” <MCMILLAM@buffalostate.edu>

Commercial SNP development

G’day,

I’m looking for companies that will develop SNPs for nonmodel organisms (just like some other companies develop microsats). I’m interested in using them for population genetics. Any suggestions?

Sincerely,

Manoel

silvamanoel33@yahoo.com

Manoel Silva <silvamanoel33@yahoo.com>

CostaRica Volunteer MonkeyEvolution

Field assistant position for study of capuchin life histories in Costa Rica.

The Lomas Barbudal Monkey Project has 6 volunteer field assistant positions available annually, with a rolling deadline for applications. The job includes collecting behavioral data and fecal samples. These positions require a 1-year contract with a flexible start date (though most positions begin in early summer or in January). Room and board are paid by the project, and airfare up to a certain amount is covered contingent upon the completion of the 1-year contract.

Further information about the research goals, working conditions, project publications, and application procedure are available at the following website:

http://www.sscnet.ucla.edu/anthro/faculty/sperry/jobs.html Any questions not answered by this website can be addressed to Susan Perry (sperry@anthro.ucla.edu)

Susan Perry <Sperry@anthro.ucla.edu>

Daphnia DNA extractions

Dear all

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

Many thanks for your help!

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

WALSER Barbara <barbara.walser@unifr.ch>

Darwin links

Hello all,

The 200th birthday of the founder of evolutionary biology, Charles Darwin, is being celebrated in 2009. This year also marks the 150th anniversary of the first publication of his work “On the Origin of Species”. vifabio, the Virtual Library of Biology, takes this opportunity to compile the most important internet resources on the subject, and other information. Please visit our comprehensive collection of “Internet resources on Charles Darwin and on evolutionary biology” at: http://www.vifabio.de/darwinjahr2009/?lang=en In case you find that important resources are missing, please make a proposal here: http://tinyurl.com/cwpzqo (follow the link “suggestion form” at the bottom of the page).

The Virtual Library of Biology (vifabio) is a project of the University Library “Johann Christian Senckenberg”, Frankfurt/Main (Germany) in cooperation with other libraries and biological organisations. vifabio aims to offers rapid access to biological literature and information.

—

Many thanks, best regards - Gerwin Kasperek

Dr. Gerwin Kasperek Virtuelle Fachbibliothek Biologie http://www.vifabio.de Universitaetsbibliothek Johann Christian Senckenberg Bockenheimer Landstr. 134-138 60325 Frankfurt am Main - Germany - Tel. +49 69 798 39365 g.kasperek@ub.uni-frankfurt.de

Gerwin Kasperek <g.kasperek@ub.uni-frankfurt.de>

Data analysis for polyploids

Hi

I am working on a tetraploid tree species and want to compute some population genetic parameters.

Does any one have a compilation of programmes that handles data sets for polyploids?

Contribution of single programmes will also be ok as well as algorithms for more advanced calculations, and then I’ll compile a list and distribute it upon request.

Cheers

Anders

Anders S. Larsen Mimersgade 118, 5.tv. 2200 Copenhagen N Phone no. +4535854345 Mobile no. +4561334345

anderslarsen333@hotmail.com

DNA Bank Database

DNA Bank Network Database Goes Online Web portal of biological DNA collections launches its searchable database system at www.dnabank-network.org< http://www.dnabank-network.org >

The DNA Bank Network links DNA banks of major biological research collections in Germany: Botanic Garden and Botanical Museum Berlin-Dahlem German Collection of Microorganisms and Cell Cultures, Braunschweig Zoologisches Forschungsmuseum Alexander Koenig, Bonn Bavarian State Collection of Zoology, Munich

The network’s web portal enables scientists to query and order DNA samples of organisms collected from natural habitats. It is thereby possible to obtain well determined DNA and tissue material to conduct, extend or complement investigations in phylogenetics, population and conservation genetics as well as in biogeography.

The DNA Bank Network ensures long-term DNA availability by storage under optimal conditions at -80C after project completion or data publication. Full documentation of each sample accessible online is provided, including provenance of the material, place of voucher deposit, DNA extraction techniques and links to existing molecular data. Additionally high resolution digital images of specimens (voucher) are generated, available online via the web portal.

The network aims at bridging the gap between natural history repositories, DNA collections and molecular sequence databases. It so supports good scientific practice as the deposition of DNA samples facilitates the verification of published results.

The establishment of this network is financially supported by the Deutsche Forschungsgemeinschaft (DFG).

“Gemeinholzer, Birgit” <B.Gemeinholzer@BGBM.org>

DNAMarkers SexDetermination GreenIguana

Dear EvolDir members,

I want to determine the sex of Green Iguana hatchlings using DNA markers. The company Zoogen offers DNA sex determination in the Green Iguana but doesn’t supply details. I’d be interested to hear from anyone who knows of or has used DNA markers to determine sex in this species.

Thanks

Paul

Paul Bloor Coordinador/Investigador Principal Unidad de Especies Silvestres Instituto de Genética Universi-

dad Nacional de Colombia Bogotá D.C - COLOMBIA

Tel.: +57-1-3165-000 Ext. 11611 Fax.: +57-1-3165-526

email: pbloor@gmail.com

DPGP releases 50 Drosophila

The Drosophila Population Genome Project released today a preview of the initial sample of Drosophila melanogaster genomes sequenced by the DPGP using first generation (single-end and 36 bp) Solexa/Illumina technology and assembled using maq 0.6.8. This data preview is intended to clearly show the scope and quality of the data. Release 1.0 will be a reference dataset.

The sample consists of the sequences for the 5 major chromosome arms (X, 2L, 2R, 3L and 3R) for 39 inbred genomes from Trudy Mackay's set of inbred lines sampled in Raleigh, NC and a set of sequenced chromosomes (8 chrXs, 6 chr2s and 5 chr3s) from a sample of Malawi isofemale lines that were inbred using balancers. Regions of residual heterozygosity and repeated sequence are filtered (set to "N"). The "raw data" are available in the NCBI Short Read Trace Archive. This Release 0.5 data are in the form of fasta files for each of the major chromosome arms for each sampled genome. The average coverage of the unique portions of all these genomes is >10X. The called bases are those with a consensus (Solexa) nominal quality score >= 30. Bases in repetitive sequences or in regions of (inbred) residual heterozygosity are not called, i.e. "N".

Release 0.5 data can be accessed at < http://www.dpgp.org/ >. The reference release (1.0) is expected in several weeks.

chuck <chlangley@ucdavis.edu>

Drosophila lines

Hi all,

I am close to finishing up my PhD and have 25 temperature-adapted fly lines from a large experiment that we will no longer be able to maintain (Drosophila melanogaster). If anyone is interested in using these fly lines for further experiments, please get in touch! It would be a shame to reward their efforts with W = 0.

The lines:

5 lines: Cold temperature (16 degrees) 5 lines: Warm temperature (25 degrees) 5 lines: Spatial heterogeneity with panmictic migration (one cage in 16, one cage in 25 degrees, 50% migration every 4 weeks) 5 lines: Spatial heterogeneity with limited migration (one cage in 16, one cage in 25 degrees, 2 gravid females migrate reciprocally every 4 weeks) 5 lines: Temporal heterogeneity (cages move between 16 and 25 degrees every 4 weeks)

These lines were all originally derived from a single wild collected sample of flies from the Okanagan valley in BC, Canada. They have been maintained under the treatment conditions for over 3 years at populations sizes > 2000. We used them to assay genetic variance under the various treatments and the effect of the treatments on G-matrix evolution (manuscripts in prep). We found significant divergence between the Cold and Warm lines for several wing shape traits and evidence of local adaptation by differences in fecundity from reciprocal transplant assays, but no differences in genetic variance between any of the treatments.

Please contact Sam Yeaman at yeaman@zoology.ubc.ca if you are interested.

Thanks!

Sam Yeaman Whitlock Lab Department of Zoology University of British Columbia Vancouver, BC 778-834-9395

yeaman@zoology.ubc.ca yeaman@zoology.ubc.ca

Evolution Lab exercises

Dear Evoldir Members:

I am trying to develop an evolution course for undergraduates that would include a hands-on (wet) lab for the students. Some of these labs can be performed over the course of a semester rather than just contained in a single lab period. I am trying to find labs other than computer-based labs but please feel free to send computer-based exercises. I will compile the responses and post the lab suggestions for all those interested on Evoldir. Additionally, I also will be posting the labs on the web for free access to reduce student textbook costs.

Thank you.

Best regards, Valerie

Valerie Schawaroch, Ph.D. Deputy Chair and Associate Professor of Biology Baruch College

valerie.schawaroch@baruch.cuny.edu

Fungal DNA isolation

Dear Evoldir members,

I got a very good response for AFLP protocol. Thanks a lot for that. Now I am ready to start my project. I will be thankful if someone guide me to isolate good quality genomic DNA from variety of entomopathogenic fungus. Primarily I am going to deal with Beauveria spp. Please send your reply as soon as possible.

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

“Shajahan, Johny” <jshajah@ilstu.edu>

FungalDNA isolation

Dear EvolDir members,

I got lots of information about DNA isolation from fungus. Now I am end up with a question: Should I go with DNA extraction from single conidia (what I mean is I should make a subculture from single conidia) or should I use a pack? I want to know about the merits & demerits of both. The goal is to make phylogenetic analysis for a variety of strains/species. Please anwer this.

Very best Johny

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

“Shajahan, Johny” <jshajah@ilstu.edu>

HIV XML annotations

HIV Evolution colleagues,

I have updated the Los Alamos HIV Sequence DB query tool at http://fortinbras.us/hivq to allow retrieval of sequence annotation data (disease progression, sampling country, phenotype, and the like) in XML format, validated against a set of XML Schema definitions available at http://fortinbras.us/HIVDBSchema/1.0. Sequence data can also now be retrieved in NeXML format, an enhanced XML version of the NEXUS format developed by Rutger Vos at UBC. Standard FASTA format is still available.

My objective is to make the wealth of epidemiological data associated with the LANL sequence data more accessible and computable. As usual, this is a service to the HIV research community, and use of it does not put you on any list of mine or anyone else’s, or at any excess risk of being pestered in any way.

Please do pester me, however, if you encounter any bugs or have ideas for enhancements. Many thanks to the other participants at the NESCent Database Interoperability Hackathon (March 2009) for their expertise and encouragement in this project.

Best, Mark Jensen

maj@fortinbras.us

Megabace sequencer 1000 info

Dear Evoldir members,

My institute is considering buying a Megabace 1000 DNA sequencer. I am not familiar with this make and would be grateful to anyone who could tell me about their experiences (good or bad) of this machine.

Thanks,

Paul

Paul Bloor Coordinador/Investigador Principal Unidad de Especies Silvestres Instituto de Genética Universidad Nacional de Colombia Bogotá D.C - COLOMBIA

Tel.: +57-1-3165-000 Ext. 11611 Fax.: +57-1-316-5526 alt. email: pbloor@unal.edu.co

pbloor@gmail.com

Microsats amplification answers

Dear all,

I posted a request on evoldir a while ago trying to find out if anyone had the following problem:

Below is the original email: We've encountered a strange problem with fluorescently labeled >> microsat markers in a gastropod - all are amplifying well (and >> produce distinct bands on agarose gels) but when we genotype them on >> our sequencer, we get extremely weak (in most cases unscorable) >> peaks. This problem is taxon-specific: in a fish that we run along >> as a control, we get PCR products with approximately the same >> concentration, but the peaks are easily scorable, so there doesn't >> seem to be anything wrong with our reagents. >> >> Changing the number of cycles (we've tried between 30 and 40) and/or >> salt concentration (2.5 - 6 mM) doesn't solve it.

Quite a few people have actually come across this phenomenon, and many said they have been unable to solve it. The most common solution was to use a different species (the problem has been encountered in certain gastropods, ascidians, insects and bryophytes). Below are a number of suggestions [my own comments in square brackets].

Thanks to everyone who responded, Peter

1. Use 1/10 of pre-primer concentration as compared to M13 primer concentration [we were already using 1 uM vs. 5 uM, and diluting it further did not help] 2. Use a different extraction method [we were using either Qiagen kit or a salting out protocol, and salting out was usually the better method. I've now tried CTAB, but that didn't improve genotyping results] 3. Dilute samples 1 in 3 or 1 in 5 [this seems to improve it - particularly diluting 1 in 10 or more te seems to decrease the concentration of whatever inhibitors are in the DNA extractions. The peaks still aren't great, perhaps because DNA concentration also becomes extremely low, but this is really the only modification of the protocol that's improved things a bit] 4. Reduce the concentration of MgCl2 [no improvement, neither was increasing its concentration] 5. Dilute PCR products 1:2, 1:5 or 1:10 prior to adding HiDi [no improvement, in fact, peaks were weaker] 6. Use 2 ul of pooled DNA + 10 ul of HiDi [we were using 1 ul previously, and this doesn't improve it] 7. Boil DNA extractions in Chelex [this seems like a good idea, but I haven't tried it yet. The idea is that boiling destroys the inhibitors and any inhibiting ions stick to the beads] 8. During genotyping, use a lower injection voltage with longer injection time [no improvement] 9. Use different primers [OK, some work better than others, but that's common - replacing all 12 of our species-specific primers is not an option]

Dr Peter R. Teske Postdoctoral Researcher Molecular Ecology Lab Dept. of Biological Sciences, E8C Macquarie University Sydney, NSW 2109 Australia Phone: +61 2 9850 8203 Fax: +61 2 9850 8245 E-mail: Peter.Teske@bio.mq.edu.au Website: http://www.bio.mq.edu.au/molecularecology/-people.htm Publications: http://www.ru.ac.za/-academic/departments/botany_research/peter/ Peter.Teske@bio.mq.edu.au Peter.Teske@bio.mq.edu.au

NESCent Biodiversity DataCenter

*** Please disseminate widely to students at your institution ***

CYBERINFRASTRUCTURE SUMMER TRAINEESHIPS 2009

VIRTUAL DATA CENTER FOR BIODIVERSITY, EARTH, ECOLOGICAL, AND EVOLUTIONARY SCIENCE DATA

http://hackathon.nescent.org/-Cyberinfrastructure_Summer_Traineeships_2009
Summer traineeships are available for up to four students and postdocs interested in informatics as applied to scientific data ranging from the fields of biodiversity, ecology, and evolutionary biology. The program provides a unique opportunity for undergraduate, masters, and PhD students as well as postdocs to obtain hands-on experience writing and extending open-source software as part of a distributed collaborative software development team building a Virtual Data Center (VDC) that includes major data and metadata repositories in those fields.

Trainees accepted into the program will receive a stipend ($4,500), and with the exception of attending one meeting near the beginning and one near the end of the 3-month program period may work from their home, or home institution. Travel costs incurred in connection with the meetings will be reimbursed. Each student will have at least one dedicated mentor to show them the ropes and help them complete their project.

Initial project ideas are listed on the website. These range from validation of metadata and identifier resolution, to supporting LSID and semantic-web compliant PURLs for digital data objects, to implementing modern web-service APIs, to cataloging the diversity of metadata schemas. The project ideas are flexible and can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

The traineeships are supported by a National Science Foundation (NSF) grant to a consortium of major repositories for biodiversity, earth and environmental, ecological, and evolutionary science. The consortium includes the LTER Network Office, the U.S. Geological Survey, NASA and Oak Ridge National Laboratory, the Global Biodiversity Information Facility (GBIF), the National Evolutionary Synthesis Center(NESCent), and the National Center for Ecological Analysis and Synthesis (NCEAS). It aims to develop the cyberinfrastructure and technologies necessary to build a Virtual Data Center (VDC) based on a network of existing and new physical repositories ("nodes") that interoperate using open standards and protocols. The network will enable discovery of as well as open, stable, and secure access to data in any of its member nodes.

TO APPLY: Students apply online. Instructions for applying are at the website (see "When you apply"), along with program rules and eligibility requirements. The 15-day application period for students opens on Monday March 30th and runs through Monday, April 13th, 2009.

INQUIRIES: vdc-twg {at} ecoinformatics {dot} org. We strongly encourage all interested students to get in touch with us with their ideas as early as possible.

Cyberinfrastructure Traineeships Website: http://hackathon.nescent.org/Cyberinfrastructure_Summer_Traineeships_2009 2009 NESCent Phyloinformatics Summer of Code (NESCent's participation in the Google Summer of Code; managed separately; postdocs not eligible; ***student application period ends April 3rd***) http://hackathon.nescent.net/Phyloinformatics_Summer_of_Code_2009 To sign up for quarterly NESCent newsletters: http://www.nescent.org/about/contact.php Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center http://nescent.org

NESCent Coding

*** This is a reminder about the student application deadline. *** *** Please disseminate widely to students at your institution. ***

PHYLOINFORMATICS SUMMER OF CODE 2009 - STUDENT APPLICATION DEADLINE IS APRIL 3

http://hackathon.nescent.org/Phyloinformatics_Summer_of_Code_2009 The Phyloinformatics Summer of Code program provides a unique opportunity for undergraduate, masters, and PhD students to obtain hands-on experience writing and extending open-source software for evolutionary informatics under the mentorship of experienced developers from around the world. The program is the participation of the US National Evolutionary Synthesis Center (NESCent) as a mentoring organization in the Google Summer of Code(tm) (http://code.google.com/soc/).

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

NESCent is particularly targeting students interested in both evolutionary biology and software development. Project ideas are listed on the website and range from hardware acceleration for phylogenetic inference, to support for phyloinformatics standards within the BioPerl and BioRuby toolkits, to alignment of next-gen sequencing data, to ontology term markup for biocuration, to semantic interoperability of web-services, to 3D-printing of phylogenies. All project ideas are flexible and many can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

TO APPLY: Instructions are at the website (see "When you apply"). You can find GSoC program rules and eligibility requirements at http://socghop.appspot.com . ***The 12-day application period for students ends on Friday, April 3rd, 2009, at 19:00 UTC (3pm EDT, 12pm PDT).***

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

2009 NESCent Phyloinformatics Summer of Code: http://hackathon.nescent.net/-Phyloinformatics_Summer_of_Code_2009 Google Summer of Code FAQ: http://socghop.appspot.com/-document/show/program/google/gsoc2009/-faqs Cyberinfrastructure Traineeships (managed separately from GSoC; postdocs also eligible): http://hackathon.nescent.org/-Cyberinfrastructure_Summer_Traineeships_2009
To sign up for quarterly NESCent newsletters: http:/-/www.nescent.org/about/contact.php Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center http://nescent.org hlapp@nescent.org

NESCent SabaticalScholars

Call for Proposals V NESCent Sabbatical Scholars, Working Groups and Catalysis Groups

The National Evolutionary Synthesis Center (NESCent) is now accepting proposals for sabbatical scholars, working groups and catalysis meetings. Proposals for postdoctoral fellowships are accepted at the December 1 deadline only. Proposals for sabbatical scholars, working groups and catalysis meetings are accepted twice a year, with June 15 and December 1 deadlines. Proposals for short-term visitors are considered four times a year, with deadlines on January 1, April 1, July 1 and September 1. For more information, please see our website at https://www.nescent.org/science/-proposals.php . Karen Henry <khenry@nescent.org>

NESCent SummerProgramming Deadline

*** Please disseminate widely to students at your institution ***

CYBERINFRASTRUCTURE SUMMER INTERNSHIPS 2009 - REMINDER: Student Application Deadline is April 13, 2009

http://hackathon.nescent.org/ Cyberinfrastructure_Summer_Traineeships_2009

Summer training internships are available for up to four students and postdocs interested in informatics as applied to scientific data in such fields as biodiversity, ecology, and evolutionary biology. The program provides a unique opportunity for undergraduate, masters, and PhD students as well as postdocs to obtain hands-on experience writing and extending open-source software as part of a distributed collaborative software development team building a Virtual Data Center (VDC) that includes major data and metadata repositories in those fields.

The application deadline for students (April 13, 2009) is approaching rapidly.

Trainees accepted into the program will receive a stipend ($4,500), and with the exception of attending one meeting near the beginning and one near the end of the 3-month program period may work from their home, or home institution. Travel costs incurred in connection with the meetings will be reimbursed. Each student will have at least one dedicated mentor to show them the ropes and help them complete their project.

Initial project ideas are listed on the website. These range from validation of metadata and identifier resolution, to supporting LSID and semantic-web compliant PURLs for digital data objects, to implementing modern web-service APIs, to cataloging the diversity of metadata schemas. The project ideas are flexible and can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

The program is supported by a National Science Foundation (NSF) grant to a consortium of major repositories for biodiversity, earth and environmental, ecological, and evolutionary science. The consortium includes the LTER Network Office, the U.S. Geological Survey, NASA and Oak Ridge National Laboratory, the Global Biodiversity Information Facility (GBIF), the National Evolutionary Synthesis Center(NESCent), and the National Center for Ecological Analysis and Synthesis (NCEAS). It aims to develop the cyberinfrastructure and technologies necessary to build a Virtual Data Center (VDC) based on a network of existing and new physical repositories ("nodes") that interoperate using open standards and protocols. The network will enable discovery of as well as open, stable, and secure access to data in any of its member nodes.

TO APPLY: Students apply online. Instructions for applying are at the website (see "When you apply"), along with program rules and eligibility requirements. The 15-day application period for students end on Monday, April 13th, 2009.

INQUIRIES: vdc-twg {at} ecoinformatics {dot} org. We strongly encourage all interested students to get in touch with us with their ideas as early as possible.

