EvolDir

June 1, 2010

Month in Review

Foreword

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

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

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

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Conferences

AMNH NewYork StudentConservation Nov3-5

2010 STUDENT CONFERENCE ON CONSERVATION SCIENCE (SCCS-NY) American Museum of Natural History New York City 3-5 November 2010 http://symposia.cbc.amnh.org/sccsny/ APPLICATIONS BEING ACCEPTED THROUGH 18 MAY 2010

In November 2010, the American Museum of Natural Historyâs Center for Biodiversity and Conservation will host SCCS-NY, the Student Conference on Conservation Science in New York City. Designed for graduate students, recent post-doctoral fellows, and early-career professionals, the conference specifically targets those pursuing or considering a profession in conservation science.

This conference is a unique opportunity for those beginning their careers to present their work before leaders in science, policy, and management. In addition to formal presentations, there will be numerous opportunities to interact with established conservation professionals at workshops, informal gatherings, and networking events.

SCCS-NY is sponsored by the American Museum of Natural Historyâs Center for Biodiversity and Conservation, the Wildlife Conservation Society, and Yale School of Forestry and Environmental Studies, in collaboration with the Bard Center for Environmental Policy, Cornell Lab of Ornithology, Fordham University, Mason Center for Conservation Studies, The Nature Conservancy, New York Botanical Garden, Princeton University, Richard Gilder Graduate School, RutgersâThe State University of New Jersey, SCCS-Cambridge, the State University of New York College of Environmental Science and Forestry, and Wildlife Trust.

SCCS-NY is a sister conference to the highly successful SCCS-Cambridge, begun in 2000 by the University of Cambridge, and the newly developed SCCS-Bangalore.

GUEST SPEAKERS

Sir Peter Crane, Ph.D. - Carl W. Knobloch, Jr. Dean of the School of Forestry & Environmental Studies and Professor of Botany, Yale University, New Haven, Connecticut

James Gibbs, Ph.D. â Professor and Associate Chair, Department of Environmental and Forest Biology, State University of New York College of Environmental Science and Forestry, Syracuse, New York

Joshua Ginsberg, Ph.D. - Senior Vice President, Global Conservation Program, Wildlife Conservation Society, Bronx, New York

AndrÃ©s GÃ³mez, D.V.M., Ph.D. - Postdoctoral Fellow, Center for Biodiversity and Conservation, American Museum of Natural History, New York, New York

Martha Groom, Ph.D. - Associate Professor of Ecology and Environmental Studies, University of Washington Bothell & Seattle, Washington

MENTORING TASKFORCE Dozens of conservation professionals will be on hand during the conference to provide personalized feedback, lead workshops, host working lunches, and offer networking ideas. (See the website for a list of confirmed participants http://symposia.cbc.amnh.org/sccsny/.)

WORKSHOPS A series of workshops will be offered by experts working in diverse aspects of conservation science and education. Topics will include:

1) Ecological risk analysis for conservation biology 2) Conservation Action Planning: developing conservation strategies for applied conservation projects 3) Advances in monitoring and quantitative ecology in conservation science 4) Expanding your teaching toolbox: an introduction to active and scientific teaching approaches 5) Modeling ecological niches and geographic distributions: what, why and how¿‘

WHO SHOULD APPLY Those wishing to participate in SCCS-NY should have completed, or be conducting a research project in any conservation-related course of study within the natural sciences, social sciences, or humanities. Selection for participation will be based on the quality of oneâs application as well as its relevance to conservation. Applications are encouraged from the following:

Graduate Students Recent Post-Doctoral Fellows Early-Career Professionals Undergraduates (research project must be of thesis-level quality)

TO APPLY, please go to http://symposia.cbc.amnh.org/sccsny/ DEADLINE: 18 May 2010

Fiona Brady <brady@amnh.org>

Ankara BeePopulationGenetics Sep7-9

Ankara Bee Genetics and Genomics

Sep 7-9

Dear Evoldir readers,

We still have some slots available in our symposium “Bee Genetics and Genomics” at the 4th European Conference of Apidology EurBee 2010 in Ankara, Turkey (7-9 September 2010, http://www.eurbee2010.org/). The symposium will bring together researchers working on different aspects of genetics and genomics of bees. We are aiming at integrating different aspects of genetics and genomics including comparative genomic analysis, expression studies, QTL mapping, breeding genetics, neurogenetics, population genetics. Invited speaker is Guy Bloch. Below you find the description of our symposium. The deadline for abstract submission is 24 May 2010 and the deadline for registration (early bird) is 20 July 2010.

Honeybees already have entered the stage of being a model organism for genomic research, at least since the publication of the complete genome sequence in 2006. However, with ongoing development in sequencing techniques other social insects will follow the honeybee opening the door for comparative approaches, especially with regard to the peculiarities of social insects like caste determination and differentiation. The bumblebee, Bombus terrestris will be the second bee with a complete genome sequence available. As costs for sequencing projects will drop, more species will be selected for whole genome sequencing. As for both, honeybees and bumblebees, as well as for other pollinators rapid declines have been reported and parasites have been claimed to be the major driver for pollinator decline, genomic research may help to disentangle the basics for host-parasite interaction in social insects. Genomic research in social insects ranges from genome and transcriptome sequencing to linkage map construction and mapping of candidate genes for specific traits. QTLs have been identified for disease resistance, hygienic behaviour, foraging behaviour and ovary development amongst others. Transcriptome differences have been studied in relation to division of labour, disease resistance and caste determination.

Names and contact information of the organizers:

Michael Lattorff Institute for Biology, Molecular Ecology Martin-Luther-University Halle-Wittenberg, Germany 06099 Halle, Germany Email: lattorff@zoologie.uni-halle.de

Cédric Alaux INRA, UMR 406 Abeilles et Environnement Laboratoire Biologie et Protection de l’abeille Site Agroparc, Domaine Saint-Paul 84914 AVIGNON Cedex 9, France email: cedric.alaux@avignon.inra.fr

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/ Michael Lattorff <lattorff@zoologie.uni-halle.de>

Beijing PlantSystematics Jul7-9 3

_INTERNATIONAL CONFERENCE ON NEW FRONTIERS IN __PLANT __SYSTEMATIC__S AND EVOLUTION_ - JULY 7-9, 2010, BEIJING, CHINA

This conference aims at providing an opportunity for plant systematists and evolutionary biologists to review the progress, evaluate the current status, and look into the future of the field. It will include talks, posters, and open discussions on recent progress and future directions of the following areas: 1) Taxonomy, collections, and databases; 2) Phylogenetics, phylogenomics, and the Tree of Life; 3) Biogeography and phylogeography; 4) Speciation, hybridization, and adaptation; 5) Molecular evolution, evolutionary genetics and genomics, and Evo-Devo. There will be 40 invited talks from worldwide experts in each of these areas. The conference will be held at the Fragrant Hill (Xiangshan), one of Beijing's most famous scenic and historical sites near the precious royal garden. It is within walking distance to the Beijing Botanical Garden and the Institute of Botany.The conference is organized by the Botanical Society of China (BSC), the Chinese Academy of Sciences (CAS), and the International Association for Plant Taxonomy (IAPT).For more information, please visit: www.syst-evol.cn . Qiu-Yun (Jenny) Xiang Associate Professor Department of Plant Biology North Carolina State University Raleigh,NC 27695-7612 919-515-2728 (phone) 919-515-3436 (Fax) Jenny_xiang@ncsu.edu http://www4.ncsu.edu/ ~ qyxiang qyxiang@ncsu.edu

Brittany SocialEvolution Oct11-15

Dear colleagues,

Registration still open!