Cyberinfrastructure Traineeships Website: http://hackathon.nescent.org/ Cyberinfrastructure_Summer_Traineeships_2009

To sign up for quarterly NESCent newsletters: http://www.nescent.org/ about/contact.php

———

Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center http://nescent.org hlapp@duke.edu hlapp@duke.edu

New Population Genetics text

Dear Colleagues,

The new text Population Genetics is now available from Wiley-Blackwell.

Visit www.wiley.com/go/hamiltongenetics to see the companion web site for the book, which provides links and instructions for the interactive simulations in each chapter as well as figures that appear in the book.

The table of contents, index and a sample chapter can be found by visiting http://www.wiley.com/WileyCDA/WileyTitle/productCd-1405132779.html I hope that students and teachers find the book useful.

Sincerely, Matt Hamilton

Matthew B. Hamilton, PhD Associate Professor Georgetown University Department of Biology, Reiss 406 37th and O Streets NW Washington, DC 20057 202-687-5924 (office) 202-687-5662 (fax) http://www9.georgetown.edu/faculty/hamiltm1/ hamiltm1@georgetown.edu

Nst Gst answers

Dear all

I'm very grateful for the suggestions received. Here are the replies:

Request:

Hi all,

I'm trying to use the approach suggested in SPAGeDi 1.2 (O. Hardy and X. Vekemans 2007) to test for the existence of a significant phylogeographic signal, using mtDNA sequence data. However there is an issue that is not entirely clear to me: in cases when a Nst > Gst > 0 but the slope of pairwise Nst vs geographic distance is not significant, what could be plausible explanations? Can anyone give me any suggestions about this issue or can suggest some paper, book, that could be of help if further questions or doubts storm me?

many thanks Marco Carriso

——

Answers:

Dear Marco,

there are two different issues in the problem you are describing. One is whether there is some phylogenetic signal in your mtDNA data on top of the differences in haplotype frequencies among populations (the Nst versus Gst comparison), and the other whether the genetic differentiation that you observe has a spatial component (does or not fit an isolation by distance pattern). When you are applying the test implemented in Spagedi that gives Nst>Gst, you are implicitly assuming an Island model of migration, with GST measuring average genetic differentiation among populations due to differences in haplotype frequencies, and Nst measuring average genetic differentiation taking into account differences in haplotype frequencies plus phylogenetic differences among haplotypes. Your observation that Nst>Gst suggests that the set of distinct haplotypes that are co-occuring whithin populations are on average more similar to each other than random sets of haplotypes at the total species level. Another way to put it, is to say that genetic drift along cannot explain the data and thus the mutational process is participating to genetic differentiation among populations. When you are computing the slope of the regression of pairwise Nst vs geographic distance, you are implicitly assuming an Isolation by distance model (i.e. restricted dispersal), and if the slope is ot significantly different than zero this means that this model should be rejected. Hence in your case there is no clear spatial component in genetic differentiation. It may be that the slope for Gst is significant but not the one on Nst. This could happen simply because of the larger variance of the estimates of pairwise Nst as compared to pairwise Gst.

best regards,

Xavier Vekemans

– Xavier VEKEMANS

Laboratoire de Genetique et Evolution des Populations Vegetales GEPV - UMR CNRS 8016 Batiment SN2 Universite des Sciences et Technologies de Lille - Lille 1 59655 Villeneuve d'Ascq Cedex FRANCE Tel: +33 3 2043 6753 - Fax: +33 3 2043 6979 http://www.univ-lille1.fr/gepv=0A=C2=A0=0A=C2=A0=0AÂ Hi Marco,

you might obtain such pattern if you have a complex history of colonisation by long term differentiated gene pools (Nst>Gst) that spread over large and/or disjunct areas because you could have comparable proportions of pairs of populations belonging to distinct gene pools at short distance and at large distance. For an example, have a look at http://www.pierroton.inra.fr/genetics/ComEvol/Atelier-Phylogeo/OHardy_phylogeography.pdfp.6 . Best,

Olivier

Olivier Hardy Chercheur qualifiÃ© FNRS Service Eco-Ethologie Evolutive - CP 160/12 UniversitÃ© Libre de Bruxelles 50 Av. F. Roosevelt 1050 Bruxelles Belgique

Tel: +32 (0)2 650 6585 Fax: +32 (0)2 650 2445 email: ohardy@ulb.ac.be

marcocarriso@yahoo.it

Polyploid analysis answers

Dear list members

Below, I've compiled a list of answers to my request for software that handles polyploid data along with available comments. I have not yet tested the software, so comments are taken from the answers I had.

AUTOTET (Thrall & Young, 2000) For genetic diversity of autotetraploids

PopGene 3.2 (Yeh et al., 1997) For genetic diversity of allotetraploids

Arlequin (Excoffier, Laval & Schneider, 2005) Fst

Spagedi (Hardy & Vekemans, 2002) Fst (Weir & Cockerham)

Structure (Pritchard, Stephens & Donally, 2000) Clustering

MalHapFreq (Hastings & Smith, 2008) ML estimates of allele frequencies

Adegenet (Jombart, 2008) (R package) Data manipulation, multivariate analyses and per se F-stats

Tetra/Tetrasat (Markwith, Stewart & Dyer, 2006) Allotetraploids

Lamarc For polyploids with unknown haplotype phase

Migrate-N

Popdist 1.2.0

GenoType (Meirmans & Tenderen, 2004)

GenoDive (Meirmans & Tenderen, 2004) AMOVA

MLTR (Ritland, 2002) Inbreeding/outcrossing

Anders S. Larsen Mimersgade 118, 5.tv. 2200 Copenhagen N Phone no. +4535854345 Mobile no. +4561334345

anderslarsen333@hotmail.com

Program for haplotypes

Dear all,

I will greatly appreciate any pointers to find a program that would help estimate or determine individual haplotypes (i.e., gametic phase) from a set of direct sequences of heterozygote individuals. I plan to use it to identify MHC alleles (ca. 170 bp). Basically I am trying to cut down the number of individuals needed to clone all alleles, times are tough!

Thanks in advance!

Best.

Axa

Axayacatl Rocha-Olivares, Ph.D. Biological Oceanography Department CICESE P. O. Box 434844 San Diego, CA, 92143-4844

DOMESTIC: Apartado Postal 360 Ensenada, Baja California, CP 22830 Mexico

COURIER: Km 107 Carretera Tijuana-Ensenada Ensenada, Baja California, CP 22860 Mexico

Office: +52(646)175-0500 (ext. 24240) Lab: +52(646)175-0500 (ext. 24318) Fax: +52(646)175-0587

Email: arocha@cicese.mx http://dob.cicese.mx/labs/ecolmolecular/index.html

Axayacatl Rocha <arocha@cicese.mx>

qBase Program

Greetings, I am looking for the free qBase program for qPCR analysis that was published in genome biology (citation below). The authors stopped distributing the program and released the (expensive) qBasePlus commercial program shortly thereafter. If anyone has the qBase program that served as a the basis for this publication, please email me. Again, this was published as a free program - the original qBase remains a free program and sharing hopefully does not violate copyright as a result.

Thanks,

Brendan Hunt

Hellemans, J., G. Mortier, A. De Paepe, F. Speleman, and J. Vandesompele. 2007. qBase relative quantification framework and software for management and automated analysis of real-time quantitative PCR data. Genome biology 8:14.

– Brendan Hunt Goodisman Lab / Yi Lab School of Biology Georgia Institute of Technology 310 Ferst Drive Atlanta, GA 30332 www.goodismanlab.biology.gatech.edu/hunt brendan.hunt@gatech.edu

Rocking Darwin

Dear all,

A small team of evolutionary ecologists from Tuebingen, Germany, just finished a rock music clip about evolution which is called “Struggle for love”, together with a computer program that allows the user to “select and evolve” music tunes following biological principles. This program was also used to generate the underlying tunes for the song.

All this is the result of a one-year project that was generously supported by the VolkswagenFoundation (www.volkswagenstiftung.de) following a creativity contest called “Evolution Today”. We cooperated with composers, musicians, film-makers, informaticians and a whole series of creative students, about one hundred in total!

Both the clip and the program are meant to attract the attention from non-biologists and make them think and talk about evolution. Hence, if you like it, please feel free to share it with your friends, relatives and students. If you have questions or suggestions, send your comments to johannes.faber@uni-tuebingen.de or nico.michiels@uni-tuebingen.de

Everything is online and freely downloadable at www.darwinrocks.de/en If you just want the video, check www.youtube.com/user/darwinrocks09 All materials are in German and English.

The Darwin Rocks! Team: Johannes Faber Suska Sahm Gregor Schulte Nico Michiels

Nico Michiels, Prof. Dr. Animal Evolutionary Ecology Group Institute of Evolution and Ecology Faculty of Biology Auf der Morgenstelle 28 72076 Tuebingen Germany

+49 7071 29-74649 (work) +49 170 4758003 (mobile)

nico.michiels@uni-tuebingen.de www.darwinrocks.de www.evoeco.uni-tuebingen.de www.eve.uni-tuebingen.de Nico Michiels <nico.michiels@uni-tuebingen.de>

Software adegenet1 2-3

Dear List,

A new version (1.2-3) of the adegenet package for the R software has been released. This package is devoted to the multivariate analysis of genetic markers.

The package can read data from many usual formats, and can handle both codominant and presence/absence markers, for any level of ploidy. It can also extract SNPs from aligned DNA sequences. Despite dedicated to multivariate analysis, adegenet also proposes a wide variety of other tools, including advanced data manipulation, classical population genetics tools, spatial genetics (the spatial Principal Component Analysis, Monmonier’s algorithm), and the simulation of hybridization.

Literature, tutorials, dedicated forums, and other information can be found on adegenet’s website: http://adegenet.r-forge.r-project.org/ Like other R packages, adegenet is available for various platforms, including Linux, MacOS X, and windows, from the Comprehensive R Archive Network (CRAN): http://cran.r-project.org/ or simply from the R software.

Best regards,

Thibaut Jombart.

–

Dr Thibaut JOMBART MRC Centre for Outbreak Analysis and Modelling Department of Infectious Disease Epidemiology Imperial College - Faculty of Medicine St Mary's Campus Norfolk Place London W2 1PG United Kingdom Tel. : 0044 (0)20 7594 3658 t.jombart@imperial.ac.uk http://www1.imperial.ac.uk/medicine/people/t.jombart/ http://adegenet.r-forge.r-project.org/ t.jombart@imperial.ac.uk t.jombart@imperial.ac.uk

Software bms runner 1 3

Dear Evoldir,

bms_runner is free software to predict functional linkage among gene products, on the basis of correlated gain and loss of genes from genomes < http://dx.doi.org/10.1093/bioinformatics/btl558 >. It does this by helping the user to configure and repeatedly launch the separate BayesTraits program < http://dx.doi.org/10.1080/10635150490522232 >.

bms_runner version 1.3 has just been released, with improvements over the previous version. bms_runner works on Linux or Mac OS X. It may be downloaded here:

http://biology.st-andrews.ac.uk/cegg/downloads.aspx I will be happy to receive any questions and feedback on bms_runner.

In future, I will only email Evoldir about bms_runner if major new functionality is added. If you prefer to receive an email every time bms_runner is updated, please let me know, and I will add you to my list of users.

Best regards,

Daniel

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

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

Software Circuitscape3 1 1

Dear all,

We've just released Circuitscape 3.1.1 connectivity analysis software. Circuitscape uses circuit theory to predict connectivity for gene flow and animal movement. It is particularly applicable to landscape genetics.

We now have executable versions for Windows and Mac, and Python source files for Linux, all freely available. You can download these and read about applications of circuit theory in ecology, evolution, and conservation at www.circuitscape.org . Best, Brad McRae

Brad McRae <mcrae@circuitscape.org>

Software Concatenator

Dear evoldir members,

I wish to announce the release of the program CONCATENATOR available at:

http://cobig2.fc.ul.pt . CONCATENATOR is a simple and user-friendly software that implements two very useful functions for phylogenetics data analysis. It concatenates NEXUS files of several fragments in a single NEXUS file ready to be used in phylogenetics software, such as PAUP and MRBAYES and it converts FASTA sequence data files to NEXUS and vice-versa. Additionally, concatenated files can be prepared for partition tests in PAUP. It is freely available in http://cobig2.fc.ul.pt . Pina-Martins F, Paulo OS (2008). Concatenator: Sequence Data Matrices Handling Made Easy. Molecular Ecology Resources 8, 1254-1255

Octávio S. Paulo Ph.D. Assistant Professor Centro de Biologia Ambiental Departamento de Biologia Animal Faculdade de Ciências da Universidade de Lisboa P-1749-016 Lisboa Portugal

Tel: 00 351 217500614 direct Tel: 00 351 217500000 ext22359 Fax: 00 351 217500028 email: octavio.paulo@fc.ul.pt url: http://webpages.fc.ul.pt/~ofpaulo/ url: http://cobig2.fc.ul.pt/ url: http://bbc.fc.ul.pt/ ofpaulo@fc.ul.pt

Software NOBLAST JAMBLAST

Dear Evoldir members,

I am happy to announce the release of the: NOBLAST and JAMBLAST softwares freely available with source code, docs, packages and standalone executables available for a variety of systems (linux windows, sources..) from SourceForge: http://sourceforge.net/projects/NOBLAST http://sourceforge.net/projects/JAMBLAST General presentation:

NOBLAST(New Options for BLAST) provides:

1) a new extended user-friendly tabular output format that can be directly analysed with any spreadsheet (OpenOffice, Excel...) and/or any database engine (e.g. MySQL) without any use of a parser. This new option extends (-m parameter) the blastall, blastcl3 and blastpgp software and is available for various NCBI BLAST programs: Blastn, Blastp, Blastx, Tblastn, Tblastx, Mega BLAST and Psi BLAST.

2) distributed/parallel BLAST functionality with exact E-value adjustment when split database are used.

NOBLAST is an open source patch for blastall, blastcl3, blastpgp and formatdb from the NCBI toolkit.

JAMBLAST (Java Application Manager for BLAST results) is an additional Java cross-platform application which can be used optionally for the management of the BLAST outputs produced by NOBLAST, using MySQL. It also offers visualization, sorting, ï, exporting... of the results according to user-deïcriteria.

citation: Lagnel J, Tsigenopoulos CS, Iliopoulos I (2009) NOBLAST and JAMBLAST: New Options for BLAST and a Java Application Manager for BLAST results. Bioinformatics 25: 824-826.

http://www.ncbi.nlm.nih.gov/pubmed/19181685 Please, feel free to report any comments to me and enjoy...

Jacques Lagnel

Jacques Lagnel Hellenic Centre for Marine Research (HCMR) Institute of Marine Biology/Genetics Gournes Pediados P.O.Box 2214 Heraklion 71003 Crete, Greece

email: lagnel@her.hcmr.gr

Tel. + 302810 337719 Fax: + 302810337820

– Hellenic Center For Marine Research, Crete Network Operation Center This message has been scanned for viruses and dangerous content by MailScanner, and is believed to be clean.

lagnel@her.hcmr.gr lagnel@her.hcmr.gr

SSCP gel solutions

Dear list members

I am about to perform a sequencing based analysis of individuals for population genetics. For this I will separate alleles by SSCP gel electrophoresis as an alternative to cloning. I've done this succesfully using MDE from Cambrex (assume the equivalent product in Europe is that from Lonza).

This product, however, is hugely expensive, so I want to hear if anyone has experience with SerdoGel (Serva), SequaGel (Apelex) or maybe some other product.

Any other experiences with separation of large (600-800 bp) fragments using SSCP is also welcome. By now I run fragments at 4 deg using 0.7X gels and cut bands stained with SYBRgold for further analysis.

Cheers

Anders

Anders S. Larsen Mimersgade 118, 5.tv. 2200 Copenhagen N Phone no. +4535854345 Mobile no. +4561334345

anderslarsen333@hotmail.com

StatGenetics ScholarshipDeadline Apr13

SISG Scholarship Deadline is April 13

Applications for scholarships to attend the 14^th Summer Institute in Statistical Genetics at the University of Washington, June 15-July 2, 2009 are due on Monday April 13. Details are available at http://sisg.biostat.washington.edu/ Bruce Weir bsweir@u.washington.edu

Bruce Weir <bsweir@u.washington.edu>

Sturgeon problems

Dear evoldir members

I am PhD student and I am going to study about gdf9 in sturgeons (Acipenser), but I have difficulties to sampling (peeling the ovum and isolating the follicle layers). I would appreciate receiving advices in this regards.

Best regards Mahtab

mahtab yarmohammadi <mahtab_yarmohammadi@yahoo.com>

Tree of Life Poster Answers

Dear EvolDirists

Some days ago I asked for good resources to obtain a "tree of life" poster. Some people asked me to compile a list of all the answers I received. Voila:

There is one available from the BBC/Open University (http://www.open2.net/darwin/poster.html). This seems to be the THE one and the bulk of all answers pointed me to this one. And it is for free! However, they send it only to the UK and the Republic of Ireland. So you might have to get in touch with someone there that can order it for you. I contacted BBC about it and they were happy to send a poster to Switzerland, but I am not sure how often we can play that game...

Some nice posters can be bought in German online shops:

www.wissenladen.de has some: http://www.wissenladen.de/catalog/product_info.php/products_id/43 http://www.wissenladen.de/catalog/product_info.php/cPath/27_56/products_id/56 http://www.wissenladen.de/catalog/product_info.php/cPath/49_132/products_id/33?osCsid=3ec31cf8fa09 ...and www.amazon.de has also some: http://www.amazon.de/Systematik-Poster-Zoologie-Anlehnung-Lehrbuch-Speziellen/dp/3827416639/ref=sr_1_1?ie=UTF8&qid=1237795662&sr=8-1 http://www.amazon.de/Systematik-Poster-Botanik-Andreas-Bresinsky/dp/3827417295/ref=pd_bxgy_b_img_b In the US, you find these:

1. From www. historyshots.com: http://www.historyshots.com/OtherArtists/4014.cfm 2. From The Natural History Museum of New York: http://www.amnhshop.com/09-015941.html 3. Zazzle has two: http://www.zazzle.com/tree_of_life_evolution_poster-228150266536416257 http://www.zazzle.com/tree_of_life_poster-228591242647081166 One of which is actually available as pdf: http://tellapallet.com/tree_of_life.htm 4. From Amazon: http://www.amazon.com/Milestones-Evolution-Art-Poster-36/dp/B001A2IPA4/ref=pd_bbs_sr_1?ie=UTF8&s=home-garden&qid=1237998364&sr=8-1 http://www.amazon.com/Evolution-Humor-Poster-Print-24x36/dp/B001AXI666/ref=pd_bbs_2?ie=UTF8&s=home-garden&qid=1237998364&sr=8-2 5. And finally this one: http://www.worldviewposters.com/treeoflife.htm "Alternative" suggestions:

There is a self made one by Ainsley S. Painted for last year's Darwin Day celebration at UC Berkeley. http://nature.berkeley.edu/~seago/art/dday-08-painting_medium.jpg. You might get a high resolution file directly from the artist: seago at nature dot berkeley dot edu

A good class project would be to have kids make a nice set of photographs of the local fauna/flora and then draw the tree that links them all. Most of the exercise would be determining the KPCOFGS classification, for which there are lots of online resources.

Contact somebody like Louise Mead (mead at ncse dot org) at the center for Science Education and ask for help.

***

Hope this is useful

Dominik

dominik.refardt@gmail.com

Tree topologies BIC

Dear EvolDir:

Is there an established way to measure the number of 'free parameters' distinguishing an unconstrained tree topology from an a priori constrained tree topology? Might it be the number of TBR rearrangements required to move from one to another?

We have been asked to test whether sequence data (dated, and so analysed in BEAST, meaning we cannot do a SH test) 'reject' a priori groupings in favour of an unconstrained topology.

Sincerely,

Arne Mooers

–

Dr. Arne Mooers Biological Sciences, Simon Fraser University Burnaby, BC Canada V5A 1S6 tel. +1 778 782 3979 skype: arnemooers http://www.sfu.ca/~amooers (lab) http://www.sfu.ca/fabstar (evolution@sfu) http://www.scientists-4-species.org (endangered species) http://www.vanevo.ca (Vancouver Evolution Festival)

amooers@sfu.ca amooers@sfu.ca

UCaliforniaLosAngeles Volunteer LomasBarbudalMonkeys

Field assistant position for study of capuchin life histories in Costa Rica.

The Lomas Barbudal Monkey Project has 6 volunteer field assistant positions available annually, with a rolling deadline for applications. The job includes collecting behavioral data and fecal samples. These positions require a 1-year contract with a flexible start date (though most positions begin in early summer or in January). Room and board are paid by the project, and airfare up to a certain amount is covered contingent upon the completion of the 1-year contract.

Further information about the research goals, working conditions, project publications, and application procedure are available at the following website:

http://www.sscnet.ucla.edu/anthro/faculty/sperry/jobs.html Any questions not answered by this website can be addressed to Susan Perry (sperry@anthro.ucla.edu)

Susan Perry <Sperry@anthro.ucla.edu>

PostDocs

BrighamYoungU Biodiversity

POSTDOCTORAL POSITION AVAILABLE U.S. National Science Foundation Partnerships for International Research and Education (PIRE) Patagonia Biodiversity Project http://patagonia.byu.edu The NSF PIRE project administered at Brigham Young University is seeking a postdoctoral scientist to join our research and education team. The successful candidate will be involved in the development and application of methods in comparative phylogeography, targeted specifically at understanding patterns of evolutionary diversification across multiple co-distributed taxa in southern Argentina and Chile. The postdoctoral position will be housed at Brigham Young University in Provo, Utah. However, opportunities exist for interaction with our PIRE team scientists in the U.S., Canada, Argentina, and Chile (see our web site for a list of team members), as well as summer exchange visitors and another post-doctoral researcher dedicated to this project. Applicants should be familiar with molecular laboratory techniques required to generate DNA sequence data, and should be comfortable with a broad range of phylogeographic analyses. Although there are no requirements for experience with particular taxonomic groups, our team is currently focused on freshwater fishes, freshwater crabs, lizards, frogs, and terrestrial flowering plants. Opportunities also exist to participate in mentoring graduate students and undergraduate students involved in our educational exchange program. The position is open to U.S. and international applicants. We will begin reviewing applications on May 10, 2009 and the search will remain open until the position is filled. We are targeting a start date of September 1, 2009 or sooner, although there is some flexibility. Salary is $36,000 per year plus health insurance benefits. The position will be for up to two years, with the second year of funding conditional upon performance. Interested candidates should direct their inquiries to: Jerald B. Johnson, Director, Patagonia PIRE Project, Department of Biology, Brigham Young University (jerry.johnson@byu.edu); a list of project co-PIs and senior personnel, and a description of their research interests, can be found on our web site. Applications should include a cover letter, a c.v., and a list of three references. Individuals that make our first cut will be invited to solicit and send recommendation letters. Formal applications should be submitted to: 401 WIDB, Department of Biology, BYU, Provo, UT 84602 by conventional mail; or electronically to PIREpostdocs@byu.edu. A condition of employment at Brigham Young University is a willingness to abide by the BYU Honor Code of conduct (http://honorcode.byu.edu).

“Jerald B. Johnson” <jerry.johnson@byu.edu>

BrownU DrosophilaFitness

Postdoc: Drosophila mitochondrial fitness interactions at Brown University

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

Applicants must have completed their PhD before starting the position, and have a strong record of accomplishment from their dissertation work. Applicants should have some combination of experience with molecular genetic techniques, Drosophila genetics, quantitative genetics, biochemical assays, molecular evolution, computational analysis, and an interest in evolution or genetics. The appointment is open for up to 3 years, and successful candidates will receive guidance in the preparation of an NIH NRSA Fellowship to pursue related projects.

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

David Rand

email: David_Rand@brown.edu

Department of Ecology and Evolutionary Biology

Box G-W, 80 Waterman Street

Brown University

Providence, RI 02912

Phone:

(401) 863-2890 (Office)

(401) 863-1063 (Lab)

Fax: (401) 863-2166

web pages:

http://research.brown.edu/research/profile.php?id=1100924991&r=1 http://www.brown.edu/Departments/EEB/rand/index.htm The Department of Ecology and Evolutionary Biology at Brown is an interactive group with strengths that span genomics, evolutionary biology, functional morphology, ecology, and environmental science. There are close ties to the Department of Molecular and Cellular Biology, and the Center for Computational Molecular Biology, as well as the Marine Biological Laboratory in Woods Hole

http://www.brown.edu/Departments/EEB/index.html http://www.brown.edu/Departments/Molecular_Biology/ http://www.brown.edu/Research/CCMB/ http://www.mbl.edu http://jbpc.mbl.edu/ http://ecosystems.mbl.edu/ Information on postdoctoral studies at Brown can be found here:

http://biomed.brown.edu/grad-postdoc/ Providence is widely recognized (by Rhode Islanders) as the Venice of New England and is wonderful place to live.

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

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CornellU PrimatePhylogenomics

Postdoctoral position in primate phylogenomics at Cornell University

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Adam Siepel in the Department of Biological Statistics and Computational Biology at Cornell University (Ithaca, NY). The research focus will be in the general area of comparative and evolutionary genomics, with a particular focus on computational analyses of newly sequenced primate genomes. Specific topics of interest include positive selection in coding and noncoding elements, lineage-specific selection, regulatory element turnover, and methods for combined phylogenetic and population genetic analysis. The candidate will be expected to participate in both methods development and data analysis. The ideal candidate will be highly motivated and independent, will have a strong background in genetics/genomics, good skills in mathematics and computer science, and a strong record of accomplishment in research. For general information about the research group, see http://compgen.bscb.cornell.edu/~acs .

Qualifications

- Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field. - Research experience (with strong first-author publications) in computational/comparative genomics and/or molecular evolution. - Fluency in probabilistic modeling and computational statistics. - Proficiency in programming, ideally in C or C++ as well as in scripting languages such as perl, matlab, or R. Should be comfortable in a linux environment, with large data sets, computer clusters, and databases.

Term

The term for this position is flexible but most likely will be 2-3 years (contingent on acceptable performance). The proposed start date is Summer 2009.

About Cornell

Cornell is home to a large, active community of researchers interested in evolutionary genomics, population genetics, and other areas of mathematical and computational biology. General information on postdoc life at Cornell is available from the Office of Postdoctoral Studies (http://www.postdocs.cornell.edu/index.php)

To Apply

Submit a CV, a short description of research interests and experience, and contact information for three references by e-mail to acs4 at cornell dot edu. Informal inquiries are welcome.

Adam Siepel 101 Biotechnology Building Cornell University Ithaca, NY 14853

Cornell University is an affirmative action/equal opportunity employer.

Adam Siepel <acs4@cornell.edu> Adam Siepel <acs4@cornell.edu>

France PlantGenomics

Postdoctoral level Researcher

Genoscope belongs to the Genomics Institute of the CEA (French government organization for technological research in energy). It provides a high-tech facility for sequencing and bioinformatics and is a major actor in evolutionary genomics. In the last few years, we have coordinated international eukaryotic genomic programs (animals, fungi, protists, plants), with results published in first ranked scientific journals.

We offer a 18-month position for a postdoctoral level candidate in evolutionary and structural genomics of plants.

He/she will participate in the analysis of newly-sequenced large plant genomes of interest both for industry and for fundamental evolutionary analysis. Using comparative genomics approaches and large-scale analysis, he/she will study genetic diversity with the goal of addressing fundamental questions on the evolution of the angiosperm group, and look for traits subject to recent selection. The candidate will have genomics and/or bioinformatics expertise and skills in the domain to adapt or develop tools of genomic analysis and statistical methods to support the project.

We are looking for a highly motivated and autonomous candidate with an interest in comparative genomics and the evolution of flowering plants. The candidate must have a good sense of initiative and of communication within a collaborative project including scientists from various fields.

He/she must have a background in the fields of genomics/bioinformatics.

The position is available immediately. Applicants must send CV + letters + recommendation to JobEvolGen@genoscope.cns.fr Location: Evry (near Paris), France.

For further information about Genoscope and CEA, please visit www.genoscope.cns.fr and www.cea.fr.

For further information, please contact : Olivier Jaillon, email : ojaillon[@]genoscope.cns.fr, tel : 00 33 1 60 87 25 30

Olivier Jaillon <ojaillon@genoscope.cns.fr>

IndianaU SpeciationGenetics

POSTDOC IN SPECIATION GENETICS

A full-time NSF-funded postdoctoral position is available in Leonie Moyle's lab, Department of Biology, Indiana University, Bloomington. The work will focus on identifying the molecular players involved in hybrid incompatibility ('speciation genes'), using classical genetics, QTL mapping, fine-mapping, and positional cloning. Our lab conducts research in evolutionary genetics, focusing on the genetic basis of reproductive isolating barriers and adaptive differentiation, especially in the plant group Solanum (http://www.bio.indiana.edu/~moylelab/). The postdoctoral candidate will also have ample opportunity to develop independent lines of research in these areas.

We seek a collegial, self-motivated, and intellectually curious individual with a PhD in Evolutionary Biology, Genetics, or related field. Applicants must have experience with molecular genotyping and analysis, and demonstrated written and oral communication skills. Skills or experience with plants, informatics, and/or embryology/development are highly desirable. The position is initially available for 12 months, with possible extension for up to 3 years. Salary will be commensurate with experience, and full benefits are included.

Indiana University has a large and interactive group in evolutionary genetics. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

To apply, please send a letter of interest, CV and contact information for 3 references to Dee Verostko (dverostk@indiana.edu), using 'Moyle Postdoctoral Fellow' as the subject line. Review of applications will start immediately and will continue until the position is filled. Inquires about the position can be directed to Leonie Moyle (lmoyle@indiana.edu). Some past and ongoing lab research projects, and references, can be found at: http://www.bio.indiana.edu/facultyresearch/faculty/Moyle.html Indiana University is an Equal Opportunity/Affirmative Action Employer.

lmoyle@indiana.edu lmoyle@indiana.edu

INRA France NematodeEvolutionaryGenomics

A 18 month PostDoc position in comparative and evolutionary genomics in Nematodes is available. The succesful candidate will be involved in a collaborative project between the French national sequencing centre (Genoscope) and a research team of the French national institute for agricultural research (INRA).

This project will comprise analysis of data produced by pyrosequencing of the transcriptomes of plant parasitic nematodes as well as development of a bioinformatic pipeline for the identification of genes of interest in the development of new control measures against these pest of high agricultural impact.

Plant-Nematode Interactions team from INRA (French National Institute for Agricultural Research) has coordinated genome sequencing and analysis of the first plant-parasitic animal, the root knot nematode /Meloidogyne incognita/. The laboratory is located in the south-east of France, in the French Riviera, near the city of Antibes. Genome sequencing and assembly as well as the analysis of genome structure have been performed by the Genoscope, the French National Sequencing Centre. The Genoscope is located in Evry, a city in the close vicinity of Paris. The candidate will work in close interaction and collaboration between the two laboratories. Clustering, analysis and parsing of sequences coming from pyrosequencing of the transcriptomes of new plant-parasitic species will be done at the Genoscope (Evry). The part of the project concerning identification of candidate targets and the development of a database will take place in the Plant-Nematodes Interactions team (Antibes). The major part of the project will take place in this latest laboratory and thus the candidate will spend most of his time in Antibes.

Contact @ INRA Antibes: Etienne DANCHIN : etienne.danchin@sophia.inra.fr Pierre ABAD : pierre.abad@sophia.inra.fr

Contact @ Genoscope Evry : Olivier JAILLON : ojaillon@genoscope.cns.fr François ARTIGUENAVE : artigue@genoscope.cns.fr

Links: -Full description of the project: http://www.sophia.inra.fr/physiologie_vegetale_enseignement/stages/niveau_doctorat/post_doc_genoscope_and_inra_sophia_antipolis_compa

-Meloidogyne incognita genome paper @ Nature Biotech: http://www.nature.com/nbt/journal/v26/n8/full/nbt.1482.html -Meloidogyne incognita genome portal: http://meloidogyne.toulouse.inra.fr/ – WARNING !! NEW ADDRESS !!

Etienne G.J. Danchin

Institut National de la Recherche Agronomique

U.M.R. - I.B.S.V. INRA-UNSA-CNRS – Centre de recherche de Sophia-Antipolis 400 route des Chappes, BP 167 06903 Sophia-Antipolis Cedex – http://www.sophia.inra.fr/ Tel. +33 492 386 494 Fax. +33 492 386 587

http://edanchin.free.fr

mailto:Etienne.Danchin@sophia.inra.fr

INRA Versailles TE evolution

20 months Postdoc Position available at INRA-Versailles

Characterization of Transposable Elements (TEs) in the tobacco genome

A 20 months postdoctoral position is available in the team "Host-Transposons Interactions and Plant Biodiversity" (http://www-ijpb.versailles.inra.fr/en/bc/equipes/Transposons/index.html), at the Institut Jean-Pierre Bourgin, Laboratoire de Biologie Cellulaire, INRA-Versailles, France.

The project will focus on the bioinformatic evaluation of TEs present in the tobacco allotetraploid genome. The analysis will be based on available tobacco genomic shotgun and EST sequences, and will aim at reconstructing consensus TE sequences to evaluate the diversity of TE lineages present in the tobacco genome. It will provide a global overview of the various TE lineages present in tobacco, with a specific emphasis on LTR retrotransposons. It will also allow to evaluate their expression conditions, and identify chimeric co-transcripts indicative of a possible impact of TE insertions on tobacco cellular genes.

Good experience in bioinformatic tools used for genome annotation is required. Expertise in eucaryotic TE classification et evolution would be highly appreciated. This work will be performed in collaboration with the team of Hadi Quesneville, URGI, INRA-Versailles (http://urgi.versailles.inra.fr/). The possibility of experimental molecular analysis of TE stress activation, of which our team has good expertise, is also open for candidates that may also be interested by these aspects. But the core of the project will be bioinformatics.

Emergency!!!! The starting date is 1st of May, 2009 (or as soon as possible)

Send a curriculum vitae, research interests, and two recommandations contacts to:

Dr Marie-Angèle GRANDBASTIEN (gbastien@versailles.inra.fr) Laboratoire de Biologie Cellulaire Institut Jean-Pierre Bourgin INRA-Centre de Versailles 78026 Versailles cedex, France gbastien@versailles.inra.fr tel: 33 1 30 83 30 24 fax: 33 1 30 83 30 99

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Marie-Angèle GRANDBASTIEN Institut Jean-Pierre Bourgin Laboratoire de Biologie Cellulaire INRA - Centre de Versailles 78026 Versailles, France Tel: 33 (1) 30 83 30 24 Fax: 33 (1) 30 83 30 99 Email: gbastien@versailles.inra.fr

"marie-angele.grandbastien" <marie-angele.grandbastien@versailles.inra.fr>

INRA Versailles TE evolution 2

21 months Postdoc Position available at INRA-Versailles

Annotation and identification of Transposable Elements in tobacco (Nicotiana tabacum): evolution, diversification and potential involvement in stress responses

A 21 months postdoctoral position is available in the team "Host-Transposons Interactions and Plant Biodiversity" (http://www-ijpb.versailles.inra.fr/en/bc/-equipes/Transposons/index.html), at the Institut Jean-Pierre Bourgin, Laboratoire de Biologie Cellulaire, INRA-Versailles, France.

The project will focus on the evaluation of TE families present in the tobacco allotetraploid genome, in order to obtain a global picture of the TE content of tobacco and of the potential impact of these TEs on adjacent genes. The analysis will be based on available tobacco genomic shotgun and EST sequences, and will aim at reconstructing consensus TE sequences to evaluate the diversity of TE lineages present in the tobacco genome. It will provide a global overview of the various TE lineages present in tobacco, with a specific emphasis on LTR retrotransposons. The project will also allow to evaluate their expression conditions, and identify chimeric co-transcripts indicative of a possible impact of TE insertions on tobacco cellular genes.

Good experience in bioinformatic tools used for genome annotation and sequence assembly is required. Expertise in TE classification et evolution will be highly appreciated. This work will be performed in collaboration with the team of Marie-Anne Van Sluys (GaTE, University of Sao Paulo, Brazil, http://www.ib.usp.br/-gate/), and with the team of Hadi Quesneville, URGI, INRA-Versailles (http://urgi.versailles.inra.fr/). Depending on the candidate profile and interests, the possibility of experimental molecular analysis of TE stress activation is also open. However the required profile is primarily a bioinformatics expertise profile.

Expected starting date: 1st of september 2009.

Two major administrative requirements are: - to have obtained a PhD for less that 5 years - no previous post-doc at the INRA-Versailles Center

Send a curriculum vitae and two recommandations contacts to:

Dr Marie-Angèle GRANDBASTIEN (gbastien@versailles.inra.fr) Laboratoire de Biologie Cellulaire Institut Jean-Pierre Bourgin INRA-Centre de Versailles 78026 Versailles cedex, France gbastien@versailles.inra.fr tel: 33 1 30 83 30 24 fax: 33 1 30 83 30 99

Marie-Angèle GRANDBASTIEN Institut Jean-Pierre Bourgin Laboratoire de Biologie Cellulaire INRA - Centre de Versailles 78026 Versailles, France Tel: 33 (1) 30 83 30 24 Fax: 33 (1) 30 83 30 99 Email: gbastien@versailles.inra.fr

"marie-angele.grandbastien" <marie-

angele.grandbastien@versailles.inra.fr>

Italy PlantConservationGenetics

Title: Post doc in Plant Conservation Genetics / Phylogeny

Research Centre: The research carried out at the Environment Department of Edmund Mach Foundation encompasses both ecological and molecular studies. It focuses on the functional integrity and biodiversity of aquatic (mainly plankton, diatoms and salmonid fishes) and land taxa (mainly vertebrate fauna and their parasites, higher plants including annual species and forest trees) that are subject to anthropic pressure and global climate changes. The ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential) Major Proposal is a collaborative project funded by the Autonomous Province of Trento involving three regional institutions (Edmund Mach Foundation, Natural History Museum of Trento, Civic Museum of Rovereto) and one external partner (University of Davis, California).

Description: We are seeking a highly motivated and independent individual to carry out a research project on the phylogeny/conservation genetics of selected, endemic taxa. The successful candidate will be responsible of sampling, selection of suitable molecular markers and phylogenetic reconstruction for three angiosperm taxa with uncertain taxonomy (within the Erysimum, Brassica and Aquilegia genera). Upon taxonomic status confirmation, population genetics, demographic and ecological studies will be carried out to provide conservation guidelines for the most interesting species. The position, initially granted for a time span of three years, may be renewed and upgraded depending on the successful completion of the project.

IT knowledge: Software for sequence processing, alignment and editing (e.g. Staden Package, Phred, Bioedit, ClustalW). Programs for population genetics/evolutionary analyses (e.g. Arlequin, Structure, Phylip). The ability to write/use Perl, Linux Shell scripts or VBA macros and the use of software for phylogenetic analyses (Paup, Phylip, Mega) are considered as optional qualifications in the selection.

More information and application: http://www.fondazioneedmundmach.it/-sperimentazione_context2.jsp?ID_LINK=3140&area=6

Deadline for application: 30th April 2009

Daniele Barbacovi Fondazione Edmund Mach Research Centre - Human Resources Office Via Mach 1, 38010 S. Michele all'Adige (TN) - Italy Phone +39 0461 615542 - Fax + 39 0461 650956 Skype daniele.barbacovi_crfem http://www.fondazioneedmundmach.eu daniele.barbacovi@iasma.it daniele.barbacovi@iasma.it

KansasStateU PlantEvolutionaryGenet

POST-DOCTORAL POSITION AVAILABLE TO STUDY EVOLUTIONARY GENETICS IN PLANTS

A postdoctoral position is currently available in the laboratory of Mark Ungerer at Kansas State University in the Division of Biology. The successful candidate will contribute to ongoing research investigating the possible causes and evolutionary consequences of massive retrotransposon proliferations that have occurred independently in the genomes of three hybrid sunflower species. Specific responsibilities of the postdoctoral researcher will include oversight of one or more major subprojects that examine the impacts of retrotransposon proliferation on genome function and structure and the environmental and genomic conditions under which such proliferation events take place. The position will require both laboratory and greenhouse work as well as seasonal trips to the southwestern US to collect from natural populations and natural hybrid zones. Candidates must have strong molecular biology skills (including experience working with RNA) and/or interest in the fields of molecular and genome evolution.

To apply, send a cover letter describing your research interests/past research achievements, a C.V., and the names and contact information for three individuals willing to provide letters of recommendation. Materials should be sent to the address below. Review of applications will begin on May 25, 2009 and continue until the position has been filled. Ph.D. degree must be completed by start date. Email applications preferred. KSU is an equal opportunity employer and actively seeks diversity among its employees. Background check required by university policy.

Mark Ungerer Division of Biology Kansas State University Manhattan KS 66506 mcungere@ksu.edu office: 785.532.5845 fax: 785.532.6653 mcungere@ksu.edu mcungere@ksu.edu

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LundU 3 AnimalEvolution

Dear All,

CAnMove (Centre for Animal Movement Research) at Lund University is seeking three postdoctoral fellows in the fields:

1) Insect flight and morphological trade-offs: adaptations for dispersal or escape flight performance (ref no. 1182)

2) Genetics of migration in willow warblers (ref no. 1183)

3) Partial migration in aquatic systems (ref no. 1184)

Please find more information at

http://www.science.lu.se/the-faculty/vacant-positions The application with reference number and including CV, signed transcripts and other documents should have arrived at Lund University at: Registrator, Lund University, Box 117, 221 00 LUND, SWEDEN, not later than 22 April 2009. (or at registrator@lu.se)

Anders Hedenström and Susanne Åkesson

CAnMove is a new centre for research on Animal Movement, funded primarily by a Linnaeus grant from the Swedish Research Council. We aim at understanding the underlying ecological and evolutionary causes for animal movements, with an emphasis on the process of migration across a large range of scales. To achieve these goals we plan to implement a sophisticated technological innovation lab, a sophisticated database and facilitate communication about new research results.

The CAnMove research program consists of 14 principal senior researchers and a number of graduate students and research partners at Lund University and elsewhere. Our facilities will be located at the Ecology Building at Lund University. The program was granted in 2008 and started during the autumn 2008. We have already recruited experts to our new technical lab and database facility, and to strengthen the program further we are now seeking suitable postdoc candidates in three research areas.