We organize a conference on “Social systems: demographic and genetic issues” next October (11-15^th) in Paimpont, Brittany, France. We propose the conference to be organized around 2 major themes:

1. /Social organization and demographic structure/ – The influence of philopatry, polygyny, dispersal bias among sexes, natal sex ratio, social reproductive suppression, kin selection and kin discrimination, on demographic structure

2. /Social organization and genetic structure/ –The effects of social organization and group dynamics, the role of group fission, fission-fusion social systems, sex biased dispersal, the influence of dominance rank (lineages or individuals), mate choice on the distribution of relatedness and gene diversity of neutral and functional (for instance MHC) genes. The conference will mix theoretical and empirical approaches, scientific questions with methodological issues.

The conference will be limited to about 75 people, with space for about forty oral communications and for posters. We invite people who wish to communicate at the conference to send us a tentative title for an oral communication or a poster before May 31^st .

Organization and registration details including a provisional program can be found on http://socior.univ-rennes1.fr/ Nelly Ménard 1, Nicolas Perrin 2, Eric Petit 1 & Jean-Sébastien Pierre 1

1 Department for the study of Ecology, Biodiversity and Evolution at the University of Rennes 1 and CNRS (National Centre for Scientific Research, France)

– Nelly Ménard, UMR 6553 ECOBIO, Ecosystème, Biodiversité, Evolution; CNRS/Université de Rennes 1; Station Biologique 35380 Paimpont-France;

http://www.sbp.univ-rennes1.fr http://ecobio.univ-rennes1.fr/ tel: 02.99.61.81.72; from abroad: 33.2.99 etc... mail: nelly.menard@univ-rennes1.fr

Heidelberg ExperimentalEvolution Sep29-Oct3

EMBO Conference Series Experimental Approaches to Evolution and Ecology using Yeast EMBL Heidelberg, Germany

Wednesday 29 September - Sunday 3 October 2010

The cellular and molecular basis of life is the outcome of a long process of evolution governed by variation and selection. The intention of this conference series is to explore the concept of using yeast as a model system in evolution and ecology, building on our deep understanding of its physiology and genetics, and taking advantage of sophisticated techniques to manipulate the yeast cell. It shall concentrate on four core issues in evolutionary biology:

1. The overall architecture of the genome and the major processes that have contributed to its evolution. 2. The ecological and genetic structure of natural populations that forms the stage on which this evolution has taken place. 3. The mechanisms of selection that lead to adaptation, and in particular how these can be studied experimentally in the laboratory. 4. The use of yeast to illuminate important problems in adaptation, especially the evolution of sex and mating systems.

The conference series aims to bring scientists engaged in technology development together with evolutionary biologists, population geneticists and classical cell biologists and geneticists in order to explore experimental strategies to study the mechanisms and design principles of evolution.

Kind regards,

Nicki Vegiopoulos Marketing Officer

European Molecular Biology Laboratory Course and Conference Office Meyerhofstr. 1 D-69117 Heidelberg

Tel: +49-6221-387 8764 Fax: +49-6221-387 8158

Please visit www.embl.org/events for a complete list of all EMBL events Please subscribe at www.embl.de/events/newsletter for our newsletter Follow us on www.twitter.com/embl_events and www.friendfeed.com/embl

Nicola Vegiopoulos <nicola.vegiopoulos@embl.de>

Hilo Hawaii ConservationGenomics Jul26-28 2

Our program is complete and registration is open! http://www.theaga.org/2010 The American Genetic Association will hold its annual meeting in Hilo, Hawaii from 26-28 July, 2010.

AGA meetings focus on a single topic and last for 2.5 days. This year's topic is Conservation Genomics, and will include talks by a series of genomicists and conservation biologists, including those who are already shaping this emerging discipline. Our goal is to provide a focused forum for discussion, brainstorming, and development of collaborative efforts that leverage emerging genomic resources for applications in conservation biology.

Ollie Ryder, Director of Genetics, San Diego Zoo's Institute for Conservation Research, will give the Wilhelmine Key Lecture.

To encourage broad attendance, we have kept registration low ($150), which includes an opening mixer and evening luau. We have negotiated very reasonable hotel accommodation in Hilo as well as dormitory space at UH.

Funds are available, on a competitive basis, for student registration and accommodation.

More details and registration are available at the meeting website: http://www.theaga.org/2010 Please join us- Hilo is an amazing setting, and we look forward to an engaging, enlightening three days.

Conference organized by Brad Shaffer

Any questions, contact:

Brad Shaffer mailto:hbshaffer@ucdavis.edu, President of the AGA, or

Anjanette Baker mailto:agajoh@oregonstate.edu, Managing Editor, Journal of Heredity

agajoh@oregonstate.edu

Hilo Hawaii ConservationGenomics Jul26-28 DormRooms

June 10 Deadline to reserve Dorm Rooms –

UH Hilo has dorm rooms available for any nights from 25-31 June. The housing is "apartment style", with 2 bedrooms (each has two beds, and sleeps two people), a common area, and a kitchen. The rate is $20/night per person, and a one-time $10 fee for linens.

If you would like to stay in the dorms, please contact Brad Shaffer, mailto:hbshaffer@ucdavis.edu by Thursday, June 10.

Symposium details and registration at: http://www.theaga.org/2010 AGA meetings focus on a single topic and last for 2.5 days. This year's topic is Conservation Genomics, and will include talks by a series of genomicists and conservation biologists, including those who are already shaping this emerging discipline. Our goal is to provide a focused forum for discussion, brainstorming, and development of collaborative efforts that leverage emerging genomic resources for applications in conservation biology.

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agajoh@oregonstate.edu

Hilo Hawaii ConservationGenomics Jul26-28 StudentGrants

GRANTS FOR STUDENTS AND POSTDOCS

The American Genetic Association is offering grants of up to $400 to assist students and postdocs wishing to attend the annual symposium.

To apply for a grant, please send 1) a short statement indicating your position (undergraduate student/ graduate student/postdoc) and why you wish to attend, and 2) a poster abstract to: Brad Shaffer hbshaffer@ucdavis.edu.

A brief supporting statement should be sent separately by your advisor.

You must be an AGA member to apply for these grants. Student membership is $20/year, and includes the online and print issues of the 2010 "Journal of Heredity", as well as access to the complete online archive (105 years!). To join, go to: http://www.oxfordjournals.org/our_journals/jhered/access_purchase/price_list.html Decisions and notification on grants will be made by June 1, 2010.

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agajoh@oregonstate.edu

KansasCity Genomics Nov5-7

8th Genomics Symposium, November 5 - 7, 2010, in Kansas City

Save the dates.

and plan to attend the 8th Annual "Genes in Ecology, Ecology in Genes" Symposium on November 5, 6, & 7, 2010, in Kansas City. We will convene in the Muehlebach/Marriott Hotel in downtown Kansas City at 6:00 p.m. and conclude on Sunday at noon. Registration will be opening soon!

Ecological Genomics is a field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context.

We have an outstanding lineup of speakers for the 2010 Symposium and we encourage you to attend! Speakers and other information will soon be announced and posted on our website, ecogen.ksu.edu, as details are finalized.

POSTER SESSIONS: Poster sessions will be held on Friday night and Saturday. Poster topics should be related to the field of Ecological Genomics. A LIMITED NUMBER OF SUBMITTED POSTER ABSTRACTS WILL BE SELECTED FOR ORAL PRESENTATIONS.

Please share this announcement with colleagues and students who are interested in learning more about the field of Ecological Genomics. If you have questions, please contact us at (785) 532-3482 or dmerrill@ksu.edu.

Funding for this symposium is provided by the National Science Foundation and Targeted Excellence at Kansas State University.

Ecological Genomics Institute Directors:

Dr. Loretta Johnson

Dr. Michael Herman

Kansas State University, Division of Biology

Ackert Hall, Manhattan, KS 66506-4901

(785) 532-3482, www.ecogen.ksu.edu dmerrill@ksu.edu

LaurentianU OEEC Jul14-16

The 40th Ontario Ecology and Ethology Colloquium (OEEC) will be held July 14-16, 2010 at Laurentian University, Sudbury, Ontario, Canada.

The OEEC is a two-day graduate student-run conference, intended to provide a supportive and enthusiastic atmosphere for approximately 100 upper level undergraduate students, graduate students, Post Docs and faculty to present research and to facilitate networking between institutions and people at all levels. Over the past 40 years, the scope of the conference has increased both geographically and conceptually, welcoming interprovincial and international speakers on subjects ranging from ecology, evolutionary biology, physiology to psychology.

For the 40th anniversary of the OEEC here at Laurentian University, the planning committee has high standards. Our goal is to create a truly significant conference experience for those who will be influencing the direction of scientific research. We are pairing with Science North, an internationally recognized centre for public science education. We also plan to create a prominent presence for the many local groups involved in the successful, yet ongoing, reclamation of the Sudbury area in order to emphasize the link between theoretical and applied research. To further support a relationship between research and community, OEEC will highlight eco-friendly fair-trade and local products for all catering and amenities.

Registration Deadline - 1 June 2010

Abstract Deadline - 28 June 2010

Conference Dates - 14-16 July 2010

For further information and registration, visit our website: http://oeec2010.jimdo.com/ and contact the the 2010 OEEC Planning Committee at oeec2010@laurentian.ca

dlesbarreres@laurentian.ca

LeedsU EvolutionSociety Sep7-9

The British Evolution Society Annual Meeting

7-9th September 2010, Leeds University, Leeds, UK

Abstract Submission is Open

SUBMIT YOUR ABSTRACT NOW: DEADLINE HAS BEEN EXTENDED TO MONDAY 10 MAY

http://abstracts.britishecologicalsociety.org/dass/-login.php Ensure you are part of the programme that includes renowned speakers such as ILKKA HANSKI, ALAN COVICH and MICHEL LOREAU.

We are also pleased to announce that ANDREW WATKINSON will be presenting the BES Lecture and CHARLES GODFRAY will be giving the Presidential Address.

And don't miss our exciting set of Thematic sessions:

Thematic Topic 1 : On the synthesis of size- and species- based approaches in community and ecosystem ecology Organiser: Richard Law and Julia Blanchard

Thematic Topic 2 : Ecological Networks: community robustness and persistence Organiser: Daniel B. Stouffer

Thematic Topic 3 : Marine Renewable Energy: the ecological implications of altering hydrodynamics Organiser: Mark Shields

Thematic Topic 4 : Understanding the impact of disturbance on plant communities Organiser: Tim Baker, Katy Roucoux, Geertje van der Heijden

Thematic Topic 5 : Promoting adaptation of species to global environmental change Organiser: Jane Hill, Chris D. Thomas and Barb Anderson

Thematic Topic 6 : Can species distribution modelling be predictive? Organiser: Drew W. Purves and Greg J. McInerny

Thematic Topic 7 : Advances in modelling ecological data Organiser: Dylan Childs and David Murrell

For more information on abstract submission, booking discounts, thematic topics and the venue, visit the Annual Meeting webpages.

http://www.britishecologicalsociety.org/meetings/-current_future_meetings/2010_annual_meeting/-index.php a.beckerman@sheffield.ac.uk

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Madison Florida SEPEEG Oct8-10

Colleagues in the southeastern US,

Early notice: Please mark your calendars for SEPEEG 2001: 8-10 October. SEPEEG is the Southeastern Population Ecology, Evolution, and Genetics meeting, to be held this year at Camp Cherry Lake in Madison, Florida. Details to follow.

Thanks, Charlie Baer & Marta Wayne

Charles F. Baer Department of Biology / University of Florida Genetics Institute 621 Bartram Hall P. O. Box 118525 University of Florida Gainesville, FL 32611-8525 USA

Office: 352-392-3550 Lab: 352-273-0143 Fax: 352-392-3704 Email: cbaer@ufl.edu web: http://www.biology.ufl.edu/People/faculty/cbaer.aspx cbaer@ufl.edu

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Norman Oklahoma SSB Jun17-21 CallSymposia

SECOND ANNOUNCEMENT

Society of Systematic Biologists Call for Symposia for the 2011 Annual Meeting

The Society of Systematic Biologists invites proposals for symposia at the 2011 Evolution meeting to be held in Norman, Oklahoma, from 17-21 June 2011. The meeting will be held jointly with the American Society of Naturalists and the Society for the Study of Evolution.

Proposals should include (1) a descriptive title, (2) one or two paragraphs explaining the purpose of the symposium and its relevance to systematics, (3) a list of presentations including proposed speakers, their institutions or affiliations, and their presentation titles, and (4) an indication of whether the speakers have been invited and whether they have agreed to participate.

Symposia are restricted to half-day sessions (6 half hour talks). 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 2010 annual meeting in Portland, Oregon. Soon after, organizers will be notified of the status of their proposals. Selected symposia will receive funds to partially defer participant costs or honoraria.

Deadline: for full consideration, please submit proposals by June 15, 2010.

E-mail proposals (Word or PDF format) to the Program Chairperson. Please use the subject heading: SSB Symposium Proposal.

Kelly R. Zamudio Department of Ecology and Evolutionary Biology Cornell University Ithaca, NY 14853 Email: kelly.zamudio@cornell.edu Phone: 607 254 4212

The program chair will confirm receipt of submitted proposals, please inquire if you do not receive e-mail confirmation.

kelly.zamudio@cornell.edu

Oregon PhylogeneticsEvolutionInformatics Jun29-30

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

The Software Bazaar features presenters demonstrating their software live on a laptop. At iEvoBio, this session takes the place of a poster session, and will be between 1.5-2 hours in duration. Conference attendees will be able to walk from one demonstration to the next and open a conversation with the presenters. Please also see our FAQ for this information (http://ievobio.org/faq.html#software). The Software Bazaar is part of the interactive afternoon program on the first conference day.

Entries should be software aimed at advancing research in phylogenetics, evolution, and biodiversity, and can include interactive visualizations that have been precomputed (such as SVGs, or Google Earth-compatible KML files).

Submissions consist of a title, which will typically be the name of the software (or visualization method) being presented, the URL of a website where more information about the software can be obtained, and the license under which the source code is available. The provided website must contain a link to where the source code (and possibly binaries) can be downloaded. If it is not obvious from the provided website, the submission must describe what the software does. Reviewers will judge whether a submission is within scope of the conference (see above), and need to be able to verify whether the open- source requirement(*) is met.