Anders Hedenström <Anders.Hedenstrom@teorekol.lu.se>

LundU AnimalMovement

CAnMove (Centre for Animal Movement Research) at Lund University is seeking three postdoctoral fellows in the fields:

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Yours sincerely,

Anders Hedenström

Professor of Theoretical Ecology

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Anders.Hedenstrom@teorekol.lu.se Anders.Hedenstrom@teorekol.lu.se

Lyon SexChromosomeEvolution

Postdoctoral position on the origin and evolution of young plant sex chromosomes

An ANR-funded postdoc position (2 years) is available in Gabriel Marais' lab at the University of Lyon (France).

The project will focus on Silene latifolia a dioecious plant species with X and Y chromosomes. This species is emerging as a model species for the understanding of the evolution of sex chromosomes. The aim of the project will be to use the genomic resources that have recently become available in S. latifolia (BAC sequences, ESTs and microarrays) to investigate several points in relation to the origin and evolution of XY in this species: XY recombination suppression, Y degeneration, and sex determination. We collaborate on this project with Prof. Alex Widmer's lab (ETH Zurich).

We seek a highly motivated candidate with skills in data analysis and a strong interest in genome evolution and evolutionary biology in general. A PhD in one or several of the following fields is expected: bioinformatics, genomics, molecular evolution, population genetics, biostatistics. The applicant does not need to be a French speaker.

We are part of the Bioinformatics and Evolutionary Genomics group, which includes about 25 people (including Laurent Duret and Manolo Gouy). The BGE group has a long-standing experience in bioinformatics and offers a very stimulating scientific environment (highest rate by CNRS at last evaluation in 2006). We have a vast range of locally available bioinformatics tools and excellent computing facilities (UNIX servers, PC clusters). Our weekly lab meeting and journal club are held in English. Find more details at http://lbbe.univ-lyon1.fr/ . Lyon is the 2nd largest French city. Its city center has been classified "world heritage" by UNESCO and Lyon is considered French capital of gastronomy. Excellent public transports exist within the city (metro, bus, tramway, public bikes), and to the nearby Alps, Paris (two hours by train) and the rest of Europe.

To apply, please send to Gabriel Marais (email: marais@biomserv.univ-lyon1.fr): a letter describing your research motivation and experience, a CV including publication list, full contact details of two scientific referees.

The position should start on fall 2009. Annual gross salary will be about 28,000 euros. Review of materials will begin late April and will continue until the position is filled. For further information, please contact:

Dr. Gabriel Marais Bioinformatics and Evolutionary Genomics group Institute for Biometrics and Evolutionary Biology University of Lyon Campus de la Doua, Villeurbanne Email: marais@biomserv.univ-lyon1.fr Website: http://lbbe.univ-lyon1.fr/--Marais-Gabriel-.html?lang=en Gabriel Marais <marais@biomserv.univ-lyon1.fr>

Marseille GorgonianGenetics

Dear all,

A 12 months post-doc position, funded by the CNRS, is opened in the DIMAR laboratory in Marseille (UMR 6540 / Centre d'Oceanologie de Marseille). The research project will deal with the genetic study of some mediterranean gorgonians which have been impacted by massive mortalities potentially linked with climate change (Garrabou et al., Global Change Biology, in press, 2009). The candidate will develop and analyse some nuclear markers for the analysis of the phylogeography of the studied species. Some gene expression analyses in response to thermal stress will also be done. The candidate should have either a strong background in polymorphism sequence analyses (coalescence, neutrality tests...) or a good experience with real-time PCR. A good knowledge of marine ecosystems might be an advantage but is not a prerequisite. The DIMAR laboratory (http://www.com.univ-mrs.fr/DIMAR/) is fully equiped for populations genetics and gene expression analyses, including experimental facilities. The researches of this laboratory mainly focus on the development and the evolution of marine biodiversity, from genes to ecosystems.

The starting date will be on 2009 september 1st or october 1st. The net salary will be around 2044 € / month. Please send a CV (including references) and motivations to didier.aurelle@univmed.fr, jean-pierre.feral@univmed.fr and anne.chenuil-maurel@univmed.fr

The deadline for application is june 5th.

With many thanks Didier Aurelle

– Didier AURELLE

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

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

didier.aurelle@univmed.fr didier.aurelle@univmed.fr

Marseille GorgoniansGenetics

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With many thanks Didier Aurelle

– Didier AURELLE

Courriel: didier.aurelle@univmed.fr

Maître de Conférences UMR 6540 DIMAR Université de la Méditerranée / Centre d'Océanologie de Marseille Station Marine d'Endoume Rue de la batterie des Lions 13007 Marseille FRANCE Tel: + 33 4 91 04 16 18 Fax: + 33 4 91 04 16 35

didier.aurelle@univmed.fr didier.aurelle@univmed.fr

Maryland PintailPopulationModeling

Postdoctoral Position U.S. Geological Survey, Patuxent Wildlife Research Center Northern Pintail Population Modeling

The U.S. Geological Survey, Patuxent Wildlife Research Center (Laurel, Maryland) is seeking candidates for a postdoctoral position to develop a spatially-implicit population model for Northern Pintails (Anas acuta) that integrates the effects of habitat and harvest management. The model will serve as a key component in addressing the challenges posed by recent reviews to better integrate objectives of waterfowl habitat and population management in a single modeling framework. Model development will occur through a process of iterative prototyping, with the initial focus on capturing the right general structure of the model, and detail and functionality added over time. The model design will be driven by the decision contexts provided by the North American Waterfowl Management Plan, and the setting of annual harvest regulations. We hope that this work will also build a solid platform for developing future population models for other species of conservation concern.

The postdoctoral position will be part of an interagency research team, including scientists from USGS, U.S. Fish and Wildlife Service, Ducks Unlimited, Environment Canada, UC Davis, and Utah State University, among others. The research team will provide substantial support in the overall framework for the model, access to appropriate data, and review of model details. Travel funds will be provided to support visits with study team members and outside cooperators, to attend regional workshops during model development, and to attend professional conferences.

The ideal candidate will have a background in population modeling, structured decision making, adaptive management, waterfowl population dynamics, and Bayesian hierarchical estimation. Proficient programming skills are required, with some preference given to candidates with a background in MATLAB. The successful candidate will also have excellent writing and personal communication skills. Applicants are expected to have earned a Ph.D. degree in a relevant discipline, preferably within the last 5 years.

The position will be located in Laurel, Maryland. The desired start date is summer 2009, and the position is funded at least through September 2010, with additional funding likely. The salary level is very competitive.

Applications are due no later than May 29, 2009. If you are interested, send a curriculum vitae, a letter describing your background and interests, and the names of three references to Michael Runge (mrunge@usgs.gov).

For further information, contact either: Michael Runge (mrunge@usgs.gov), USGS Patuxent Wildlife Research Center 12100 Beech Forest Road, Laurel, MD 20708-4017 (301) 497-5748

Scott Boomer (scott_boomer@fws.gov), USFWS Division of Migratory Bird Management 11510 American Holly Drive, Laurel, MD 20708 (301) 497-5970

mrunge@usgs.gov mrunge@usgs.gov

Munich PlantAdaptation

Post-Doc position in Plant Evolutionary Genetics at LMU Munich (Germany)

A post-doctoral position is open for two years in the Biology Department at the University of Munich LMU for someone interested by molecular evolution and population genetics in plants (wild tomato species). The applicant will be based in the Section of Evolutionary Biology in the group of Prof. Wolfgang Stephan. The applicant will pursue research on molecular adaptation of wild tomato species (Solanum peruvianum and S. chilense) to abiotic stress such as drought tolerance or cold resistance. These species are found in a wide range of habitats (high mountains, deserts) in South America, and are a good model to study plant adaptation at the genetic level. The objective of the post-doctoral period is to use polymorphism (SNP data) to detect natural selection at candidate genes involved in adaptation to different habitats. The applicant is also expected to perform functional validation at those candidate genes. Therefore, the project will involve molecular and quantitative genetic assays of wild tomato accessions, and inferences from molecular population genetics and evolution.

Applicants must have completed their PhD before starting the position. We seek highly motivated candidates with a strong record of accomplishment from their Master's/PhD thesis work. Ideally, applicants should have some experience with molecular genetic techniques, and a strong background in population genetics, evolution and statistics. However, we wish to encourage the application of plant geneticists, experienced in molecular functional analysis, who are interested in evolution.

The Ludwig-Maximilians University of Munich is rated the best in Germany by international standards. The Department of Biology comprises research groups working on both plant and animal genetics. The Section of Evolutionary Biology also includes the group of Prof. J. Parsch working on evolution of gene regulation in Drosophila melanogaster, and the group of Prof. D. Metzler developing statistical and mathematical methods in population genetics. The group of Prof. Stephan focuses on statistical methods for detecting genes under selection in D. melanogaster. In wild tomato species we focus on the evolution of genes involved in plant-parasite interactions (Dr Rose), and theoretical aspects of species history (Dr. Tellier).

The start date is spring or summer 2009. Applications will be reviewed until the position is filled. To apply please email 1) a CV, 2) a short statement of research interests and experience describing your qualifications for this position, and 3) contact information for three references.

Contact: Prof Wolfgang Stephan (stephan@bio.lmu.de) Dr Aurelien Tellier (tellier@bio.lmu.de)

Section of Evolutionary Biology LMU BioCenter Grosshaderner Str. 2 82152 Planegg-Martinsried Germany Tel: +49 89 2180 74 105 Fax: +49 89 2180 74 104 www.evol.bio.lmu.de Aurelien Tellier <tellier@zi.biologie.uni-muenchen.de>

NCStateUniversity MolecularPhylogenetics

Postdoc: Molecular Phylogenetics

A postdoctoral position is available at North Carolina State University (NCSU) for someone with interests in molecular evolution and phylogenetics. The selected applicant will be associated with the NCSU Insect Museum, working closely with Dr. Andrew R. Deans on an

NSF- funded project that touches many other aspects of evolutionary biology: divergence time estimation to address biogeographic and host/ parasite questions, DNA barcoding to test hypotheses of mimicry and beta diversity, new informatics to manage/incorporate morphological and fossil data, and novel methods for revisionary systematics. This position is an opportunity to join a growing lab of enthusiastic and approachable biologists with a broad array of expertise.

As a vertex of North Carolina's Research Triangle NCSU benefits from close proximity to a large community of evolutionary biologists at NCSU (e.g., in the Entomology, Genetics, and Biology departments) and our affiliation with the National Evolutionary Synthesis Center (NESCent).

Required: PhD in Biology or related field. Experience in primer design, PCR, molecular data analysis. Excellent written and oral communication skills.

Desirable: Experience with insects, informatics, and ontologies, penchant for international travel and field work.

Details: The position is available from July 1, 2009 (negotiable) and is offered for one year, with the possibility of reappointment for another year. Salary is $38,000 per annum. Information of benefits can be found here: http://www7.acs.ncsu.edu/hr/job_applicants/ Applicants must apply online - http://jobs.ncsu.edu/applicants/Central?quickFind=83352 (position # 01-07-0902) for instructions. Proper documentation of identity and employability will be required before the hiring process can be finalized. Applicants should upload a two-page (maximum) statement of research interests, a CV, and contact information for three references. Review of applicants commences May 1, 2009 and continues until the position is filled.

PI contact information: Andrew R. Deans Department of Entomology North Carolina State University Campus Box 7613 2301 Gardner Hall Raleigh, NC USA 27695-7613

ncsu.edu email: andy_deans@ phone: +1 (919) 515-2833 fax: +1 (919) 515-7746 skype: ardeans

More information: http://ncsu.edu/ http://deanslab.org/ http://gsl.cals.ncsu.edu/ http://insectmuseum.org/ http://entomology.ncsu.edu/ /AA/EOE. ADA Accommodations: Dr. Andrew R. Deans andy_deans@ncsu.edu 919-515-2833.// NC State welcomes all persons without regard to sexual orientation./

andy_deans@ncsu.edu andy_deans@ncsu.edu

Netherlands TheoryAnimalMovement

Theoretical/Animal Ecologist POSTDOC (M/F)

vacancy number CL-PGM-09441

to study the movement of animals linked to resource distributions and personality traits.

The Netherlands Institute of Ecology (NIOO) is a top research institute of the Royal Netherlands Academy of Arts and Sciences (KNAW). It comprises three centers: the Centre for Estuarine and Marine Ecology (CEME) in Yerseke, the Centre for Limnology (CL) in Nieuwersluis, and the Centre for Terrestrial Ecology (CTE) in Heteren. Mission of the NIOO (http://www.nioo.knaw.nl) is to carry out excellent fundamental and strategic research in ecology.

The Project Group Movement Ecology of the NIOO develops a universal framework to understand movement of animals in terrestrial, freshwater and marine habitats.

General Program Description:

Movement is a fundamental characteristic of life. Power-laws, in the form of so-called Lévy walks, have been put forward as a generic description for the foraging trajectories of free-ranging animals, as an alternative for the traditional Brownian walks. Lévy walks give rise to scale-free, super-diffusive movement trajectories that are hypothesized in the literature to improve the efficiency of searching for food in complex landscapes. The aim of the project is to develop theoretical models to describe animal movements, and to use large databases of movements by great tits and swans to test whether their movements can be best described by Lévy walks. In experimental setups specific hypothesis on individual movement patterns can be tested in great tits with known individual history.

This project is supervised by Marc Naguib (CTE), Bart Nolet (CL), and Johan van de Koppel (CEME). It is initiated to stimulate cooperative research among groups from these different centres of NIOO, and is financed by the Strategic Fund of the KNAW.

Function description: The candidate will be the principle researcher of the project: 'Universal movement laws in terrestrial, marine and freshwater animals: the link with prey distribution and individual strategies'.

The project will entail (1) a theoretical study of animal movement in explicit resource landscapes, (2) analyses of existing data from terrestrial, marine and freshwater systems, and (3) a laboratory or field experiment with Great Tits that addresses the effects of individual variation and resource heterogeneity on movement trajectories.

Requirements: We are looking for a highly motivated and skilled candidate with a PhD degree in ecology, having affinity for and experience with at least two of the following: (a) modelling / programming, (b) statistical analyses of complex data, (c) experimental studies with animals. The candidate is expected to promote new techniques to measure and analyse animal movement. The candidate should be a team player, be legally qualified to design animal experiments, and have good communication skills, both orally and in writing,

Location: The candidate will initially be based in Nieuwersluis, but needs to visit the other two centres on a regular basis. In the course of 2010 the base will change to Wageningen after the merger of CTE and CL.

Appointment: Temporary appointment for 3 years, starting in the course of 2009.

Salary: Salary depends on training and work experience, the maximum gross monthly salary coming with a full-time appointment will amount up to EUR3.755,00 (scale 10, Collective Agreement for Dutch Universities (CAO-Nederlandse Universiteiten), excluding 8% holiday pay and a year-end bonus. We offer an extensive package of fringe benefits.

Information: To request additional information and a pdf of the project proposal please contact the members of the project group by e-mail: movement@nioo.knaw.nl <mailto:movement@nioo.knaw.nl> . General information on the NIOO can be found at the Internet at: http://www.nioo.knaw.nl < https://webmail.cte.nioo.knaw.nl/exchweb/bin/redir.asp?URL=http://www.nioo.knaw.nl/ > .

Applications: Applications with CV (including a list of publications and a statement of research interests), mentioning the vacancy number should be addressed to prof. dr. Louise E.M. Vet, director of the NIOO, P.O. Box 40, 6666 ZG Heteren, The Netherlands, or by e-mail to g.giesen@nioo.knaw.nl. The closing date for application is May 1th 2009

Prof. Dr. Marc Naguib Netherlands Institute of Ecology (NIOO-KNAW) PO Box 40 6666 ZG Heteren The Netherlands m.naguib@nioo.knaw.nl <mailto:m.naguib@nioo.knaw.nl> Tel: +31 (0)26 4791 255 Fax: +31 (0)26 4723 227 http://www.nioo.knaw.nl/PPAGES/mnaguib/ < http://www.nioo.knaw.nl/CTE/PVD/index.htm >

"Naguib, Marc" <M.Naguib@nioo.knaw.nl>

NewYorkBotanicalGarden PBI Miconieae

Postdoctoral Position at The New York Botanical Garden

The New York Botanical Garden, a National Historic Landmark and one of New York City's premier cultural institutions seeks a full-time Post-Doctoral Research Associate to join our Institute of Systematic Botany Science department. This is a grant funded position. Salary commensurate with experience. Excellent benefits, including paid vacation.

The candidate will join the PBI: Miconieae (Melastomataceae) project. This NSF-funded research will produce an online monograph of all 1,800 species in this neotropical tribe, including complete descriptions, images, keys for their identification, and distribution maps for each species, while continuing to research phylogenetic relationships within the tribe. This project presents a unique opportunity for a highly motivated individual to carry out field work in the Neotropics, and to take a leading role in the analysis of large data sets (800+ species; 1000+ terminals) using molecular and morphological data. Funding is available for a minimum of 1 year, and may be extended upon mutual agreement and grant renewal. Applicants should have a Ph.D. at the start date, experience in phylogenetic analyses and sequencing techniques, as well as desire to be involved in all aspects of a multidisciplinary and international project on angiosperm systematics. (http://sweetgum.nybg.org/melastomataceae)

Applicants should send a cover letter with a brief description of research interests, curriculum vitae, up to four reprints if available, and the names and contact information for at least three references to: HR@nybg.org or mail to The New York Botanical Garden, 200th St. & Kazimiroff Blvd., Bronx, NY 10458, Attention Human Resources/Dr. Fabian Michelangeli - Position Application Number SC-1632.

The review of applications will begin on May 4th, 2009.

The New York Botanical Garden is an Equal Opportunity Employer.

fabian@nybg.org

UBourgogne NeuroEvoParasito

Project title: Neurophysiological basis of parasite manipulation: how do acanthocephalan parasites interfere with the serotonergic pathway of their crustacean host ?

A postdoctoral associate is sought to collaborate on a highly original project at the interface between invertebrate neurophysiology and behavioral ecology. The main goal of the project is to understand the neurophysiological basis of parasite manipulation. Parasite manipulation is defined as the ability, shared by several parasite groups, to modify their hosts behaviour in ways that enhance their own transmission, for instance through increasing the intermediate hosts vulnerability to predation by the final host. We are specifically investigating how parasites interfere with the serotonergic system of their host to alter behavioural perception and/or response to environmental cues (such as phototactism or chemotactism). The project will use the amphipod Gammarus pulex and its acanthocephalan parasites Pomphorhynchus sp. as a model system. It will address how reaction to light and/or odor is controled by serotonin (receptors involved) and whether parasites are altering certain components of the serotonergic pathway (serotonin brain/hemolymph concentrations, post-traductional changes in 5HT-receptors, changes in SERT gene expression...).

The candidates should have a PhD in neurophysiology, or in behavioural ecology with research experience in invertebrate neurobiology. Experience with biochemical techniques (western blot, ELISA, HPLC, immunocytochemistry, analysis of post-traductional modifications) are requested. Skills in proteomics or gene expression analysis will also be considered.

The successful applicant will join the evolutionary ecology lab at University of Dijon, France, and be jointly supervised by Professor Frank Cezilly (www.u-bourgogne.fr/BIOGEOSCIENCE/cv/cezilly) and Dr. Marie-Jeanne Perrot-Minnot (www.u-bourgogne.fr/-BIOGEOSCIENCE/perrot). The position will be appointed for two years with a net salary of 2500 euros/month Start date is negotiable from september to december 2009. Applicants are requested to email a letter of introduction and motivation, CV, and references to fcezill@u-bourgogne.fr and mjperrot@u-bourgogne.fr. The deadline for application is may the 28th, 2009

*** Marie-Jeanne Perrot-Minnot Associate Professor Ecology Evolution lab UMR CNRS 5561 Biogeosciences Univ. Bourgogne 6 Bd Gabriel 21000 Dijon France

Marie-Jeanne Perrot-Minnot <mjperrot@u-bourgogne.fr>

UBristol DrosophilaAdaptation

NERC-funded PDRA available in Biological Sciences, University of Bristol, UK

Limits to evolution along ecological gradients in rainforest Drosophila

Applications are invited for a Postdoctoral Research Assistant to work on a NERC-funded project with Dr Jon Bridle. This research will combine ecological and quantitative genetic studies of natural populations to test population genetic models for limits to adaptation at range margins. It will focus on estimating adaptive divergence and fitness along several ecological gradients in northern Queensland. Addressing these issues is crucial for assessing dangerous levels of environmental change.

The research involves collaboration with Profs Mark Blows (Queensland), Ary Hoffmann (Melbourne), and Nick Barton (Vienna), and will require spending extended periods in the field, and approximately six months per year in Australia.

Successful applicants for will need to show evidence of successful research and that they are capable of working independently under difficult field conditions. Experience in the design and successful performance of detailed quantitative genetic experiments and fitness assays (particularly in Drosophila) would be a distinct advantage, as well as an understanding of population and quantitative genetic theory.

A full driving license is essential. The position will be for 36 months, with a start time of January 2010 at the latest. Further details and informal enquires are welcome (jon.bridle@bristol.ac.uk).

A full-time technician position is also available for this project, to be advertised at a later date.

The deadline for applications is 29th May 2009.

Please see https://www.bris.ac.uk/boris/jobs/ads?ID=

78747 for full details of the application procedure.