Presenters are expected to bring their own laptops for presentation, and any auxiliary devices necessary (such as a mouse). Power will be available at the presentation tables (110V/60Hz, US-style plugs; international presenters need to bring a suitable adaptor). Please let the organizing committee know as much in advance as possible if you expect to have unusually high demands for wireless network bandwidth. Note that commercial marketing activities are not permitted - presenters wishing to promote commercial or proprietary services or products should contact the Evolution conference about exhibitor space.

Review and acceptance of Software Bazaar submissions will be on a rolling basis. The deadline for submission is the morning of the first day of the conference (June 29). As the number of Software Bazaar presentation slots is finite, we cannot guarantee the availability of slots up until the day of the conference. We cannot accept submissions until the open-source requirements are met.

We ask all submitters of Software Bazaar presentations to be willing to also serve as reviewers of such, as described above.

Softwar Bazaar demonstrations are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Lightning talks, 3) Challenge entries, and 4) Birds-of-a- Feather gatherings. The Calls for Challenge entries (http://ievobio.org/challenge.html) and Lightning Talks (same submission URL as above) remain open, and information on the Birds-of-a-Feather session is forthcoming.

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

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

(*) iEvoBio and its sponsors are dedicated to promoting the practice and philosophy of Open Source software development (see http://www.opensource.org/docs/definition.php) and reuse within the research community. For this reason, software to be demonstrated to conference attendees must be licensed with a recognized Open Source License (see http://www.opensource.org/ licenses/), and be available for download, including source code, by a tar/zip file accessed through ftp/http or through a widely used version control system like cvs, Subversion, git, Bazaar, or Mercurial. Authors are advised that non-compliant submissions must be

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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

RutgersU EvolutionaryPopulationGenetics

New Directions in Evolutionary and Population Genetics

June 15-17, 2010

Rutgers University, Piscataway, NJ

URL http://www.biomaps.rutgers.edu/index.php?option=com_content&task=blogcategory&id=22&Itemidy Course Description The course is a three-day intensive investigation of evolutionary and population genetics. There will be sessions covering new research directions in protein evolution, human evolution, mathematical modeling and evolutionary genetics of model organisms.

To attend please submit a Registration form. There is no registration fee but registration is required. If you have any questions on the Summer School, need travel assistance, or help in arranging for hotel accommodations, please contact info@biomaps.rutgers.eduThis e-mail address is being protected from spam bots, you need JavaScript enabled to view it .

Inquiries - Please contact one of the organizers (emails at bottom of this message).

Schedule of Speakers

June15, Tuesday Morning Session: “Protein Evolution” 9:30 - 10:15 AM: Jody Hey (Rutgers University) 10:15 - 11:00 AM: Wei Wang (UCSD) 11:00 - 11:45 AM: Konstantin Zeldovich (UMass Medical School) 11:45 - 12:30 PM: Martin Weigt (Institute for Scientific Interchange) 12:30 - 2:00 PM: Lunch Break

Afternoon Session: “Functional Selection” 2:00 - 2:45 PM: Robert Trivers (Rutgers University) 2:45 - 3:30 PM: Chang Chan (Institute for Advance Study) 3:30 -4:00 PM: Break 4:00 - 4:45 PM: Daniel Segre (Boston University) 4:45 - 5:30 PM: Prashanth Ak (Institute for Advance Study)

June 16, Wednesday Morning Session: “Mathematical Models” 9:30 - 10:15 AM: Joshua Plotkin (UPenn) 10:15 - 11:00 AM: John Wakeley (Harvard University) 11:00 - 11:45 AM: Sergio Lukic (Rutgers University) 11:45 - 12:30 PM: Sang-Chul Choi (Rutgers University) 12:30 - 2:00 PM: Lunch Break

Afternoon Session: “Microbial Evolution” 2:00 - 2:45 PM: Joshua Rest (SUNY at Stony Brook) 2:45 - 3:30 PM: Paul Sniegowski (UPenn) 3:30 - 4:00 PM: Break 4:00 - 4:45 PM: Laura Landweber (Princeton University) 4:45 - 5:30 PM: Siobain Duffy (Rutgers University) 5:30 - 6:15 PM: Jesse Bloom (Cal Tech)

June 17, Thursday Morning Session: “Computational Methods” 9:30 - 10:15 AM: Adam Siepel (Cornell University) 10:15- 11:00 AM: Jeffrey Townsend (Yale University) 11:00- 11:45 AM: Itsik Pe'er (Columbia University) 11:45- 12:30 PM: Matthew Hahn (Indiana University) 12:30 - 2:00 PM: Lunch Break

Afternoon Session: “Human and Model Organism Evolution” 2:00 - 2:45 PM: Soojin Yi (Georgia Tech) 2:45 - 3:30 PM: Marcus Kronforst (Harvard University) 3:30 - 4:00 PM: Break 4:00 - 4:45 PM: Sarah Tishkoff (UPenn) 4:45 - 5:30 PM: Matthew Rockman (NYU)

Location: Life Sciences Auditorium, Life Sciences Building Busch Campus, Rutgers University, Piscataway, NJ Links for directions and travel: http://maps.rutgers.edu/building.aspx?1085 http://maps.rutgers.edu/directions/nb.aspx

Organizers: Kevin Chen, Rutgers University: kcchen@biology.rutgers Gyan Bhanot, Rutgers University: gbhanot@rci.rutgers.edu Jody Hey, Rutgers University: hey@biology.rutgers.edu Ronald Levy, Rutgers University: ronlevy@lutece.rutgers.edu Alexandre Morozov, Rutgers University: morozov@physics.rutgers.edu

The course is sponsored by the BioMaPS Institute for Quantitative Biology at Rutgers University. The National Institutes of Health provides partial funding of the BioMaPS Summer School through the NIH Roadmap for Medical Research, Grant 5 K07 GM72919. Information on this RFA, “Curriculum Development Award in Interdisciplinary Research” can be found at http://nihroadmap.nih.gov/ .

Jody Hey Professor, Department of Genetics Rutgers University Nelson Biological Labs (rm B326) 604 Allison Rd. Piscataway, NJ 08854-8082

732-445-5272 fax 732-445-5870

http://genfaculty.rutgers.edu/hey/home
hey@biology.rutgers.edu

Hey@Biology.Rutgers.Edu

RutgersU EvolutionaryPopulationGenetics FixedURL

URL (previous EVOLDIR posting had incorrect URL) http://www.biomaps.rutgers.edu/index.php?option=com_content&task=blogcategory&id=22&Itemidy New Directions in Evolutionary and Population Genetics

June 15-17, 2010

Rutgers University, Piscataway, NJ

Course Description The course is a three-day intensive investigation of evolutionary and population genetics. There will be sessions covering new research directions in protein evolution, human evolution, mathematical modeling and evolutionary genetics of model organisms.

To attend please submit a Registration form. There is no registration fee but registration is required. If you have any questions on the Summer School, need travel assistance, or help in arranging for hotel accommodations, please contact info@biomaps.rutgers.edu.

Inquiries - Please contact one of the organizers (emails at bottom of this message).