Dr Jon Bridle School of Biological Sciences University of Bristol Bristol BS8 1UD

Tel. (+44) 117 928 7482 Fax. (+44) 117 331 7985 jon.bridle@bristol.ac.uk

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

UBritishColumbia InfluenzaEvolution

Postdoctoral Researcher The CIHR Team in Functional Infectomics of H5/H7 Influenza A virus

The CIHR Team in Functional Infectomics of H5/H7 Influenza A virus, coordinated by team leader Dr. François Jean in the Department of Microbiology and Immunology at the University of British Columbia invites applications for Postdoctoral researchers. Three-year terms are available for comparative studies in functional infectomics of Influenza A (infA) to reveal host-dependent factors and associated biological networks determining pandemic. www.microbiology.ubc.ca/-fjean The following position is open for immediate hire:

Evolutionary Biology/Knowledge Translation/Bioinformatics/Public Health Postdoctoral Fellow CIHR Team in Functional Infectomics Research Laboratory, Vancouver, B.C., Canada

You will participate in public health research initiatives, including collaborations between all CIHR Pandemic Preparedness Team members. The successful candidate must synthesize and translate the functional infectomics data into useful resources for the media, public health educators and policy-makers. A strong working knowledge of bioinformatics, particularly in the areas of comparative genomics, proteomics and pandemic modeling is highly preferred. Proficiency with computers, and effective use of relevant database, spreadsheet, statistical, graphical, presentation, communication and web application is highly recommended. The successful applicant will keep up-to-date regarding new initiatives, developments and trends in virology, genomics, bioinformatics, proteomics, infectious diseases and population health issues. Your excellent communication skills will be the foundation for the synthesis and presentation of related data and information in concise and meaningful ways. The ideal candidate also has considerable data management and problem-solving skills. This is a unique position requiring a well-rounded individual looking for a challenging postdoctoral experience.

The appointments will be for one year initially, and may be renewable for up to 3 years at the postdoctoral level. The CIHR Team in Functional Infectomics expects to hire multiple researchers who will work with one another and with researchers in other disciplines participating in the team project worldwide.

Due to repeated outbreaks of avian influenza around the world, including the most recent one in the province of British Columbia, the Government of Canada, and the Canadian Institutes of Health Research (CIHR) have prioritized resources and co-operation to eradicate avian influenza as soon as possible, and prevent any future human infection with highly pathogenic strains of the virus. This has guaranteed funding for multiple Postdoctoral fellowships. We seek individuals to work with a world-class team of faculty from the University of British Columbia, British Columbia Centre for Disease Control, University of Calgary, Canadian Food Inspection Agency, Centers for Disease Control Atlanta, Ohio State Medical College and the University of Hong Kong to develop and coordinate worldwide research efforts pandemic preparedness. Travel between various laboratories may be required.

Candidates should have: completed their Ph.D. within the last three years in Bioinformatics, Public Health, Virology, Microbiology or a related discipline, or hold a CIHR-eligible Health Professional degree (i.e., Physician, or Veterinarian). An equivalent combination of education, training and experience will be considered, but must conform to CIHR eligibility guidelines. The successful candidate will have excellent organization, interpersonal, and communication skills, and have a strong personal commitment to public health. The team grant is composed of five research projects in genomics, proteomics, RNA profiling, cell biology, and bioinformatics, with postdoctoral positions available to each project. The work will involve driving an increase in our molecular, cellular and functional understanding on infA-induced pathogenesis. Subsequently, using this novel biological knowledge, researchers will develop trans-disciplinary models for real-time risk management of influenza pandemic, and disease surveillance in Canada and around the world.

Applicants should submit a resume, statement of research interests and the names and complete contact information (including phone, fax and e-mail) of four references to Dr. Michelle Krakowski, Department of Microbiology & Immunology, Life Sciences Centre, 3559-2350 Health Sciences Mall, Vancouver, B.C., V6T 1Z3. (mkrakow@interchange.ubc.ca). Review of applications will begin immediately and will continue until the positions are filled.

UBC hires on the basis of merit and is committed to employment equity. We encourage all qualified persons to apply; however, Canadians and Permanent Residents of Canada will be given priority. The positions

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UCaliforniaIrvine StatisticalGenetics

One or more Postdoctoral Scholar positions are available to carry out bioinformatics analyses of population and quantitative genetics datasets. The project will be jointly supervised by Anthony Long and Stuart Macdonald (University of Kansas), with the position located at U.C. Irvine. There will be opportunity to interact with a diverse group of evolutionary geneticists at the University of California, Irvine (http://ecoevo.bio.uci.edu). This position provides an opportunity to develop an independent line of research and to collaborate with our group on several quantitative problems. Potential projects include computational analyses of fifteen resequenced Drosophila genomes, computation analyses of ~2000 recombinant inbred lines genotyped at >1500 SNP loci, and developing quantitative genetic and population genetic models relating phenotype to genotype.

This position requires a Ph.D. and a record of published research in areas related to population/quantitative/statistical genetics, computational or mathematical biology. Project will involve working with massive datasets so demonstrated competency with Unix/Perl/MySQL will be required (and R an added plus). Positions are initially for one year, with possibility of renewal. The positions are currently open, and the starting date is negotiable.

All qualified candidates, including minorities and women, are strongly encouraged to apply. Applicants should submit a cover letter, a curriculum vitae, and the names, addresses and phone to:

Tony Long, Department of Ecology and Evolutionary Biology, 321 Steinhaus Hall
University of California, Irvine, Irvine, CA 92697-2525

email: tdlong@uci.edu

The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program.

Anthony Long Professor, Ecology and Evolution U.C. Irvine 92697-2525 Ph: 949-824-2562 http://cstern.bio.uci.edu tdlong@uci.edu tdlong@uci.edu

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UCollegeLondon MappingPreferenceGenes

Position available: POSTDOCTORAL RESEARCH ASSOCIATE

Department of Genetics, Evolution and Environment, University College London

Project title: Genetic basis of female sexual preference in a stalk- eyed fly

Investigators: Dr Kevin Fowler & Prof Andrew Pomiankowski

1) OUTLINE OF PROJECT

A NERC-funded postdoctoral position is available from 01 June 2009 (flexible) for up to 36 months to investigate the genetic basis of female mate preference in the stalk-eyed fly, Diaesemopsis meigenii. The project combines evolutionary genetic analysis and quantitative trait locus (QTL) mapping approaches. Quantitative genetic analysis will be carried out on condition-dependent female mate preferences and examine a range of correlated traits in males and females. In addition, a QTL mapping analysis of variation in preference will be carried out on inbred lines, using genomic markers (microsatellites and SNPs). The study is a collaboration with Dr Jon Slate and Prof Terry Burke at the University of Sheffield, and will use the resources of the NERC Molecular Genetics Facilities at Sheffield and Liverpool. The post holder will be assisted by a research technician (full-time) and join the thriving stalk-eyed fly research group.

2) FURTHER RESEARCH DETAILS OF PROJECT

This project aims to provide a integrated analysis of the genetic basis of female mate preferences using a combination of quantitative genetic and quantitative trait locus (QTL) mapping approaches.

There have been few rigorous studies of variation in female mate preferences. In part, this reflects the difficulty of accurately estimating preferences, requiring the repeated measurement of female response to a range of male stimuli in controlled conditions. We have established an excellent system for quantifying variation in female mate preference in the African stalk-eyed fly Diasemopsis meigenii. In this species, females actively reject unwanted male mating attempts and this has enabled us to accurately measure mate preference of individual females. We have shown that the strength of directional preference increases with female eyespan. This suggests.that preference is condition-dependent as females raised under good larval food conditions have larger eyespan. More recently, we showed that adult food conditions alter preference in a condition-dependent manner, as females kept on good adult food had stronger directional preferences for males with larger sexual ornaments than females reared on poor quality food.

In this project we will investigate the genetics of condition- dependent preference. We will carry out a half-sib quantitative genetic analysis in three environments which vary in food quality. We will estimate genetic parameters and see how they vary with environmental stress. Also, we will test for genetic covariation of female preference with other female traits known to affect preference (eyespan and fecundity) and examine condition-dependent association with the male ornament (eyespan).

We will also will carry out a QTL mapping study of the genetics of preference. A genomic map will be generated for D. meigenii. A microsatellite library for D. meigenii has been partially constructed at the NERC MGF-Sheffield. We aim to increase this to a map composed of ~50 polymorphic microsatellites. We will also identify and evaluate SNPs using 454 pyrosequencing of a cDNA library at the NERC MGF- Liverpool. To identify female preference QTL we will exploit inbred lines of D. meigenii that we have already generated. Inbred lines will be quantified for female preference and then we will carry out an F2 cross between high and low lines. We will then map the genetic architecture underlying variation in preference, to establish the number, distribution of effects and linkage patterns of the QTLs underlying preference. We will also use the QTL approach to test whether QTL for preference are genetically correlated with female eyespan and fecundity QTL and assess the co-localisation of female preference QTL and male eyespan QTL.

3) GENERAL INFORMATION

Applicants must have a PhD in a relevant genetics, behavioural or evolutionary discipline, be enthusiastic and well organised. Experience in handling large-scale experiments with insects, population genetics, behavioural assays and statistical analysis of genomic marker data would be advantageous.

Starting salary will be in band 7 of the national pay scale (between £28,839 and £31,513 plus £2,781 London Allowance, according to experience).

To apply, please download the application form. Job description and person specification from: http://www.ucl.ac.uk/biosciences/vacancies . Applicants should send a cover letter, CV, contact details of 3

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UEastAnglia WarblerFitness

The following postdoc position has become available again due to the previously chosen candidate being unable to take up the position

Telomeres as biomarkers of costs and quality in the Seychelles warbler

UEA SCHOOL OF BIOLOGICAL SCIENCES

SENIOR RESEARCH ASSOCIATE Ref: RA519

29,704 to 35,469 per annum

This NERC funded postdoctoral position is available from June 2009 for a period of two years and nine months to undertake a comprehensive longitudinal study of telomere shortening in a wild avian population. The researcher will help to develop and then utilise molecular protocols to screen for telomere length in the Seychelles warbler. You must have, or shortly obtain, a PhD (or equivalent) in a relevant discipline, have a keen interest in understanding life history trade-offs and senescence and have practical experience in modern molecular techniques.

Closing date: 12 noon on Thursday 2 April 2009. This is a readvertisement but previous applicants are welcome to apply.

Further particulars and an application form are available on our website: www.uea.ac.uk/hr/jobs/

<file:///C:\Documents%20and%20Settings\k483\ Local%20Settings\Temporary%20Internet%20Files\ OLK1A\www.uea.ac.uk/hr/jobs/> or Tel. 01603 593493.

David S Richardson Centre for Ecology, Evolution and Conservation School of Biological Sciences University of East Anglia e-mail: david.richardson@uea.ac.uk Norwich NR4 7TJ ph: (44) 01603 591496 ENGLAND fax: (44) 01603 592250

http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=325

"Richardson David Dr (BIO)" <David.Richardson@uea.ac.uk>

UGeneva Bioinformatics

Postdoc / Research Associate position Systems genetics and evolution of animal molecular systems

We are looking for a highly motivated, innovative and independent project leader to work at the exciting interface of the emerging fields of systems genetics, linking genetic variations with phenotypes, and evolutionary systems biology, studying trends in molecular systems evolution. This computational project will bring together the group's expertise in comparative genomics and the forthcoming human genome variation data, possibly, in conjunction with artificial evolution simulations.

Candidates must have a PhD and demonstrate clear evidence of successful work in computational biology, including a thorough understanding of evolutionary concepts, genomics and genetics. Practical programming experience in the Unix environment and fluency in English are required. Experience in a multidisciplinary research environment, familiarity with graph and data analysis algorithms, Bayesian statistics, and MATLAB is a plus.

The Computational Evolutionary Genomics group, headed by Prof. E. Zdobnov, is part of the Department of Genetic Medicine and Development of 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. Salaries: 68'000-94'000 CHF/y depending on experience.

Closing date for applications: 31 May 2009.

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

Prof. Evgeny Zdobnov University of Geneva CMU / Dpt GEDEV Rue Michel-Servet 1 1211 Genève 4 Switzerland

Stefan.Wyder@unige.ch Stefan.Wyder@unige.ch

UGeorgia Infectious disease dynamics

NONLINEAR DYNAMICS & NOISE AMPLIFICATION IN INFECTIOUS DISEASE DYNAMICS

A postdoctoral associate is sought to collaborate on a project to study the interaction between nonlinearity, resonance and noise amplification in the dynamics of directly transmitted infectious diseases. The main goal of the project is to understand the relative importance of exogenous and endogenous nonlinearities and stochastic processes in the outbreak dynamics of endemic pathogens. The successful applicant should have a background in population biology of infectious diseases or epidemiology. Experience with stochastic processes and analyzing nonlinear dynamical systems is required. The project is housed at the University of Georgia Odum School of Ecology and will be jointly supervised by Professors Pej Rohani (http://www.uga.edu/rohanilab/) and John Drake (http://dragonfly.ecology.uga.edu/drakelab/). The position will be initially appointed for one year with a starting salary of $37,000. Start date is negotiable. Potential applicants are requested to email (jdrake@uga.edu) a letter of introduction, CV, and expression of interest. The position will remain open until filled.

andrea.silletti@gmail.com

UGeorgia PathogenEvolution

University of Georgia - Post-Doctoral Associate â Modeling pathogen evolution

We are seeking candidates with skills and interests in evolutionary biology and computer modeling to become involved in one or more ongoing infectious disease projects with Dr Andrew Park at the Odum School of Ecology, including:

â short-term pathogen evolution â the emergence of immune escape pathogen strains â the role of host heterogeneity in maintaining pathogen diversity â characterizing disease evolution trajectories

Funding (plus health and retirement benefits) is available for 18 months, with the possibility of extension Applicants should email a statement of interest, CV, and arrange to have 3 letters of recommendation sent to Dr Park (awpark@uga.edu). Applications received before 10 May 2009 will be reviewed and the position can be taken up from July 2009, or later.

The University of Georgia is an equal opportunity, affirmative action employer.

Andrew Park <andrew.william.park@gmail.com>

UGuelph Parasite Vector DNABarcoding

Postdoctoral position in molecular identification ("DNA barcoding") of pathogens and disease vectors

Outstanding applicants are sought for a two-year postdoctoral position at the University of Guelph, focusing on the development of molecular identification methodology ("DNA barcoding") for a wide range of pathogens, parasites, and disease vectors. This will include both original research and participation in the assembly and coordination of large-scale international collaborations.

Experience is required in PCR, DNA sequencing, and related analytical approaches, as well as expertise in one or more of protists, nematodes, flatworms, or insect vectors. In addition, applicants must possess excellent written and oral communication skills in English as well as strong leadership qualities.

Salary and benefits will total $45,000 (CDN) per year, with a further $5,000 per year in individual research support. The successful candidate will have access to a high-throughput biodiversity genomics facility under the co-supervision of Ryan Gregory (Department of Integrative Biology) and Paul Hebert (Biodiversity Institute of Ontario). The position will be co-funded by the Ministry of Research and Innovation through the Ontario Post-Doctoral Fellowship Program, Round 3.

Candidates must meet the following additional requirements: * Have completed their PhD no earlier than June 15, 2007. * Be available to begin work no later than Oct. 31, 2009. * Be eligible to work in Ontario, Canada.

Applicants should send a CV including a brief overview of experience and research interests to rgregory@uoguelph.ca

Review of applications will commence June 15, 2009.

For more information, visit: * Canadian Centre for DNA Barcoding: http://www.dnabarcoding.ca/- * International Barcode of Life (iBOL) project: http://www.dnabarcoding.org/ * University of Guelph: http://www.uoguelph.ca/ * Gregory Lab: http://-www.gregorylab.org/ rgregory@uoguelph.ca

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UIllinois HumanPathogenEvolution

Postdoctoral Research Fellowship, Genetic Diversity and Clinical Outcome Organization: University of Illinois Medical Center Department of Medicine, Section of Infectious Diseases

Our laboratory seeks to understand the role of human and pathogen diversity in the outcome of human fungal infections.

We are seeking an enthusiastic and highly motivated evolutionary biologist/yeast geneticist to join a large group of clinical and basic science investigators. The overall goal of the funded projects is to identify and characterize regions of high genetic plasticity in both the human and pathogen genome that have strong associations with parameters of clinical outcome. Focus will be on infections of the AIDS-related pathogen, Cryptococcus neoformans as well as Candida albicans, the fourth most common blood stream infection in the US. Novel pathways related to virulence identified by a number of genomics methods will be further characterized using yeast and mammalian genetics and immunology in mouse models. Research is supported through multiple NIH and Veteran's Administration grants and has just received additional NIH-supported funding.

The successful applicant will be responsible for designing and carrying out experiments, analyzing experimental results, preparing manuscripts and helping with the supervision of students. A PhD is required with a strong and published history in molecular genetics. Experience in bioinformatics is also preferred. No previous experience in pathogenic fungi is required although experience in yeast genetics would be valuable. Our laboratory provides strong support for the development of independent projects leading to a productive career for post-doctorate candidates. Applicants who are non-residents must possess a valid visa for working in the U.S. UIC is AA/EOE

Send a curriculum vita and a short discussion of career plans to: Peter R. Williamson, MD/PhD Section of Infectious Diseases, M/C 735 Department of Medicine, 808 S. Wood St, Rm 888 Chicago, IL 60612 email: prw@uic.edu

Peter R. Williamson, MD/PhD Associate Professor of Medicine, Pathology, Microbiology and Immunology University of Illinois at Chicago School of Medicine Section of Infectious Diseases Rm 888, Bld 910, m/c 735 808 S. Wood St. Chicago, IL 60612 tel: (312) 996-6070 fax: (312) 413-1657

Peter Williamson <prw@uic.edu>

ULeeds HostParasiteEvolution

Job: Postdoctoral Research Assistant in host-parasite evolutionary ecology.

Institute of Integrative and Comparative Biology, Faculty of Biological Sciences, University of Leeds

A 36 month fixed-term Postdoctoral Research Assistant position (University Grade 6: £23,002 - £27,466) is available in the research group of Dr. William Hughes (http://www.personal.leeds.ac.uk/ ~ fbswohh/). The project will use honeybees and their chalkbrood fungal parasite as a model system to investigate the effects of host and parasite genetic diversity on parasite transmission and evolution. You will work with honeybee colonies with different levels of genetic diversity and will use microsatellite genotyping to determine the effect of host genotype on parasite virulence and fitness. You will conduct controlled infections with single and multiple parasite strains and use real-time PCR to quantify within-host parasite dynamics. You will carry out serial passage experiments to establish experimentally how host and parasite genetic diversity impact the evolution of the parasite. The project's results will help inform management strategies for our increasingly vulnerable ho neybee populations and will significantly advance our understanding of the evolutionary biology of host-parasite interactions in general.

You will be joining a young and dynamic research group, which will be growing significantly over the course of 2009. The molecular laboratory is well-equipped with a real-time and four conventional PCR machines, while capillary sequencers are provided by a Faculty facility. The project will utilise a large experimental apiary at the nearby University Farm and will be supported by a full-time Research Technician. Work will be in collaboration with the National Bee Unit and the University of Copenhagen; training visits to both will take place over the course of the first year.

You should have a first degree and PhD in a relevant subject, an excellent publication/results record for your career stage, and research experience in evolutionary biology or molecular ecology. You should be hard working, self-motivated and able to work both independently and as part of a team. You must have experience with molecular techniques, preferably real-time PCR. Experience with social insects, beekeeping or mycology, and a driving licence would also be useful.

The position is to start 1 June 2009 or as soon as possible thereafter. Applications will be reviewed on 24th April 2009, but will continue to be considered until the position is filled.

Informal enquiries (please include CV) to Dr William Hughes, email w.o.h.hughes@leeds.ac.uk. To apply on line please visit http://www.leeds.ac.uk and click on jobs.

W.O.H.Hughes@leeds.ac.uk
W.O.H.Hughes@leeds.ac.uk

UManchester MicrobialEvolution

Postdoctoral Research Associate, Microbial Evolution

Faculty of Life Sciences, University of Manchester, UK

We seek an enthusiastic and highly motivated evolutionary biologist/microbial ecologist to study competitive interactions between bacteria and burying beetles for access to carrion. We have previously shown that microbial decomposers of carrion cause significant harm to beetle larvae. Furthermore, we have shown that beetles can reduce this harm by providing various forms of parental care for the larvae. The specific aims of this project are to: 1) Determine the fitness effects of microbes on beetles when competing for access to carrion. 2) Identify the bacterial species that decompose carrion, the nature of the anti-competitor compounds they secrete, and against whom these toxic products are targeted. 3) Determine the effects of behavioural, physiological and biochemical counterstrategies used by beetles and beetle larvae to contend with microbial competitors. The ideal candidate will have interest and experience in microbiology and evolutionary biology.

The successful applicant will be responsible for designing and carrying out experiments, analyzing experimental results, preparing manuscripts, and helping with the supervision of students. You should hold a PhD in a relevant biological discipline and have a strong background in evolutionary biology. Experience in microbial ecology is desirable.

This work is a collaborative project between Dr. Rozen and Dr. Andrew McBain at the University of Manchester and Dr. Per Smiseth at the University of Edinburgh. Occasional travel to Edinburgh will be required.

Funded by the Leverhulme Trust, this position is tenable from 1st June 2009 for three years.

Informal enquiries can be addressed to: Dr Daniel Rozen, Tel: +44 (0) 161 275 5094, Email: Daniel.rozen@manchester.ac.uk

Application forms and further particulars can be obtained at http://www.man.ac.uk/news/vacancies Daniel Rozen University of Manchester Faculty of Life Sciences Michael Smith Building Oxford Road Manchester M13 9PT

Tel: +44161 275 5094 Fax: +44161 275 5082

Daniel.Rozen@manchester.ac.uk

UmeaU ClimatechangeBiodiversity

Two post-doc positions (2 years) on the role of climate change for the evolution of biodiversity

The aim of the project is to understand how climate change affects evolution and the global distribution of species. The earth is subject to recurrent and rapid climate shifts at various time-scales, but the consequences of this has not been incorporated into models of evolution. Climate shifts cause extinction, splitting, and merging of gene pools, potentially affecting rates of speciation and species extinction. There are two opposing views on the effect of climate change on species diversification. According to one view, climate shifts enhance speciation by promoting lineage splitting. The alternative view is that climate shifts curb speciation by causing extinction or merging of diverging gene pools, as well as leading to species extinction. In the project, models of past climate change are combined with phylogenetic data to address how diversification of species and spatial patterns in genetic divergence within species are affected by climate variability. A paper providing a background to the project is found in Annu. Rev. Ecol. Syst. 33:741-777.

Position 1 investigates the role of climate variability for the diversification of species. Data on past climate change from climate models are used together with phylogenies from a range of taxa to test for an association between climate variability and species diversification.

Position 2 tests how climatic variability affects the degree of genetic divergence among populations. Data on levels of genetic divergence among populations are combined with data on past climate change from climate models to test for a correlation between genetic divergence and climatic stability, both within species (in cases where climatic stability varies across its geographic range) and between species inhabiting regions differing in climatic stability.

To qualify for the positions you should have a PhD degree or equivalent. Experience with geographic information systems and bioclimatic modelling is meriting for both positions. Position 1 requires good knowledge on methods of statistical inference from phylogenetic data. Position 2 requires familiarity with theories on causes for spatial patterns in genetic variation and knowledge on statistical inference using genetic data. The positions are for two years and available immediately, preferably starting no later than September 1, 2009.

For further information, please contact Associate Professor Roland Jansson, Department of Ecology and Environmental Science, phone: +46-(0)90-786 95 73, roland.jansson@emg.umu.se, or look at < http://-www.emg.umu.se/roland >www.emg.umu.se/roland.

Your application, in English, should include: (1) a short summary of your previous research achievements and other experience relevant for the positions, (2) a short description of why you are a good candidate for the position and how you could contribute to the research, (3) a curriculum vitae with a list of publications, and (4) names and contact details of three references.

Union information is available from SACO, +46-(0)90-786 53 65, SECO civil, +46-(0)90-786 52 96, and ST,

+46-(0)90-786 54 31.

If you are applying for both positions, you need to send in one application for each position. Applications will be discarded or, if the applicant so wishes, returned two years after the position has been filled. Documents sent electronically should be in MS Word or PDF format.

Your complete application, marked with reference number 315-301-09, should be sent to jobb@umu.se (state the reference number as subject) or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive May 31, 2009 at the latest.

Roland Jansson, Associate professor Dept. of Ecology and Environmental Science Umeå University SE-901 87 Umeå, Sweden phone: +46-90-786 95 73 fax: +46-90-786 78 60 web: < http://www.emg.umu.se/roland >http://www.emg.umu.se/roland

roland.jansson@emg.umu.se
roland.jansson@emg.umu.se

UmeaU SticklebackGenetics

2-year postdoc position: stickleback ecological genetics

Umeå University, Sweden. Dept. Ecology & Environmental Sciences

We are looking for a post-doc to study local adaptation and phenotypic plasticity in isolated populations of sticklebacks in northern Sweden. After the most recent ice age, some stickleback populations became land-locked in ponds in which they are the only fish species, while other populations coexist with predators. This project aims to study the effect of predator presence on local adaptation. The successful applicant will genotype sticklebacks from natural populations, perform common garden breeding experiments, and analyse genetic and phenotypic data. As a joint project of the research groups of Professor Göran Englund (spatial fish ecology) Professor Frank Johansson (phenotypic plasticity) and Dr. Folmer Bokma (phylogenetics) this offers an interesting, cross-disciplinary scientific environment. Highly motivated candidates with relevant expertise in ecology and molecular genetics are encouraged to get in contact. Previous experience with stickleback research is considered an advantage.

The position is available at the earliest possible time point. For further information, please contact Dr. Folmer Bokma, (+46 90 786 7121) or folmer.bokma@emg.umu.se, or look at http://www.emg.umu.se/projects/macroevolution/ . To qualify for the position you should have a PhD degree or equivalent, preferably not more than three years old. Your application, in English, must include a short summary (max 1 page) of your previous experience, curriculum vitae, list of publications, and names and contact details of three references. Union information is available from SACO, +46-(0)90-786 53 65, SEKO civil, +46-(0)90-786 52 96 and ST, +46-(0)90-786 54 31. Documents sent electronically should be in MS Word or PDF format. Your complete application, marked with reference number, should be sent to jobb@umu.se (state the reference number as subject) or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive April 24, 2009 at the latest.

Folmer Bokma Dept. Ecology & Environmental Science Umeå University, Sweden folmer.bokma@emg.umu.se

folmer.bokma@emg.umu.se
folmer.bokma@emg.umu.se

UMontreal Bioinformatics

Posting is also accessible via my website http://megasun.bch.umontreal.ca/People/burger/ ===Postdoctoral position in bioinformatics (-omics analysis) ^^^^^

A post-doctoral position is available to analyze and integrate data from genomics, transcriptomics, proteomics, and RNA catalysis. The aim is to understand the evolution of cellular machineries involved in RNA editing and trans-splicing. For more details on the research projects ongoing in the lab see < http://megasun.bch.umontreal.ca/People/burger/research.html >.

Training background —– PhD in molecular biology, biochemistry, or bioinformatics. Training in computer science.

Expertise —– The candidate should have expertise in computer-based large-scale data analysis, including genome and cDNA assembly and annotation, comparative genome and proteome analysis, and software tool development under Unix/Linux. Experience in database development is desirable.

Starting date —– Immediately.

=== Graduate student position (PhD) in bioinformatics ^^^^^

A position is available to identify (primary and secondary structure) motifs involved in a novel RNA trans-splicing process that we discovered recently (Marande & Burger 2007, Science 318:415). Predicted motifs and postulated mechanisms will be the basis for in-vitro experiments, which, in turn, will help to narrow the search space of in-silico analyses.

Training background —– MSc in bioinformatics or bi-disciplinary training in computer science & molecular biology.

Expertise —– Methods and tools in pattern searching, motif prediction, RNA secondary structure prediction, gene prediction. Programming expertise in Perl, C(++), Java on the Unix/Linux platform.

Starting date —– Immediately.

===Application ^^^^^

Interested candidates are encouraged to send by e-mail their CV, addresses for potential reference letters, student transcripts, and Master/PhD thesis to

Gertraud Burger, PhD Robert-Cedergren Centre for Bioinformatics and Genomics Departement de Biochimie Universite de Montreal, Pavillon Roger Gaudry 2900 Blvd Eduard-Montpetit Montreal, Quebec, H3T 1J4, CANADA

e-mail: jobs@bch.umontreal.ca (Subject:“PhD-bioinfo”)

=== ~~~~ Gertraud Burger, PhD Professeur titulaire Leader of bioinformatics training programs Departement de biochimie Robert-Cedergren Center for Bioinformatics and Genomics Pavillon Roger Gaudry (P. principal) H-307-13 Universite de Montreal 2900 Edouard-Montpetit Montreal QC, H3T 1J4, Canada Tel (514) 343-7936, Fax -2210 http://megasun.bch.umontreal.ca/People/burger ~~~~

OO OO OO OO OO OO ROBERT-CEDERGREN CENTER for OO OO BIOINFORMATICS and GENOMICS OO ——————————— OO OO UNIVERSITE de MONTREAL OO OO

Gertraud Burger <Gertraud.Burger@Umontreal.ca>

UPittsburgh PlantSexChromosomes

POSTDOCTORAL FELLOW in PLANT EVOLUTIONARY GENETICS A postdoctoral fellow is sought to participate in work furthering the understanding the evolution of sex chromosomes in strawberry (Fragaria species) (see Spigler et al 2008 Heredity 101:507; Moore 2009 Heredity 102: 211). The project will include comparative genetic mapping and QTL analysis of sexual traits.

The ideal candidate will be an independent thinker but be able to work creatively on a team, have a PhD in quantitative, population or molecular genetics, evolution, or related field, and have proven experience with AFLP, SSR and/or genome-wide DNA sequences, use of relevant programs for statistical analysis and mapping of genetic data and evidence of ability to complete manuscripts. Experience with polyploidy, outbred crosses, GISH/FISH, BAC libraries and bioinformatics tools is desirable.

The position is available from July 1, 2009 and is offered for two years, with the opportunity of renewal. Applicants should email (tia1@pitt.edu<mailto:tia1@pitt.edu>) a letter of interest, CV and the names/contact information for three references. Review of applications will begin immediately and continue until the position is filled.

Tia-Lynn Ashman Professor Department of Biological Sciences 4249 Fifth Ave. & Ruskin University of Pittsburgh Pittsburgh, PA 15260-3929 phone: 412-624-0984 fax: 412-624-4759 web: http://www.pitt.edu/ ~ biohome/Dept/Frame/Faculty/ashman.htm tia1@pitt.edu tia1@pitt.edu

USouthFlorida Bioinformatics

DESCRIPTION: Post-Doctoral Researcher position in Mya Breitbart’s laboratory at the University of South Florida, College of Marine Science (http://www.marine.usf.edu/genomics).

RESPONSIBILITIES: The post-doc will work on an NSF-funded project to design and implement a platform for the annotation of bacteriophage genes. This new resource will be used to provide high quality annotations to over 1000 existing phage and prophage genomes, and dozens of environmental phage metagenomes. Research tasks include developing and validating subsystems for phage, comparative genomics and sequence alignments, creating and refining phylogenies for specific phage groups, data-mining environmental metagenomes, and identifying novel genes that can be used for molecular detection assays for various phage groups. This project will involve interactions with many phage researchers (both biologists and computer scientists), creation of computational resources, and application to biological datasets.

REQUIREMENTS: Prior experience in bioinformatics and phylogenetics is required. Programming skills are highly desirable. Prior experience with phage is considered a plus but not necessary.

LOCATION: Saint Petersburg, Florida, USA

SALARY AND BENEFITS: This Post-Doctoral Fellowship is for three years. Salary is competitive. Contact Mya Breitbart (mya@marine.usf.edu) for salary and benefit details.

HOW TO APPLY: Please email your CV and a letter of intent (including qualifications) to Mya Breitbart – mya@marine.usf.edu

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Mya Breitbart Assistant Professor University of South Florida College of Marine Science 140 7th Avenue South Saint Petersburg, FL 33701 phone: 727-553-3520 fax: 727-553-1189 mya@marine.usf.edu http://www.marine.usf.edu/genomics mya@marine.usf.edu

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UTartu LifeHistoryEvolution

Position in evolutionary ecology available: optimality modeling

We wish to recruit a post-doctoral researcher to undertake OPTIMALITY MODELING in the field of LIFE HISTORY research. The position will be opened at the recently established Centre of Scientific Excellence 'Frontiers in Biodiversity Research' (FIBIR, http://fibir.ut.ee) at the University of Tartu, Estonia (http://www.ut.ee). The successful candidate will work in Prof. Toomas Tammaru's (http://www.ut.ee/˜tammarut) research group, whose primary focus is the life history evolution of insects (the evolution of body size in particular). Having mainly relied on experimental methods to date, the group is looking to strengthen the modeling component of its research activity. We have various ideas waiting to be formalized, and empirical data are available to serve as the foundation of empirically based models. However, the work profile is largely flexible, and the researcher will be able to develop his or her own ideas. The successful candidate will be encouraged to collaborate with other research groups, both at FIBIR and elsewhere. Funding is presently available for 24 months, though there is a strong possibility that this can be extended, subject to the candidate's performance. FIBIR offers an excellent research environment within a modern infrastructure. The salary level corresponds to that of European Union framework projects and is open to negotiation. The position is available from 1st June, 2009, though the start date is flexible. The successful candidate is expected to have a strong publication record that demonstrates his or her ability to apply either analytical or numerical methods to model biological systems. Competence in the field of mathematical statistics would be an advantage. Previous experience with insect life history research is not essential. In the case of very strong candidates, it would be possible to transform the post-doctoral position into that of a senior researcher. If interested, provide your CV, a list of publications and the contact details of at least two academic referees by 11th May, 2009. For this purpose, and for informal enquiries, please contact Toomas Tammaru at toomas.tammaru@ut.ee (cc to maarika.maesalu@ut.ee).

Toomas Tammaru professor of zoology http://www.ut.ee/˜tammarut tammarut@ut.ee tammarut@ut.ee

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UTartu PhylgeneticComparativeMethods

Position in evolutionary ecology available: phylogenetic comparative methods

We wish to recruit a post-doctoral researcher in evolutionary ecology to undertake research using PHYLOGENETIC COMPARATIVE METHODS. The position will be opened at the recently established Centre of Scientific Excellence 'Frontiers in Biodiversity Research' (FIBIR, http://fibir.ut.ee) at the University of Tartu, Estonia (http://www.ut.ee). The successful candidate will work in Prof. Toomas Tammaru's (http://www.ut.ee/˜tammarut) research group, whose primary focus is the life history evolution of insects. Having mainly relied on experimental methods to date, the group is now looking to develop its expertise in the field of phylogenetically explicit comparative approaches. The strengths of the group include a rare combination of in-depth knowledge about the taxonomy and life-history of insects (mainly Lepidoptera), and a productive interest in various questions in the field of evolutionary biology. While we have well-defined research questions in mind for the post-doctoral researcher (evolution of body size, egg size, host specialization etc.), and respective data sets available, the work profile is largely flexible. The successful candidate will be encouraged to collaborate with other research groups, both at FIBIR and elsewhere. Funding is presently available for 24 months, though there is a strong possibility that this can be extended, subject to the candidate's performance. FIBIR offers an excellent research environment within a modern infrastructure. The salary level corresponds to that of European Union framework projects and is open to negotiation. The position is available from 1st June, 2009, though the start date is flexible. The successful candidate is expected to have a strong publication record that features research using a phylogenetic comparative approach. However, we may also consider candidates with experience of other phylogeny-based analyses or statistical analysis of autocorrelated data). Previous experience with insect life history research is not essential. In the case of very strong candidates (excellent publication record and very good skills in comparative analyses), it would be possible to transform the post-doctoral position into that of a senior researcher. If interested, provide your CV, a list of publications and the contact details of at least two academic referees by 11th May, 2009. For this purpose, and for informal enquiries, please contact Toomas Tammaru at toomas.tammaru@ut.ee (cc to maarika.maesalu@ut.ee).

Toomas Tammaru professor of zoology http://www.ut.ee/ ˜ tammarut tammarut@ut.ee tammarut@ut.ee

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UTromso FungalTaxonomy

The position's no: Use DocuLive no,

Research fellow position in mycology at Tromsø Museum - Tromsø University Museum, Department of Natural Sciences.

Application deadline: The reference no. 09-418 must be quoted in your application.

The University of Tromsø has a research fellow position in mycology vacant from 01.01.2010.

The period of appointment is 4 years.

For further information, please contact: Director Marit A. Hauan, phone +47 77645000, e-mail: marit.hauan@uit.no Head of Department of Natural Sciences Karl Frafjord, phone. +47 77645000, e-mail: karl.frafjord@uit.no

The position is attached to the Department of Natural Sciences, Tromsø Museum - Tromsø University Museum.

The research area will be mycology with focus on taxonomy and molecular methods.

The University of Tromsø wishes to recruit female researchers. When two or more applicants are found to be approximately equally qualified, female applicants will be given priority.

Applicants must document knowledge in mycology at Master level. They also must fulfil the requirements for admission into the Faculty's PhD-program, according to Chapter II, section 5 in "Directions for the degree philosophiae doctor (PhD) at the University of Tromsø" (http://uit.no/forsknavd/ph.d.-forskrift/-1), and also according to the Faculty's complementary regulations.

The normal period of appointment is four years, with 25% mandatory work duties annually, se guidelines for PhD students' responsibilities: http://uit.no/-getfile.php?PageId=6139&FileId=37. This mandatory work is affiliated to the activities of the Department of Natural Sciences and may include curatory work, research mediation to the public or teaching. Previous appointments as a research fellow or in other positions for recruitment are counted as part of the duration of the research fellowship, so that the combined duration of the researcher's education is three years.

The remuneration for this position is in accordance with the State wage scale code 1017 (depending on qualifications). A compulsory contribution of 2 % is made to the Norwegian State Pension Fund.

The period of the research fellowship shall be utilised for researcher education and shall normally culminate in the awarding of a PhD degree. For applications for appointment, a description outlining the academic basis of the doctoral degree project ought to be put forward. A plan shall be drawn up, preferably within one month after the appointment, as a separate application to a PhD program. A finite and accepted plan for the PhD program should be completed within maximum three months after the appointment, outlining how the research fellowship period shall be implemented with respect to both the research project and other researcher education. The plan shall state who is responsible for providing academic supervision. Acceptance into a PhD program is mandatory for the appointment as PhD student. If this agreement is not in place within the time limit, the University of Tromsø may cancel the appointment, according to §1-3(8) in "Guidelines for appointments to positions as PhD student, post doctor and research assistant": http://www.lovdato.no/-for/sf/kd/kd-20060131-0102.html . The research in mycology at the Department of Natural Sciences focuses on phylogenetic relationships between taxa at the species and genus levels, and between families within the pyrenomycetes s. lato (Ascomycota). The ongoing research in mycology addresses taxa within the families Lophiostomataceae and Xylariaceae.

The Department of Natural Sciences presently employs 2 professors, 7 associate professors, 6.5 technical staff members, 2 Post Doctors and 7 PhD students. The department has large collections, documenting more that 130 years of research in North Norway and other northern regions. The research at the department covers both taxonomy and ecology, and the DNA-laboratory is dedicated to the study of molecular phylogeny and taxonomy of various organisms including fungi, plants and animals.

Applicants will be assessed by an expert committee. The main emphasis of the assessment will be on the applicant's potential for research as is evident from: * Master's thesis or equivalent * Other scientific works * Project description (if available)

Supervised professional training and other activities of significance for the implementation of a doctoral degree programme and possible teaching qualifications will also be taken into consideration. Administration and organisational experience will be viewed favourably. Information and material to be considered must be submitted within the closing date for applications.

Applicants must submit a list of all their scientific works including

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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

UWashington SalmonSNPs

University of Washington Postdoctoral Openings

SNP Discovery and Applications in Pacific Salmon

Position Overview:

Organization: School of Aquatic and Fishery Sciences, College of Ocean and Fishery Sciences

Title: Research Associate

Position details:

The School of Aquatic and Fishery Sciences (SAFS < http://fish.washington.edu/ >) at the University of Washington has openings for up to two postdoctoral Research Associates (100% time) to conduct research on SNP discovery using next generation sequencing or possibly SNP applications in Pacific salmon. These are 2-year positions with the possibility to extend depending upon funding. The positions are not eligible for tenure.

The general scope of the appointments may include but is not limited to:

* Development SNPs using next generation sequencing and resequencing. * Bioinformatics. * Original research on salmon population genetics and conservation. * Work with regional fisheries managers to apply SNP research to contemporary problems. * Formulation of problems, analysis of data, production of scientific papers, and presentation at scientific meetings. * Mentor and otherwise assist graduate students who are doing projects in salmon genetics and supervise hourly help involved in data analysis.

Requirements:

* Ph.D. in genetics, biology, or a related field

The following experience is desired: * DNA sequencing * Bioinformatics

Positions are located at the University of Washington, Seattle, WA. The University of Washington is an affirmative action, equal opportunity employer. The University is building a culturally diverse faculty and staff and strongly encourages applications from women, minorities, individuals with disabilities and covered veterans.

"University of Washington faculty engage in teaching, research and service."

Interested persons should send CV, short letter of intent including names and contact information for three references via email to Dr. Jim Seeb, School of Aquatic and Fishery Sciences, University of Washington (jseeb@u.washington.edu <mailto:rayh@u.washington.edu>). Review of applications will start April 24, 2009 and continue until the positions are filled. For successful candidates, a background check for criminal history is required.

Jim Seeb Research Professor International Program for study of Salmon Ecological Genetics School of Aquatic and Fishery Sciences University of Washington 1122 NE

Boat Street, Box 355020 Seattle, WA 98105-5020, USA Phone: 206 685 2097

Jim Seeb <jseeb@u.washington.edu>

WorkshopsCourses

Bialowieza Poland EvolutionaryAdaptation Jun28-Jul2

ESF workshop on evolutionary and physiological adaptation to climate induced environmental changes - deadline for applications extended to April 10. Dear all,

We would like to invite young scientists to submit abstracts for oral and poster presentations for a workshop on evolutionary and physiological adaptation to climate induced environmental changes.

The European Science Foundation finances the workshop through the networking programs ConGen and ThermAdapt. In the workshop, we will merge knowledge from population genetics and molecular and evolutionary physiology in a multidisciplinary fashion and discuss possible approaches to get a deeper understanding of mechanisms behind adaptation to thermal changes.