Schedule of Speakers

June15, Tuesday Morning Session: "Protein Evolution" 9:30 - 10:15 AM: Jody Hey (Rutgers University) 10:15 - 11:00 AM: Wei Wang (UCSD) 11:00 - 11:45 AM: Konstantin Zeldovich (UMass Medical School) 11:45 - 12:30 PM: Martin Weigt (Institute for Scientific Interchange) 12:30 - 2:00 PM: Lunch Break

Afternoon Session: "Functional Selection" 2:00 - 2:45 PM: Robert Trivers (Rutgers University) 2:45 - 3:30 PM: Chang Chan (Institute for Advance Study) 3:30 -4:00 PM: Break 4:00 - 4:45 PM: Daniel Segre (Boston University) 4:45 - 5:30 PM: Prashanth Ak (Institute for Advance Study)

June 16, Wednesday Morning Session: "Mathematical Models" 9:30 - 10:15 AM: Joshua Plotkin (UPenn) 10:15 - 11:00 AM: John Wakeley (Harvard University) 11:00 - 11:45 AM: Sergio Lukic (Rutgers University) 11:45 - 12:30 PM: Sang-Chul Choi (Rutgers University) 12:30 - 2:00 PM: Lunch Break

Afternoon Session: "Microbial Evolution" 2:00 - 2:45 PM: Joshua Rest (SUNY at Stony Brook) 2:45 - 3:30 PM: Paul Sniegowski (UPenn) 3:30 - 4:00 PM: Break 4:00 - 4:45 PM: Laura Landweber (Princeton University) 4:45 - 5:30 PM: Siobain Duffy (Rutgers University) 5:30 - 6:15 PM: Jesse Bloom (Cal Tech)

June 17, Thursday Morning Session: "Computational Methods" 9:30 - 10:15 AM: Adam Siepel (Cornell University) 10:15- 11:00 AM: Jeffrey Townsend (Yale University) 11:00- 11:45 AM: Itsik Pe'er (Columbia University) 11:45- 12:30 PM: Matthew Hahn (Indiana University) 12:30 - 2:00 PM: Lunch Break

Afternoon Session: "Human and Model Organism Evolution" 2:00 - 2:45 PM: Soojin Yi (Georgia Tech) 2:45 - 3:30 PM: Marcus Kronforst (Harvard University) 3:30 - 4:00 PM: Break 4:00 - 4:45 PM: Sarah Tishkoff (UPenn) 4:45 - 5:30 PM: Matthew Rockman (NYU)

Location: Life Sciences Auditorium, Life Sciences Building Busch Campus, Rutgers University, Piscataway, NJ Links for directions and travel: http://maps.rutgers.edu/building.aspx?1085 http://maps.rutgers.edu/directions/nb.aspx

Organizers: Kevin Chen, Rutgers University: kcchen@biology.rutgers Gyan Bhanot, Rutgers University: gbhanot@rci.rutgers.edu Jody Hey, Rutgers University: hey@biology.rutgers.edu Ronald Levy, Rutgers University: ronlevy@lutece.rutgers.edu Alexandre Morozov, Rutgers University: morozov@physics.rutgers.edu

The course is sponsored by the BioMaPS Institute for Quantitative Biology at Rutgers University. The National Institutes of Health provides partial funding of the BioMaPS Summer School through the NIH Roadmap for Medical Research, Grant 5 K07 GM72919. Information on this RFA, "Curriculum Development Award in Interdisciplinary Research" can be found at http://nihroadmap.nih.gov/ .

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Hey@Biology.Rutgers.Edu

Switzerland EvolEcolGenomicsAdaptation Sept2-3

Evolutionary and ecological genomics of adaptation

2-3 September 2010

Fribourg, Switzerland

Organizers: Christoph Haag and Christian Lexer, University of Fribourg Laurent Excoffier, University of Bern

Confirmed invited speakers:

* Roger Butlin (University of Sheffield, UK)

* Adam Eyre-Walker (University of Sussex, UK)

* Hopi Hoekstra (Harvard University, USA)

* Magnus Nordborg (Gregor Mendel Institute, Vienna,

Austria)

* David Reich (Harvard University, USA)

* Outi Savolainen (University of Oulu, Finland)

Natural environments differ in many biotic and abiotic aspects, and the way in which animals and plants adapt to these different environments is one of the fundamental questions of ecology and evolutionary biology. In recent years, new genetic and genomic methods have been developed, making it possible to discover the genes involved in such adaptations. This has facilitated many new exciting insights, for instance into

* the functional mechanisms of adaptation * the molecular evolution of adaptively important genes * the genetic architecture of evolving traits * the convergent evolution of similar phenotypic traits by distinct mutations * the ecology of speciation

We organize a symposium bringing together six invited speakers including top empirical and theoretical evolutionary biologists and a number of younger researchers to discuss recent developments in this fast developing field.

Deadline for contributed talk or poster submission: 30 June 2010 Deadline for registration without presentation: 15 August 2010

For more information on program, travel, venue, registration etc. please visit: http://www.unifr.ch/biol/ecology/adaptation_genomics/ Sponsored by: 3éme Cycle Romand en Sciences Biologiques, Conférence Universitaire de Suisse Occidentale (CUSO), University of Fribourg, University of Bern

Christoph Haag, Christian Lexer, Laurent Excoffier christoph.haag@unifr.ch

Christian Lexer Associate Professor of Evolutionary Biology University of Fribourg, Department of Biology Unit of Ecology & Evolution Chemin du Musée 10, CH-1700 Fribourg, Switzerland Tel (office) +41 (0)26 300 8868 Tel (lab): +41 (0)26 300 8895 Fax: +41 (0)26 300 9698 Email: christian.lexer@unifr.ch Web: http://www.unifr.ch/biol/ecology/lexer/index.html christian.lexer@unifr.ch

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Tuebingen ESEB2011 Aug20-25 CallSymposia

The 13th Congress of the European Society for Evolutionary Biology Tuebingen, Germany, 20-25 August 2011

is now online at www.eseb2011.de with some first important benchmarks. Check again in the autumn for details on registration and submission (we'll remind you).

CALL FOR SUBMISSION OF SYMPOSIUM PROPOSALS

A substantial part of the programme relies on the assistance of fellow-scientists like you, who are prepared to organize a symposium. This is a call to submit proposals by 31 July 2010.

Symposia typically start with one or two invited speakers (40 min) and are followed by submitted talks (20 min) (actual duration will be shorter to allow participants to change rooms). Symposia take place in one, two or a maximum of three 80-min windows. On special request, symposia can take the form of a discussion round or other more interactive forms of scientific exchange.

A symposium proposal consists of:

1. One organizer (for all communication) and one co-organizer (as a replacement) with contact details. Both are committed to attend the whole meeting. We do not provide financial support for organizing a symposium.

2. Topic: Anything related to short-term or long-term evolutionary change, with preference for well-defined, emerging fields or new trends in established fields. Please provide a short, tantalizing title as well as a 5-line summary that can be used for an online overview of symposia.

3. Proposal details: Summarize in max. 1 page why you think this makes a good subject for the next ESEB Congress and propose up to 4 possible (alternative) invited speakers (please check beforehand whether these people are available V a firm commitment is not yet necessary at this stage). If feasible, attach a list of possible submitted contributions (name + institution). ESEB will waive the registration fee for the (one or two) invited speakers in symposia. Please indicate whether you can generate financial support for accommodation or traveling of the guest speakers.

4. Time window: Explain why you want to apply for one, two or three 80- min time windows.

5. Submission: Send an email before 31 July 2010 to nico.michiels@uni- tuebingen.de. Proposals will be evaluated and selected by the Local Scientific Committee. We expect to decide on symposia by the end of October at the latest. Symposia proposals on overlapping subjects may be requested to fuse.

6. A call for contributed papers will be sent out in December 2010. Symposium organizers must be prepared to screen submissions for their symposium (online evaluation system).

Looking forward to receiving a broad spectrum of exciting proposals.

Yours, Nico Michiels

Nico Michiels, Prof. Dr. Animal Evolutionary Ecology Faculty of Biology Auf der Morgenstelle 28 72076 Tuebingen Germany

Tel. +49 7071 2974649 Fax +49 7071 295634 Mobile +49 170 4758003

nico.michiels@uni-tuebingen.de http://www.evoeco.uni-tuebingen.de http://www.eve.uni-tuebingen.de Nico Michiels <nico.michiels@uni-tuebingen.de>

UCaliforniaLosAngeles GenomicDiversity Jul22-24

14th Annual Genetics & Ethics in the 21st Century: Genomic Diversity and Health Disparities. July 22-24, 2010 The Stanley Hotel Estes Park, Colorado

Sponsored By: University of Colorado Denver, University of California Los Angeles, Case Western Reserve University

Featured Speakers: - Rick Kittles, Department of Medicine, University of Chicago, “The Role of Diverse Populations in Understanding Cancer Disparities” - Sandra Soo-Jin Lee, Stanford Center for Biomedical Ethics, Stanford University. “The Search for Difference: Personalized Medicine and its Implications for Health Disparities” - Jeffrey C. Long, Department of Anthropology, University of New Mexico, “Genetic Ancestry and Race and Their Implications for Health Disparities” - Patrick Boudreault, Deaf Studies Department, California State University Northridge, and Christina Palmer, Psychiatry and Biobehavioral Sciences, Human Genetics, and the Center for Society and Genetics, UCLA, “Genetics and Deaf Communities” - Ed McCabe, Pediatrics, Human Genetics, and Center for Society and Genetics, UCLA; Physician-in-Chief, Mattel Children’s Hospital, “Ancestry and Identity: From Recreational Genetics to Personalized Medicine”

This is a call for abstracts for the fourteenth conference in an annual series that addresses current ethical, societal and legal issues related to human genetics. The focus of this year’s conference is on the issues surrounding new genomic technologies allowing for large-scale ancestry testing and health risk assessments, and how these technologies are co-evolving with societal and legal understandings about human diversity and health disparities across groups. Are the new technologies paving the way for personalized genomics, providing new identities and destabilizing old identities to individuals and groups, re-instituting biological determinism? The conference will consider multiple facets of human diversity, and how different groups and constituencies experience health disparities and are affected by new medical technologies for population screening.

The deadline for abstract submissions is MAY 21th, 2010. Please submit abstracts (250 word max.) to Ana Wevill ana@socgen.ucla.edu<mailto:ana@socgen.ucla.edu> You will be notified about your submission by June 1st. We are soliciting papers, panels and posters (note your preference in your submission). We encourage life and social scientists, ethicists, health care professionals and physicians, historians, legal professionals and students to consider a submission. Paper and poster sessions may include, but are not limited to: Ancestry Testing; Population Screening; Ancestry and Cancer; Genomics and Health Disparities in African-American, Latino/a, Asian and Native American Communities; Health Disparities in Diverse Communities.

For more information please contact: Jessica Lynch Alfaro, Ph. D. Associate Director UCLA Center for Society and Genetics 1321 Rolfe Hall Los Angeles CA 90095-7221 310 206 1889 http://www.socgen.ucla.edu/lynchalfaro@ucla.edu Janet@mednet.ucla.edu

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UColorado HumanGenomicDiversity Jul22-24

14th Annual Genetics & Ethics in the 21st Century: Genomic Diversity and Health Disparities. July 22-24, 2010 The Stanley Hotel Estes Park, Colorado

Sponsored By: University of Colorado Denver, University of California Los Angeles, Case Western Reserve University

Featured Speakers: - Rick Kittles, Department of Medicine, University of Chicago, “The Role of Diverse Populations in Understanding Cancer Disparities” Sandra Soo-Jin Lee, Stanford Center for Biomedical Ethics, Stanford University. “The Search for Difference: Personalized Medicine and its Implications for Health Disparities” Jeffrey C. Long, Department of Anthropology, University of New Mexico, “Genetic Ancestry and Race and Their Implications for Health Disparities” Patrick Boudreault, Deaf Studies Department, California State University Northridge, and Christina Palmer, Psychiatry and Biobehavioral Sciences, Human Genetics, and the Center for Society and Genetics, UCLA, “Genetics and Deaf Communities” Ed McCabe, Pediatrics, Human Genetics, and Center for Society and Genetics, UCLA; Physician-in-Chief, Mattel Children’s Hospital, “Ancestry and Identity: From Recreational Genetics to Personalized Medicine”

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The deadline for abstract submissions is Monday, May 10th, 2010. Please submit abstracts (250 word max.) to Ana Wevill ana@socgen.ucla.edu You will be notified about your submission by June 1st. We are soliciting papers, panels and posters (note your preference in your submission). We encourage life and social scientists, ethicists, health care professionals and physicians, historians, legal professionals and students to consider a submission. Paper and poster sessions may include, but are not limited to: Ancestry Testing; Population Screening; Ancestry and Cancer; Genomics and Health Disparities in African-American, Latino/a, Asian and Native American Communities; Health Disparities in Diverse Communities.

For more information please contact: Jessica Lynch Alfaro, Ph. D. Associate Director UCLA Center for Society and Genetics 1321 Rolfe Hall Los Angeles CA 90095-7221 310 206 1889 http://www.socgen.ucla.edu/lynchalfaro@ucla.edu IMPORTANT WARNING: This email (and any attachments) is only intended for the use of the person or entity to which it is addressed, and may contain information that is privileged and confidential. You, the recipient, are obligated to maintain it in a safe, secure and confidential manner. Unauthorized redisclosure or failure to maintain confidentiality may subject you to federal and state penalties. If you are not the intended recipient, please immediately notify us by return email, and delete this message from your computer.

Janet@mednet.ucla.edu

ULaval CanSocEcolEvol May9-12

Canadian Society for Ecology and Evolution 2010 Annual Meeting, University of Laval, Quebéc City, May 9-12

REGISTRATION REMINDER: There is still time to register for the 2010 CSEE Annual meeting in Québec City. We still have available slots for posters. However, titles must be received by April 16th to be listed in the printed program. We would appreciate receiving as soon as possible the remaining registrations such that we can finalise the arrangements for the social events.

You can register online at: http://www.scee2010.ulaval.ca/meeting.htm We are looking forward to hosting you in Québec!

Local Organizing Committee: Louis Bernatchez, Nadia Aubin-Horth, Stéphane Boudreau, Nathalie Brodeur, Steeve Côté, Christian Landry, Eric Normandeau, Julie Turgeon, Jeff Hutchings

Société Canadienne d’Écologie et d’Évolution Congrès annuel 2010, Université Laval, Québec, 9-12 mai

DERNIER RAPPEL POUR L’INSCRIPTION: Il est encore temps de vous inscrire pour participer à la réunion annuelle 2010 de la SCEE à Québec. Il reste encore des places disponibles pour présentation d’affiches. Notez cependant que les titres reçus après le 16 avril ne seront pas être listés dans le programme imprimé. Aussi, nous aimerions recevoir les dernières inscriptions dès que possible afin de finaliser les arrangements pour les diverses activités sociales.

Vous pouvez vous inscrire en ligne à : http://www.scee2010.ulaval.ca/meeting_fr.htm Au plaisir de vous recevoir à Québec!