We have invited approximately twenty leading researchers within the field to give talks and have space for additional 30-35 short presentations and/or poster presentations. Priority will be given to young scientists (PhD or post docs) from EU countries, particularly from those countries that support one or both of the ESF programmes (see www.esf.org/thermadapt and www.esf.org/congen for a list of countries).

The workshop will be held in Bialowieza (Poland) from 28 June (date of arrival) to 2 July 2009 in the EU Centre of Excellence (MRI PAS) Mammal Research Institute (Polish Academy of Science). Accommodation and food are covered by the ESF. Furthermore, after application some young researchers may get covered their travel expenses or parts thereof.

Further information about the workshop including application procedures, a list of invited speakers and information about accommodation and transportation from Warsaw to Bialowieza (and return) can be found at the homepage: http://asg.agrsci.dk/workshop/bialowieza. The deadline for applications is April 10.

If necessary, Torsten Nygaard Kristensen (torsten.nygaard@agrsci.dk<mailto:torsten.nygaard@agrsci.dk>) can also be contacted for further information.

Aarhus University, Denmark Department of Biological Sciences/ Department of Genetics and Biotechnology Telephone: +4589423135/+4589991076

Torsten Nygaard <Torsten.Nygaard@agrsci.dk>

Colombia Bioinformatics Aug23-30 DeadlineMay1

Hi,

Just to remind potential applicants that the closing date for applying for the EMBO course on "Advanced bioinformatic methods in the study of gene and genome evolution" in Medellin, Colombia, is Friday May 1st.

The topics covered are:

- Databases, database searching, multiple sequence alignment - Maximum Parsimony/Distance Matrices - Maximum Likelihood/Bayesian MCMC - Codon-based models of evolution - Integrating functional evolution with genomics - Developing pipelines for evolutionary genomics - Evolution of insect vectors of tropical diseases

The practicals will cover:

- Databases and data base interrogation - Multiple sequence alignment - PAUP - MrBayes - PAML - Integrating functional and evolutionary databases - Computational pipeline assembly - Student data analysis

In addition, there are a number of research seminars:

- Dr. Davide Pisani - Origin of vision in vertebrates - Dr. Chris Creevey - Metagenomic Analysis of Environmental Samples - Dr. Mary O'Connell - Mammalian protein evolution:phylogenetic challenges and functional inferences - Dr. James McInerney - The chimaeric origin of the Eukaryotic cell - Dr. David Fitzpatrick - Comparative genomics of Candida genomes

EMBO will cover the cost of tuition, housing and food. Students will have to cover the cost of travelling to the course.

You can find more information here:

http://cwp.embo.org/wpc09-04/index.html – Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@nuim.ie – Work — http://bioinf.nuim.ie/

James McInerney <james.o.mcinerney@nuim.ie>

Denmark AdaptationInAquaticEctotherms Jun15-19

Workshop announcement: "Thermal adaptation in aquatic ectotherms", Denmark, June 15-19 2009.

Dear all

We would like to announce the workshop "Thermal adaptation in aquatic ectotherms" to be held in Denmark from the 15th to the 19th of June 2009. The workshop is funded by the ThermAdapt network under the European Science Foundation and by the Nordic Network MADFish, and is organized by the Section for Population Genetics, National Institute of Aquatic Resources, Technical University of Denmark. The workshop will be held at the Mols Laboratory, a field station located in a national park near Aarhus.

Background Aquatic organisms are expected to be affected by future climate changes, but knowledge about their response to these challenges is generally lacking. Understanding thermal adaptation requires insights from cellular through organism to population levels of biological organization. In this workshop, we intend to bring together researchers from population genetics and molecular and evolutionary physiology in a cross-disciplinary environment to foster exchange of ideas and improve our understanding of responses to thermal changes in aquatic organisms and populations. The workshop will be organized as sessions with presentations by all workshop participants, leaving good time for discussions both during and between sessions.

Invited speakers Craig Primmer, University of Turku, Finland David Conover, Stony Brook University, USA Hans Otto Pörtner, AWI, Bremerhaven, Germany Luc De Meester, Katholieke Universiteit Leuven, Belgium Patricia Schulte, University of British Columbia, Canada

Attendance The workshop is intended for established researchers, postdocs and PhD students working on thermal adaptation in aquatic ectotherms. Attendance is limited to 35 participants, and accommodation and meals are funded by the networks. Please send an email to Jakob Hemmer-Hansen (jhh@aqua.dtu.dk) with a short description of your area of research if you are interested in participating in the workshop. Priority will be given to applicants from ESF member countries and members of the MADFish network.

Relevant information Getting there: The Mols field station is located just 15 minutes from Aarhus Airport (Tirstrup) and 45 minutes from the city of Aarhus. Transport to/from trains and planes will be arranged.

ThermAdapt network: http://www.esf.org/activities/research-networking-programmes/life-earth-and-environmental-sciences-lesc/current-esf-research-networking-programmes-in-life-earth-and-environmental-sciences/thermal-adaptation-in-ectotherms-linking-life-history-physiology-behaviour-and-genetics-thermadapt.html MADFish network http://madfish.lif.hi.is Section for Population Genetics, Technical University of Denmark: http://www.aqua.dtu.dk/English/Recreational_fisheries/Population_genetic_group.aspx Mols field station: http://www.naturhistoriskmuseum.dk/molslab/ Organizers Jakob Hemmer-Hansen Dorte Bekkevold Thomas Damm Als Einar Eg Nielsen Michael Møller Hansen

Section for Population Genetics National Institute of Aquatic Resources (DTU Aqua) Technical University of Denmark Vejlsoevej 39 DK-8600 Silkeborg Denmark

jhh@aqua.dtu.dk jhh@aqua.dtu.dk

Eawag Switzerland SummerSchool Jul5-18 2

This is an announcement of:

PhD Summer School 2009 at Eawag in Kastanienbaum, Switzerland (July 5-18, 2009): “Interactions between ecological and evolutionary processes in aquatic systems”

Deadline for the application is extended to April 14th, 2009 (CET). For further information and online application, please visit our website: http://www.eawag.ch/programs/phd_ss_2009/index_EN The course will confront selected PhD students with the challenge of integrating ecosystems ecology and evolutionary biology, arguably the least well-integrated pair of disciplines in ecology. Some have described this challenge as the last missing synthesis in ecology. We will take a multidisciplinary look at lake ecology, ask how nutrient fluxes shape microbial and algal activity and diversity, how these in turn exert ecological and evolutionary pressure on organisms at higher trophic levels, and lastly, how adaptive evolution at higher trophic levels exerts ecological pressures at lower levels that possibly change ecosystem dynamics. The 2009 course will be built around different aspects of ecological stoichiomentry. The course will consist of theoretical and conceptual lectures and practical research modules including laboratory and fieldwork that seek to demonstrate experimental approaches. Lectures will be given by our invited lecturers James Elser, Nelson Hairston, Eric Triplett, Andrew Hendry and Eawag scientists. Concepts taught include e.g. feedback between biogeochemical conditions and microbial ecology, microbial structure and activity, food webs, adaptive evolutionary dynamics of predator-prey relations, ecosystem effects of evolution at ecological time scales.

The Summer School course will be held at Eawag Kastanienbaum, near Lucerne, in Switzerland. Eawag is the Swiss Federal Institute of Aquatic Science and Technology, and the Kastanienbaum Centre for Ecology, Evolution and Biogeochemistry (CEEB) is situated at the shores of Lake Lucerne. It offers seminar rooms, laboratories, and on-site housing for students.

Sincerely yours, Hitoshi Araki

PhD Summer school 2009 steering committee

Eawag, Swiss Federal Institute of Aquatic Science and Technology Center for Ecology, Evolution and Biogeochemistry Seestrasse 79, CH-6047 Kastanienbaum, Switzerland http://www.eawag.ch/programs/phd_ss_2009/index Hitoshi.Araki@eawag.ch Hitoshi.Araki@eawag.ch

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Iceland ArabidopsisEvolution Aug14-17

Iceland â Arabidopsis Molecular Ecology Group (AMEGO) 14-17 August 2009

The Arabidopsis Molecular Ecology Group (AMEGO) is a network financially supported by NordForsk, including research groups from Denmark, Finland, Norway and Sweden. AMEGO will be hosting international workshops and Ph.D. courses on Arabidopsis molecular ecology and evolution in the period 2007-2009. The last

Arabidopsis molecular evolution workshop and Ph.D. course will be held 14-17 August 2009 in Reykjavik, Iceland.

Preliminary program: 14 August Arrival and registration 15 August Workshop with talks and posters 16 August Excursion to Arabidopsis lyrata sites. Participants will also get the opportunity to experience some of the natural wonders of Iceland. 17 August Ph.D. course: âNatural selection in the wild: exploring the magnitude and mechanisms of selection in the fieldâ. Participants should bring their own laptop. Responsible: Professor Jon Ãgren, Uppsala University.

Deadline for registration is 24 May 2009

For more information about AMEGO 2009 workshop and Ph.D. course, please see our home page at http://www.molecol.net. The registration page can be found at http://www.bio.ntnu.no/amego/pomelding/-skjema.php . Best regards, Sverre Lundemo

Sverre Lundemo Department of Biology Norwegian University of Science and Technology N-7491 Trondheim Norway

lundemo@bio.ntnu.no

Sverre Lundemo <lundemo@bio.ntnu.no>

ImperialCollege PopulationBiol May26-28

Dear Young Researchers,

We would like to welcome you at the 3rd young researcher symposium in applied population biology, held by the NERC Centre for Population Biology & Imperial College London, Division of Biology at Silwood Park, UK:

Populations under Pressure 26th - 28th May, 2009 [http://www.iccs.org.uk/PuP.htm] Extended deadline for applications: 30th April 2009

Background Applied population biology forms the basis for scientific conservation. Although population biology, ecology and conservation share many common research questions and interests, scientists working in one field are often unfamiliar with the techniques and approaches used in others, especially early in their career.

Aims In this symposium, we aim to provide an opportunity for interdisciplinary discussions within the broad field of applied population biology, and with a focus on conservation. We focus in particular on graduate students and post-docs who already have, or would like to develop, a more interdisciplinary perspective on their work.

Symposium structure Participants will present their own work, focussing on problematic or unsolved issues they are finding, or introducing new findings or approaches of potentially broad interest, and will have the opportunity to discuss those during the workshops with researchers from different backgrounds. The workshops will be complemented with plenary presentations by leading researchers in applied population biology, enhancing the scope of the discussions.

Workshops:

(1) Interactions between harvesting and ecological and anthropogenic processes. Invited speaker: Per Lundberg (Lund University) and E.J. Milner-Gulland (Imperial College London)

(2) How to explain global, regional and local patterns of biodiversity in a unified framework. Invited speaker: Drew Purves (Microsoft Research Cambridge), David Orme (Imperial College London)

(3) Linking ecological theory to on-the-ground action for the ecological management of landscapes. Invited speakers: Tom Nudds (University of Guelph, Canada), Dan Reuman (Imperial College London), David Murrell (Univeristy College London)

Transferable skills session: The Bayesian approach. Invited speaker: Richard Hillary (Imperial College London) How to re-unite theoreticians and field biologists. Invited speaker: Robert D. Holt (University of Florida), David Murrell (University College London)

Please check out the symposium website to find out how to apply and participate [http://www.iccs.org.uk/-PuP.htm] Cheers, Nils

Nils Bunnefeld Swedish University of Agricultural Sciences, Umea Tel: +46 90 786 86 85 www.moose-research.se http://fp7hunt.net Come to PuP: www.iccs.org.uk/PuP.htm Nils Bunnefeld <Nils.Bunnefeld@vfm.slu.se>

Italy PopulationForestGenomics Jul22-24 Reminder

Dear Colleagues,

The INTERNATIONAL WORKSHOP Population and Ecological Genomics in Changing Forest Environments will be held at the Centro di Ecologia Alpina (CEA; http: www.cealp.it), Fondazione Edmund Mach, on Monte Bondone, near Trento, Italy, July 22-24, 2009. This workshop will be hosted by CEA, in collaboration with the University of California, Davis, USA (Department of Plant Sciences).

The aim of the workshop is to provide up-to-date knowledge of theoretical and computational approaches to studying adaptation in changing forest environments. The workshop will emphasize the use bioinformatics tools and software packages. Participants must have their own laptop computer and have software applications installed before arriving at the CEA. Information regarding obtaining software and computer hardware requirements will be provided by the organizers in advance of the workshop.

The workshop is primarily intended for young researchers at the doctoral and post-doctoral stages, but is also open to people working outside academic institutions seeking to acquire basic knowledge useful for implementing practical management and conservation plans.

Organizers: David Neale (Dept. of Plant Sciences, UC Davis) Cristiano Vernesi (Centro di Ecologia Alpina, Research and Innovation Centre, Fondazione Edmund Mach) Claudio Varotto (IASMA Research and Innovation Centre, Fondazione Edmund Mach)

Course Instructors: David Neale (UC Davis, USA) , Jill Wegrzyn (UC Davis, USA), Andrew Eckert (UC Davis, USA) and Elena Mosca (UC Davis, USA). Invited speakers: Sally Aitken (University of British Columbia, Canada) and Brad St. Clair (USDA Forest Service, Corvallis, Oregon, USA)

Local committee: Cristiano Vernesi and Floriana Marin (secretary), Fondazione Edmund Mach.

Dates: July 22-24, 2009. Place: Centro di Ecologia Alpina, Viote del Monte Bondone, 38040 Trento, Italy. Registration: Enrollment is limited to 15 participants. Potential participants are kindly requested to submit an e-mail (events@iasma.it) along with a one-page cv and 1-page statement describing why they would like to attend the workshop. Deadline for registration is May 1, 2009. Applicants will be advised of acceptance by May 15, 2009. Fee: 200 includes lunches and dinners (from July 22-24) and the course manual. Contacts: Floriana Marin, Research and Innovation Centre, Fondazione Edmund Mach, (events@iasma.it), phone: +39 0461 615543 - Fax + 39 0461 615183

Cristiano Vernesi Centro di Ecologia Alpina Centro Ricerca e Innovazione - Fondazione Edmund Mach postal address: Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skypename: cvernesi

Please consider your environmental responsibility before printing this email

Cristiano Vernesi <vernesi@cealp.it>

Kunming ConservationBiol

Advanced Tropical Field Ecology and Conservation CourseThis program is an intensive 4 week course in field research methods, research design, sampling and analysis designed for graduate students and advanced undergraduates in Ecology and Conservation.

Format: The Advanced Field Ecology and Conservation-Xishuangbanna (AFEC-X) Summer Course activities will be split between lecture and field exercises. Students will participate in established long term monitoring experiments and further gain experience in independent project design. With guidance, students will design and present research proposals and further conduct field based data collection. The course concludes with a symposium, where students present results of course activities amongst their peers and instructors.

Where: The course convenes in Kunming, capital city of Yunnan Province. Orientation, Introduction to the Course and a series of lectures will be given in Kunming before moving to Xishuangbanna Tropical Botanical Garden (XTBG) in Menglun, China. Both the long term and independent research projects will take place in and around Menglun.

Topics: Tropical Ecology, Eco-Physiology, Taxonomy, Evolutionary Ecology, Plant and Animal Interactions, Biodiversity, Conservation Biology, Invasive Species and more. Further discussions will look at how these topics are affected in human dominated landscapes.

Instructors: The various topics will be taught by professors from several institutes including The Chinese Academy of Sciences, Texas Tech University, Peking University and the Smithsonian Institute. More info at: http://www.afec.ecologicalevolution.org/ Ferry Slik Associate Professor Ö¹ú¿ÆÑ§ÔºÎË«æÄÉÈÈøÖ²ÎïÔ Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences Yunnan, China

Website

http://www.phylodiversity.net/fslik/ Plants of Southeast Asia http://www.asianplant.net Trees of Sungai Wain

http://www.nationaalherbarium.nl/Sungaiwain/
Asian plant species synonym website http://www.phylodiversity.net/fslik/synonym_lookup.htm
Macaranga and Mallotus of Borneo http://www.nationaalherbarium.nl/MacMalBorneo/index.htm Ferry Slik <ferryslik@hotmail.com>

Montana ConservationGeneticDataAnalysis Aug31-Sep4

4th ConGen- Population Genetics Data Analysis Course Recent Approaches for Estimation of Population Size, Structure, Gene flow, Selection Detection focusing on conservation and beyond 31-Aug/4-Sep 2009, Flathead Lake Biological Station, Montana, USA

Applications for 2009 will open soon!

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 20 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program).

Deadline for application is 15 June, 2009

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

For detailed information see http://popgen.eu/congen2009/ < http://popgen.eu/congen2008/ >.

congen@popgen.eu

conservation genetics course <congen@mail.icav.up.pt>

Munich HostParasiteCoevolution Sep20-25

Second Call for applications for summer school on Host-Parasite Coevolution

The Munich Graduate Program for Evolution, Ecology and Systematics (EES) invites applications for the international EES summer school on Host-Parasite Coevolution held at Frauenchiemsee (80 km east of Munich) from September 20th to September 25th, 2009.

The 5-day summer school will consist of lectures, discussions and exercises organized by the local and invited instructors, as well as oral and/or poster contributions by the students. We will cover theoretical aspects of host-parasite evolution and discuss empirical approaches for studying coevolution. Specific topics will include the evolution of virulence and resistance, local adaptation and spatial structuring in host-parasite systems, and the molecular signature of coevolution.

Instructors (confirmed): Mike Boots, University of Sheffield, UK (theoretical analysis of disease dynamics in humans and wildlife) Jukka Jokela, ETH Zurich, Switzerland (maintenance of sex driven by host-pathogen coevolution) David Nash, University of Copenhagen, Denmark (coevolution on geographical scales) Peter Tiffin, University of Minnesota, USA (molecular coevolution between plants and parasites)

Local Instructors/Organizers at Ludwig-Maximilians-University Munich: Susanne Foitzik, Pleuni Pennings, Laura Rose, Aurelien Tellier, Volker Witte, and Justyna Wolinska.

The summer school is open to all graduate students (PhD, Masters, Diplom biologists). The summer school will be taught in English. Participants should plan to arrive Sunday, Sept. 20th. The summer school will wrap up on Friday, Sept. 25th in the early afternoon.

Costs: Thanks to support from the Volkswagen Foundation, the University of Munich's EES program will cover housing and meals during the Summer School. Participants are required to cover their own travel expenses and pay a 50 Euro registration fee. A small amount of funding is available to subsidize travel costs for students from the most distant locations.

The Application Procedure: Applicants should submit a single pdf file containing the following: a) a one page CV b) a one page motivation letter for attending the summer school c) a short abstract of your research project (maximum 200 words) Email applications to Dr. Elisabeth Brunner (brunner@biologie.uni-muenchen.de). Application Deadline: June 1st, 2009.

Further information is available at: http://www.eeslmu.de/eeswiki/Summer_school_2009 Dr. Laura Rose Department Biologie - Biozentrum University of Munich Grosshaderner Str. 2 82152 Planegg Germany

Phone: 49 89 2180 74 150 Fax: 49 89 2180 74 104 Email: rose@zi.biologie.uni-muenchen.de Web: www.zi.biologie.uni-muenchen.de/evol/EvoBio rose@zi.biologie.uni-muenchen.de rose@zi.biologie.uni-muenchen.de

NESCent GMOD Jul16-19

The application deadline for both GMOD summer schools is April 6, less than a week from now.

GMOD Summer School - Americas will be held 16-19 July at the National Evolutionary Synthesis Center (NESCent), in Durham, NC, USA. Student tuition is free. See http://gmod.org/wiki/2009_GMOD_Summer_School_-_Americas GMOD Summer School - Europe will be held 3-6 August at the University of Oxford, in Oxford, UK. This is a part of GMOD Europe 2009, which includes the next GMOD Meeting. Student tuition is £95. See http://gmod.org/wiki/2009_GMOD_Summer_School_-_Europe GMOD (http://gmod.org/) is a collection of interoperable open source software components for managing, visualizing, annotating and integrating biological, mostly genomic, data. GMOD is also a community of developers and users dealing with similar problems. GMOD is used in diverse contexts, with both emerging and established model organisms.

The courses includes training on several GMOD components: * GBrowse - the widely used Generic Genome Browser * Chado - a modular and extensible database schema for biological data * Apollo - genome annotation editor * BioMart - biological data warehouse system * GBrowse_syn - a GBrowse based synteny viewer * JBrowse - a brand new Web 2.0 genome browser * Artemis-Chado Integration (Europe only) * MAKER - Genome annotation pipeline (Americas only) * Tripal - Web front end for Chado (Americas only)

Please contact the GMOD Help Desk (help@gmod.org) if you have questions.

We hope to see you in Durham or Oxford,

Dave Clements GMOD Help Desk

Dave Clements <clements@nescent.org>

Neuchatel SocialEvolution Jun4-5

Dear colleagues,

We are organising a small workshop in Neuchatel on Social Evolution, for MSc and PhD students working in evolutionary biology. Please could you pass this on.

Yours,

Daniel Rankin & Ralph Bergmueller

CUSO Workshop on Social Evolution Social evolution: from theory to data (and back again)

Institute of Biology, University of Neuchatel 4th-5th June 2009

Summary The target of the workshop will be to investigate conflict and cooperation on multiple levels of organisation, i.e. cooperation among genes, cells, organisms in groups including humans and conflict and cooperation on the level of cultural transmission. We aim at disentangling similarities and differences in the concepts and empirical study of social evolution in different fields (i.e. molecular, organismic and economic) and provide a platform to students who aim at developing a research project.