Comité organisateur: Louis Bernatchez, Nadia Aubin-Horth, Stéphane Boudreau, Nathalie Brodeur, Steeve Côté, Christian Landry, Eric Normandeau, Julie Turgeon, Jeff Hutchings

Louis Bernatchez Chaire de recherche du Canada en Génomique et Conservation des Ressources Aquatiques

Département de biologie, Institut de Biologie Intégrative et des Systèmes (IBIS) Pavillon Charles-Eugène-Marchand 1030, Avenue de la Médecine Local 1145 Université Laval Québec (Québec) G1V 0A6 Canada

Tél.: 1 418 656-3402 Téléc.: 1 418 656-7176 Courriel: Louis.Bernatchez@bio.ulaval.ca Web: http://www.bio.ulaval.ca/louisbernatchez/ Louis.Bernatchez@bio.ulaval.ca

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ULisbon PolyploidEvolution Nov11-12

Dear colleagues,

The website of the THE INTERNATIONAL MEETING ON THE GENETICS OF POLYPLOIDS is now available.

http://polyploidymeeting.fc.ul.pt/ The INTERNATIONAL MEETING ON THE GENETICS OF POLYPLOIDS aims at promoting knowledge exchange and discussions on the latest developments regarding the field of polyploidy. The meeting will take place next November11th-12th, 2010 at the Faculdade de CiÃncias, Universidade de Lisboa (FCUL).

The main topics to be covered in the meeting will be gene expression, genome dynamics, sex and reproduction, and will include subjects such as epigenetics, gene regulation, genome structure and evolution, heterosis, sexual differentiation and determination will be covered.

This international meeting will feature outstanding speakers in the field of polyploidy such as Luca Comai, UC Davis, USA; James Bogart, University of Guelph, Canada; Manfred Schartl, University of Wuerzburg, Germany; Roger Butlin, University of Sheffield, UK.

We would greatly appreciate your collaboration in helping us promote this meeting.

International meeting on the genetics of polyploidshttp://t2.gstatic.com/images?q=-tbn:zveCAWSFlXy8DM:http://www.freed igitalphotos.net/images/photos/kiwi-fruit-halves.jpg

Angela InÃcio <mainacio@fc.ul.pt>

UOttawa ComparativeGenomics Oct9-11

SECOND CALL FOR PAPERS

Eighth Annual RECOMB Satellite Meeting on Comparative Genomics

October 9-11, 2010

University of Ottawa

http://recombcg.uottawa.ca/recombcg2010/ Comparison of related genomes offers enormous inferential power, revealing a wealth of knowledge about genome evolution itself and about genetic function and cellular processes. As the number of fully sequenced genomes grows, so do the opportunities and challenges for computational comparative genomics. This workshop brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and novel experimental results. The program will include both invited speakers and contributed talks.

KEYNOTE SPEAKERS

Brenda J. Andrews (University of Toronto) Andrew G. Clark (Cornell University) Nicolas Corradi (University of British Columbia) Jan Dvorak (University of California at Davis) Aoife McLysaght (University of Dublin) Nicholas Putnam (Rice University)

Contributions to this computationally-oriented workshop are welcomed on any theoretical and/or empirical approach to genome-wide comparison such as genome evolution, algorithms for genome rearrangement, comparative tools for assembly, gene identification or annotation, comparison of functional networks, genomic variation in humans and model organisms, cancer genomics, duplication patterns of genes, segments and whole genomes, and comparative epigenetics. To compete for a place in the program, papers should be submitted electronically at

https://www.easychair.org/login.cgi?conf=-3Drecombcg10 in order to be rated by a distinguished program committee.

The workshop will be held on the campus of the University of Ottawa beside the downtown area. Ottawa is served by direct flights from New York, Philadelphia, Chicago, Washington, Detroit, London, Frankfurt and many Canadian cities. The dates of the workshop coincide with the three-day Canadian Thanksgiving weekend, around the peak time for autumn foliage colour.

KEY DATES

Paper submission deadline June 7, 2010

Notification of paper acceptance June 28, 2010

Final manuscript due July 16, 2010

Poster submission deadline September 17, 2010

Notification of poster acceptance September 21

STEERING COMMITTEE

Jens Lagergren (Stockholm Bioinformatics Centre and CSC, KTH, Sweden) Aoife McLysaght (University of Dublin, Ireland) David Sankoff (University of Ottawa, Canada)

CONFERENCE CHAIR

David Sankoff (University of Ottawa)

PROGRAM COMMITTEE CHAIR

Eric Tannier (INRIA Rhône-Alpes, France)

PROGRAM COMMITTEE

LOCAL ORGANIZING COMMITTEE Anne Bergeron (Université du Québec à Montréal) Frank Dehne (Carleton University) Guy Drouin (University of Ottawa) Nadia El-Mabrouk (Université de Montréal) Evangelos Kranakis (Carleton University) Marcel Turcotte (University of Ottawa)

PROGRAM COMMITTEE Lars Arvestad (Royal Institute of Technology, Sweden) Anne Bergeron (Université du Québec à Montréal) Mathieu Blanchette (McGill University) Guillaume Blin (Université Paris-Est, France) Guillaume Bourque (Genome Institute of Singapore) Marilia Braga (University of Bielefeld, Germany) Michael Brudno (University of Toronto) Jeremy Buhler (Washington University) Sèverine Bérard (INRA Toulouse, France) Cedric Chauve (Simon Fraser University) Aaron Darling (University of Queensland, Australia) Niklas Eriksen (Göteborg University, Sweden) Patricia Evans (University of New Brunswick) Guillaume Fertin (Université de Nantes, France) Matthew Hahn (Indiana University) Joao Meidanis (UNICAMP, Brazil Bernard Moret (Ecole Polytechnique Fédérale de Lausanne, Switzerland) Craig Nelson (University of Connecticut) Aida Ouangraoua (Simon Fraser University) Michal Ozery-Flato (University of Tel-Aviv, Israel) Teresa Przytycka (NCBI) Eric Rivals (LIRMM & CNRS) Eduardo Rocha (Université Paris 6 et Institut Pasteur, France) Hugues Roest Crollius (Ecole Normale Supérieure, France) Jens Stoye (Universität Bielefeld, Germany) Krister Swenson (University of Ottawa) Glenn Tesler (UC San Diego) Elisabeth Tillier (University of Toronto) Stéphane Vialette (Université Paris-Est, France) Sophia Yancopoulos (The Feinstein Institute for Medical Research, New York) Louxin Zhang (National University of Singapore)

CALL FOR PAPERS

Papers should be submitted via the EasyChair system. Submissions must be received in electronic form by 11:59pm (any time zone), June 7, 2010. https://www.easychair.org/login.cgi?conf=-3Drecombcg10 Submissions should be no longer than 12 single-spaced 8.5“x 11” pages with 1.25-inch margins all around, everything included (title,

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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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UOxford Avian July

The Edward Grey Institute, in the Dept of Zoology, University of Oxford, is hosting two international Ornithological meetings in July 2010:

The SIXTH INTERNATIONAL HOLE-NESTING BIRDS CONFERENCE will be held at Lady Margaret Hall (one of the Colleges of the University of Oxford, close to the city's historic centre) from 13-15 July.