Invited experts Professor Redouan Bshary (University of Neuchatel CH) Dr Andy Gardner (University of Edinburgh, UK) Dr Ashleigh Griffin (University of Oxford UK) Dr Gilbert Roberts (University of Nottingham UK) Professor Carel van Schaik (University of Zurich CH) Professor Claus Wedekind (University of Lausanne CH)

Registration fees None for CUSO students (Geneva, Lausanne, Frbiourg, Neuchatel and Bern). CUSO students will have their travel refunded and receive a contribution meals. Please note that accommodation is not provided. There is a small fee of 50CHF to cover coffee and lunch over the two days for non-CUSO participants.

Registration deadline: 18th May 2009

Maximum number of participants: 30

For further details please contact: Dr Ralph Bergmüller (University of Neuchatel) ralph.bergmueller@unine.ch Dr Daniel Rankin (University of Zurich) d.rankin@bioc.uzh.ch

Registration at: http://www.3eme-cycle.ch/biologie/pages/entry.php?code=3Dab23-09

d.rankin@bioc.uzh.ch

OhioStateU PhylogeneticMethods Jul13-17

The Ohio State University and Willi Hennig Society will host a Workshop in Phylogenetic Methods in Columbus, Ohio, July 13-17, 2009. Students will participate in lectures and discussions of phylogenetic methods and principles and will receive hands-on training in various software packages.

The workshop includes a workbook (approximately 300 pages), relevant software (including TNT, POY, Nona, Winclada, Muscle, RaxML, and MrBayes), and lessons lead by Gonzalo Giribet (Harvard University), Kevin Nixon (Cornell University), Ward Wheeler (American Museum of Natural History), Christopher P. Randle (Sam Houston State) and John Wenzel (Ohio State University). A syllabus is available at http://systematics.osu.edu < http://systematics.osu.edu/ > (click on "workshop information").

This workshop can be attended either via Fellowship student enrollment or Auditor enrollment. Fellowship student enrollment includes lodging, lecture, and hands-on computer lab; Auditor enrollment does not include lodging or hands-on training with the computer programs.

Fellowship enrollment (limited to 20 students) is $1200, with one week of lodging included. These students will receive a $600 Hennig Society fellowship paid directly to the workshop, thus they will be responsible for a workshop cost of only $600, plus the cost of transportation to and from the Ohio State campus, and meals. Auditor enrollment fee is $600. No lodging is provided, but we will assist with local arrangements. Auditors also get the workbook and software packages, and are included in the reception mixer and group dinner.

Applications for full enrollment may be made through http://systematics.osu.edu < http://systematics.osu.edu/ > Click on "workshop information" for details. An application consists of a completed application form (available from the web site), a current CV for the student, and a letter from the student's advisor regarding the relevance of the course to the student's career goals. Applications are due April 30, 2009, and notification of acceptance will begin by May 15. Auditor enrollment is available by correspondence with osuphylo@osu.edu, and will close on June 15, 2009. Further information may be obtained by emailing osuphylo@osu.edu.

daly.66@osu.edu daly.66@osu.edu

Roscoff France MarineEvolutionaryGenomics

Summer Course - Marine Genomics Europe Marine Evolutionary & Ecological Genomics May 25th â June 5th, 2009 Station Biologique de Roscoff, France

Aims to give an introduction on genetic and genomic approaches to analyze biological diversity, evolution and adaptation at the species and population level in the ocean

Confirmed teachers

Sandie Baldauf, Univ of York, UK

Erik Bonivard, Univ. Paris 6, FR

Galice Hoarau, Univ of Groningen, NL

Wiebe Kooistra, SZN, IT

FrÃ©dÃ©ric Partensky, SB-Roscoff, FR?

Klaus Valentin, AWI-Bremerhaven, DE

FrÃ©dÃ©rique Viard, SB-Roscoff, FR

ClÃ©mentine Vitte, Univ. Paris 6, FR

Filip Volckaert, KULeuven, BE

Organizing committee

HÃ©lÃne Huelvan, SB-Roscoff, FR

Jeanine Olsen, Univ of Groningen, NL

Anne Saisi, SB-Roscoff, FR

Arnaud Tanguy, SB-Roscoff, FR

FrÃ©dÃ©rique Viard, SB-Roscoff, FR

Filip Volckaert, KULeuven, BE

Target group

PhD students (at least in their second year) and post docs with a solid knowledge in phylo- and/or population genetics. This course is open to MGE members as well as non-members.

Topics

The course will consist of lectures, tutorials and computer based exercises in the following subjects.

* Phylogeny - sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies * Population genetics â allele and genotype analyses, population genetic structure and gene flow, assignment tests, effective size and population dynamics, case studies * Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies * Environmental, functional and comparative genomics - 1. Genome structure and architecture. 2. Markers in the genomics realm. 3. Methods for detecting structure. 4. Introduction to functional genomics. 5. Methods for detecting adaptive variation (including selective sweeps) within and among populations; linking hydrographical/environmental and demographic data to population structure and local adaptation. 6 Quantitative genetics: evolution of traits. 7. EST libraries: why and how. 8. Introduction to comparative genomics (whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, transposable elements in marine species) 9. Case studies * Phylogenomics - 1. What is comparative genomics? 2. Genomics and genetics of speciation/ what makes a species from a genome point of view? 3. Comparative marine genomics. 4. Case studies

Costs; course, accommodation and meals

* The course fee is paid by the MGE Network for all academics (pre and post doc). Welcome reception, excursion (incl lunch) and farewell dinner are included. * All participants pay their own travel, accommodation and board (self catering is possible) * Participants are offered to be accommodated at the SBR guesthouse which is situated directly at the institute. The cost for this is 13 per night in double room incl. breakfast. The guesthouse can also offer lunch and supper for a cost of 5.50 per person and meal.

Application and contact

To apply please fill in the application form and send to Anne Saisi (saisi@sb-roscoff.fr) together with a 2-paged CV before April 10, 2009. This information + application form can also be found on the MGE website: www.marine-genomics-europe.org under Training & Education.

16 participants will be selected by the following criteria:

1. Relevance of the course for their PhD or post-doc project

2. Background and experience of applicant

3. We will aim at mixing people from different research areas and therefore probably no more then one person per institute will be considered. We will also aim at an equal distribution of women and men.

The selected persons will receive a notification at the end of April that has to be confirmed within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Contact

Anne Saisi

European Project Manager

Station Biologique de Roscoff

BP 74, 29680 ROSCOFF CEDEX

France

Email: saisi@sb-roscoff.fr

Phone: (33)2 98 29 23 45

Fax: (33)2 98 29 23 80

Disclaimer: http://www.kuleuven.be/-cwis/email_disclaimer.htm Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Roscoff France MarineEvolutionaryGenomics May25-Jun5

MGE Summer Course

Marine Evolutionary & Ecological Genomics May 25th â June 5th, 2009 Station Biologique de Roscoff, France

Confirmed teachers Sandie Baldauf, Univ of York, UK Erik Bonivard, Univ. Paris 6, FR Galice Hoarau, Univ of Groningen, NL Wiebe Kooistra, SZN, IT FrÃ©dÃ©ric Partensky, SB-Roscoff, FR Klaus Valentin, AWI-Bremerhaven, DE FrÃ©dÃ©rique Viard, SB-Roscoff, FR ClÃ©mentine Vitte, Univ. Paris 6, FR Filip Volckaert, KULeuven, BE Simon Creer, UBangon, UK Mathias Wegner, UZurich, CH

Organizing committee HÃ©lÃne Huelvan, SB-Roscoff, FR Jeanine Olsen, Univ of Groningen, NL Anne Saisi, SB-Roscoff, FR Arnaud Tanguy, SB-Roscoff, FR FrÃ©dÃ©rique Viard, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

Aims to give an introduction on genetic and genomic approaches to analyze biological diversity, evolution and adaptation at the species and population level in the ocean

Target group

PhD students (at least in their second year) and post docs with a solid knowledge in phylo- and/or population genetics. This course is open to MGE members as well as non-members.

Topics

The course will consist of lectures, tutorials and computer based exercises in the following subjects.

* Phylogeny - sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies * Population genetics â allele and genotype analyses, population genetic structure and gene flow, assignment tests, effective size and population dynamics, case studies * Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies * Environmental, functional and comparative genomics - 1. Genome structure and architecture. 2. Markers in the genomics realm. 3. Methods for detecting structure. 4. Introduction to functional genomics. 5. Methods for detecting adaptive variation (including selective sweeps) within and among populations; linking hydrographical/environmental and demographic data to population structure and local adaptation. 6 Quantitative genetics: evolution of traits. 7. EST libraries: why and how. 8. Introduction to comparative genomics (whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, transposable elements in marine species) 9. Case studies * Phylogenomics - 1. What is comparative genomics? 2. Genomics and genetics of speciation/ what makes a species from a genome point of view? 3. Comparative marine genomics. 4. Case studies

Costs; course, accommodation and meals

* The course fee is paid by the MGE Network for all academics (pre and post doc). Welcome reception, excursion (incl lunch) and farewell dinner are included. * All participants pay their own travel, accommodation and board (self catering is possible) * Participants are offered to be accommodated at the SBR guesthouse which is situated directly at the institute. The cost for this is 13 per night in double room incl. breakfast. The guesthouse can also offer lunch and supper for a cost of 5.50 per person and meal.

Application and contact

To apply please fill in the application form and send to Anne Saisi (saisi@sb-roscoff.fr) together with a 2-paged CV before April 10, 2009. This information + application form can also be found on the MGE website: < http://www.marine-genomics-europe.org/- > www.marine-genomics-europe.org under Training & Education.

16 participants will be selected by the following criteria:

1. Relevance of the course for their PhD or post-doc project 2. Background and experience of applicant 3. We will aim at mixing people from different research areas and therefore probably no more then one person per institute will be considered. We will also aim at an equal distribution of women and men.

The selected persons will receive a notification at the end of April that has to be confirmed within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Contact

Anne Saisi European Project Manager Station Biologique de Roscoff BP 74, 29680 ROSCOFF CEDEX France Email: saisi@sb-roscoff.fr Phone: (33)2 98 29 23 45 Fax: (33)2 98 29 23 80

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Shanghai ComputationalBiology Aug16-22

Dear Colleagues,

We are pleased to inform you about the upcoming workshop:

"EMBO Practical Course on Computational biology: From (meta)genomes to phenotype and environment"

in Shanghai sponsored by the EMBO World Practical Course program.

The 7-day workshop (August 16th-22nd 2009) is the third in a successful series, and has the ambitious goal to introduce advanced methods and applications of computational biology in the field of metagenomics.

Participation is restricted to 20 graduate students and postdocs, who will work on biological problems that could even lead to scientific discoveries made during the course. For all participants, fellowships will be made available covering housing, subsistence and registration. No funding are available for travel costs.

Closing date for applications: May 15th, 2009 Further information and registration at http://cwp.embo.org/wpc09-11/ Sincerely,

francesca ciccarelli, for the organizers*

* Organizing Committee of the EMBO practical course 'EMBO Practical Course on Computational biology: From (meta)genomes to phenotype and environment', August 16th-22nd, Shanghai, China

Dr. Peer Bork, EMBL Heidelberg , Germany Dr. Liping Zhao, Shanghai Jiao Tong University, China Dr. Yixue Li, Shanghai Institutes for Biological Sciences, China Dr. Chaochun Wei, Shanghai Jiaotong University, China Dr. Francesca D. Ciccarelli, EIO Milan, Italy Dr. Jan Korbel, EMBL Heidelberg , Germany Dr. Roland Krause, Max-Planck-Institute Berlin, Germany

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

UCollege Cork Bioinformatics

Topic: MSc in Bioinformatics with Systems Biology at University College Cork

Dear all,

The MSc course in Bioinformatics with Systems Biology at University College Cork, Ireland, is now open for applications for the academic year 2009/2010. The closing date for EU applicants is 1st July 2009 and for non-EU applicants is 31st May 2009.

This programme receives funding from the Irish Government under a major initiative to meet IT skills, therefore EU students will pay a reduced annual tuition fee of 2000 euros and non-EU students will pay a reduced annual tuition fee of 9960 euros. There are also scholarships available to help EU and non-EU students to cover fees and maintenance costs.

Please visit the MSc course website http://www.ucc.ie/ucc/depts/microbio/MScBioinf for information on the MSc course content, scholarships, and application procedures.

If you have any questions about the course or careers in Bioinformatics, please feel welcome to contact me, as I would be very happy to discuss with you in person or by phone or email.

Best wishes, Avril

Dr Avril Coghlan Department of Microbiology University College Cork, Ireland

"Coghlan, Avril" <A.Coghlan@ucc.ie>

UGlasgow Bio++ Jun16-18

The Bio++ workshop is a three-day, hands-on course, to be taught at the University of Glasgow from the 16th - 18th of June 2009 (9am - 5.30pm). Bio++ (http://kimura.univ-montp2.fr/BioPP/) is a highly efficient set of C++ libraries for applications in bio-sequence analysis, molecular evolution and population genetics.

The workshop is for researchers who already have some experience of programming as well as knowledge of population genetics and/or phylogenetics. The workshop will include one day with a short introduction to the C++ language for users with a background in other programming languages, followed by two days of intensive instruction in using the Bio++ libraries working on examples for population genetic and phylogenetic analyses.

In addition to providing detailed instructions in the use of these libraries, the workshop will be the founding event for a new network of bioinformatic researchers who are developing tools for data analysis in phylogenetics and population genetics (BioPhyloPop group).

This workshop is free of registration fees thanks to sponsorship from the Scottish Bioinformatics Forum but attendees will be expected to make their own lunch, travel and accommodation arrangements.

To register for the course and for more details, please email Dr Annabelle Haudry: a.haudry@bio.gla.ac.uk stating which programming language you have experience with, what you use it for.

– Dr. Annabelle Haudry Division of Ecology & Evolutionary Biology Graham Kerr Building GK 408 University of Glasgow Glasgow G12 8QQ, SCOTLAND Office: +44 (0)141 330 6637 http://www.gla.ac.uk/departments/ecologyevolutionarybiology/researchinterests/pdra/annabellehaudry/ Annabelle Haudry <a.haudry@bio.gla.ac.uk>

UNAMexico MolecularEvolution Jun22-Jul3

LATIN-AMERICAN WORKSHOP ON MOLECULAR EVOLUTION

Intensive workshop on the theory and practice of phylogenetics, molecular evolution and population genetics. It will take place at the Center for Genomic Science, Universidad Nacional Autónoma de México (UNAM), in its Cuernavaca campus (Cuernavaca, Morelos, Mexico), from June 22 to July 3, 2009. The workshop will consist of 10 full days of lecture and computer practice. It will fulfill the requirements of several UNAM graduate programs. The workshop is aimed at students and professors from Latin-America. It will be delivered in Spanish. Limited to 40 participants.

For more information and applications: http://www.ccg.unam.mx/˜vinuesa/tlem09/index.xhtml Organizers: Center for Genomic Science, Institute of Biology, Institute of Ecology, School of Science, UNAM.

TALLER LATINOAMERICANO DE EVOLUCIÓN MOLECULAR

Taller intensivo sobre teoría y práctica de filogenetica, evolución molecular y genética de poblaciones. Se llevará a cabo en el Centro de Ciencias Genómicas de la Universidad Nacional Autónoma de México (UNAM), campus Cuernavaca, Morelos, México, del 22 de Junio, al 3 de Julio, 2009. El taller constará de 10 días de clase, 8 horas diarias, cubriendo las estipulaciones de diversos programas de posgrado de la UNAM. El taller está dirigido a estudiantes y profesores de Latinoamérica. Será impartido en castellano. Cupo limitado a 40 participantes.

Para mayor información y solicitudes de inscripción: http://www.ccg.unam.mx/ ˜ vinuesa/tlem09/index.xhtml Organizadores: Centro de Ciencias Genómicas, Instituto de Biología, Instituto de Ecología, Facultad de Ciencias, UNAM.

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Susana A. Magallón Instituto de Biología Universidad Nacional Autónoma de México 3er Circuito de Ciudad Universitaria Del. Coyoacán México D.F. 04510 México

Voice: (52-55) 5622-9087 FAX: (52-55) 5550-1760 E-mail: s.magallon@ibiologia.unam.mx

http://www.ibiologia.unam.mx/directorio/m/magallon.htm
S.Magallon@ibunam2.ibiologia.unam.mx
S.Magallon@ibunam2.ibiologia.unam.mx

UNAM Mexico MolecularEvolutionPhylogenetics Jun22-Jul3

LATIN-AMERICAN WORKSHOP ON MOLECULAR EVOLUTION

Intensive workshop on the theory and practice of phylogenetics, molecular evolution and population genetics. It will take place at the Center for Genomic Science, Universidad Nacional Autónoma de México (UNAM), in its Cuernavaca campus (Cuernavaca, Morelos, Mexico), from June 22 to July 3, 2009. The workshop will consist of 10 full days of lecture and computer practice. It will fulfill the requirements of several UNAM graduate programs. The workshop is aimed at students and professors from Latin-America. It will be delivered in Spanish. Limited to 40 participants.

For more information and applications: http://www.ccg.unam.mx/ ˜ vinuesa/tlem09/ Organizers: Center for Genomic Science, Institute of Biology, Institute of Ecology, School of Science, UNAM.

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Universidad Nacional Autónoma de México (UNAM), campus Cuernavaca, Morelos, México, del 22 de Junio, al 3 de Julio, 2009. El taller constará de 10 días de clase, 8 horas diarias, cubriendo las estipulaciones de diversos programas de posgrado de la UNAM. El taller está dirigido a estudiantes y profesores de Latinoamérica. Será impartido en castellano. Cupo limitado a 40 participantes.

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Susana A. Magallón Instituto de Biología Universidad Nacional Autónoma de México 3er Circuito de Ciudad Universitaria Del. Coyoacán México D.F. 04510 México

Voice: (52-55) 5622-9087 FAX: (52-55) 5550-1760 E-mail: s.magallon@ibiologia.unam.mx

http://www.ibiologia.unam.mx/directorio/-m/magallon.htm Susana Magallon <S.Magallon@ibunam2.ibiologia.unam.mx>

UStAndrews BioinformaticsComparativeGenomics Aug15-18

Dear Evoldir,

The University of St Andrews and the Scottish Bioinformatics Forum will be hosting:

Summer School - Bioinformatics and Comparative Genomics Date: 15th August 2009, 09:00 am End Date: 18th August 2009 Location: The University of St Andrews, Scotland

http://www.genome-bioinformatics.org Confirmed Speakers: Prof Ziheng Yang FRS, University College London, UK Prof Neil Hall, University of Liverpool, UK Dr Zemin Ning, Wellcome Trust Sanger Institute, UK Dr David Martin, University of Dundee, UK Prof Geoff Barton, University of Dundee, UK Dr Daniel Barker, University of St Andrews, UK Prof Ian Korf, UC Davis Genome Center, USA Prof Dannie Durand, Carnegie Mellon University, USA Dr Chris Janssen, SBF and University of Glasgow, UK Dr David Ferrier, University of St Andrews, UK

The summer school on bioinformatics and comparative genomics will address practical bioinformatics for sequence analysis and comparative genomics for use in biological and biomedical research. Internationally renowned invited speakers will discuss current challenges, applications, and future outlook in the field. The school will consist of a series of lectures, seminars and practical classes, allowing participants both insight into theory and the opportunity to learn practical skills in data analysis and interpretation.

Registration for the summer school includes attendance at a one-day international conference on 18th August, “Comparative Genomics”. Four nights of accommodation (14th-17th August) are optionally available on registration.

Full details and registration please see:

http://www.genome-bioinformatics.org We look forward to seeing you in August.

Best regards,

Daniel

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

University of St Andrews Webmail: https://-webmail.st-andrews.ac.uk db60@st-andrews.ac.uk db60@st-andrews.ac.uk

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Valencia MolecularEvolution Jun15-19

Fourth Course on Molecular Evolution, Phylogenetics, Phylogenomics and Adaptation

15 - 19 June 2009, Valencia. Spain

Hernán Dopazo, Co-ordination

The course aims to provide the necessary background to understand the basic concepts from comparative and evolutionary biology that are frequently used in molecular biology and bioinformatics analyses. The course consists in five full-day sessions with an adequate balance between theory and computer practice, oriented to solve frequent problems and hypothesis testing. The course includes a session of phylogenomic analysis and functional annotation including the most recent developments in this area. Among other tools, attendees will become familiar with Phylip, Phyml, PAML, TreePuzzle, MrBayes, Modeltest, ProTest, JModelTest programs and tools developed in our department such as Phylemon, FatiGO and FatiScan. The course is mainly intended for professionals in the field of biology and chemistry who work on areas related to biological sequence analysis.

Course fee is 300 euros

Application Deadline: 18th May 2009

More information at: http://bioinfo.cipf.es/courses/-mol_evol_phylo_4ed/ Language: the official language of the course will be english unless all attendees speak spanish.

Phylemon web server: http://phylemon.bioinfo.cipf.es Comparative Genomics Unit Bioinformatics and Genomics Department Centro de Investigación Príncipe Felipe (CIPF) Valencia, Spain.

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

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.