Following successful meetings in The Netherlands (twice), Corsica, Switzerland and Poland, the Sixth International Hole Nesting Bird Conference is taking place at Lady Margaret Hall, Oxford from 13th July - 15th July 2010. The meeting will open with registration and a drinks reception and buffet on 13 July at Lady Margaret Hall College, and then last two full days (14th/15th July) and will provide a forum for recent studies of ecology, evolution and behaviour of all hole-nesting species, temperate or tropical, and of purely academic or more applied interest. Social events include a guided trip to Wytham Woods and barbeque, and plenary speakers include Christiaan Both, Erik Matthysen, James Reynolds & Ben Sheldon.

Immediately following this, on 16 July 2010, is the DAVID LACK CENTENARY SYMPOSIUM, to be held in the Department of Zoology, University of Oxford, to mark the centenary of the birth of David Lack on 16 July 1910. A programme of invited talks will focus on, and celebrate, the scientific contributions of David Lack to Ornithology, and the broader fields of Ecology and Evolution, and assess the development of these fields in the 21st century. Speakers include: Prof Thomas Alerstam, Prof Ted Anderson, Prof Tim Birkhead, Prof Ben Hatchwell, Dr Andrew Lack, Prof Ian Owens, Prof Chris Perrins, Prof Trevor Price, Prof Simon Verhulst. The meeting will conclude with a reception and Banquet at Wadham College.

Further details of both meetings can be found at:

http://www.zoo.ox.ac.uk/egi/newsevents/-2010conferences.html We look forward to welcoming you in Oxford this summer.

ben.sheldon@zoo.ox.ac.uk

WoodsHole CytochromeBiodiversity Oct3-7

We are pleased to announce the

10th International Symposium on Cytochrome P450 Biodiversity and Biotechnology, 3-7 October 2010 in Woods Hole, Massachusetts, USA.

This symposium addresses all aspects of cytochrome P450 biodiversity, biotechnology, and evolution. The overall goal of this 10th symposium is to foster a synthesis of understanding of cytochrome P450 (CYP) structural and functional evolution, and new directions in application of this knowledge in environmental assessment, remediation, and synthesis of new potential drugs.

Sessions in this meeting include evolutionary and mechanistic comparisons among available P450 structures, functional comparisons among microbial, insect and plant P450s in synthetic and detoxification pathways, as well as bioengineering of P450 catalytic sites for technological and environmental applications.

Presentations (talks and posters) by graduate students and post-docs are strongly encouraged.

Abstract Submission and Registration are now open ##### http://www.whoi.edu/-conferences/p450 Abstract Deadline is August 1, 2010

A list of plenary speakers will be posted in the coming weeks. We hope to welcome you to Woods Hole in October!

Please share this announcement with students and colleagues.

John Stegeman and Jed Goldstone, Woods Hole Oceanographic Institution Mary Schuler and Stephen Sligar, University of Illinois, Urbana-Champaign p450@whoi.edu

jedgold@gmail.com

GradStudentPositions

Dublin MammalEvolution

Dear All,

Applications are invited for a 4-year PhD position to study the evolution of innate immunity in mammalian clade the Bioinformatics and Molecular Evolution Group at Dublin City University, Ireland.

Suitable candidates will have a background in genetics/mathematics/computer science/evolutionary biology, have a keen interest in molecular evolution and must be highly motivated.

For further information please contact Dr Mary O'Connell directly (email given below).

If you are interested in applying for the position, please send your CV (with referee detailsx2) and personal statement to mary.oconnell@dcu.ie

Application deadline: 30th May 2010. Project start mid-late September 2010.

Best wishes,

Mary

Dr Mary J. O'Connell, Bioinformatics and Molecular Evolution Group leader, Chair of Bioinformatics DCU, School of Biotechnology, Dublin City University, Glasnevin, Dublin 9.

Phone: +353 1 700 5112 Fax: +353 1 700 5412 Email: mary.oconnell@dcu.ie website: http://bioinf.dcu.ie dr mary o'connell <mary.oconnell@dcu.ie>

Edinburgh 2 FungalPathogenEvolution

Hi all, these 2 PhD studentships are available for EU citizens:

PhD Studentship 1

What is driving the rapid evolution of Ramularia collo-cygni?

Scottish Agricultural College

Scottish Agricultural College and BASF

Ramularia collo-cygni is a pathogen of increasing importance on barley crops in Northern Europe and can cause significant yield losses. This Project will use a combination of lab and field based experimentation to develop increased understanding of the biology of this pathogen. The use of population genetic markers will be deployed to examine the variation found in populations, whilst examining the functionality and evolutionary potential of the asteromella stage of the fungus. This studentship is fully funded by BASF and will be based at SAC, whilst being registered at the University of Edinburgh.

This postgraduate position is for three years, with a proposed start date of October 2010, ending October 2013. The full award (stipend and fees) is available to EU Citizens only.

The successful candidate must have or expect to obtain a minimum of an upper second class degree in a scientific discipline from a UK University or equivalent. They should have familiarity and demonstrated use of current Windows office packages. and data handling packages. Oral and writing skills in English are required to a high standard. A valid EU driving license is also desirable.

The studentship offers a stipend of £13290 per annum. The student will be based at the SAC, King's Buildings, West Mains Road, Edinburgh, EH9 3JG.

Application packs are available from Frances Stratford (frances.stratford@sac.ac.uk) quoting reference SAC/CSS/BASF

For further particulars or to have an informal discussion about this studentship, contact Dr Neil Havis neil.havis@sac.ac.uk (0131 535 4136) or Dr James Fountaine james.fountaine@sac.ac.uk (0131 535 4370) SAC, West Mains Road, Edinburgh EH9 3JG.

Closing date for the return of applications is 9 July 2010

PhD Studentship 2

Scottish Agricultural College

Scottish Agricultural College and Syngenta Crop Protection

Characterisations of mutations in the succinate dehydrogenase gene for potential fungicide resistance development in Ramularia collo-cygni populations.

This postgraduate position is for three years, with a proposed start date of October 2010, ending October 2013. The full award (stipend and fees) is available to EU Citizens only.

Ramularia collo-cygni is a pathogen of increasing importance on barley crops in Northern Europe. It is a disease that occurs late in the season and is characterised by small necrotic spots, usually with a yellow halo. Recently, Syngenta Crop Protection have launched a new succinate dehydrogenase inhibitors (SDHI) fungicide, this project will characterise the potential mutations in R. collo-cygni that could cause fungicide resistance with the use of lab derived mutants. The implications of these mutants and 'wild type' samples will then be assessed using a range of bioassays, field and glasshouse experiments and high-throughput genotyping (such as pyrosequencing), additionally population genetic markers will also be developed to help understand the potential impact of resistance on the wider populations of R. collo-cygni at a plot, field and a wider scale. This project is a jointly funded project between SAC and Syngenta Crop Protection and will be registered at the University of Edinburgh.

The successful candidate must have or expect to obtain a minimum of an upper second class degree in a scientific discipline from a UK University or equivalent. They should have familiarity and demonstrated use of current Windows office packages. and data handling packages. Oral and writing skills in English are required to a high standard. A valid EU driving license is also desirable.

The studentship offers a stipend of £13290 per annum. The student will be based at the SAC, King's Buildings, West Mains Road, Edinburgh, EH9 3JG.

Application packs are available from Frances Stratford (frances.stratford@sac.ac.uk) quoting reference SAC/CSS/Syng

For further particulars or to have an informal discussion about this studentship, contact Dr James Fountaine, james.fountaine@sac.ac.uk (0131 535 4370) or Dr Fiona Burnett, fiona.burnett@sac.ac.uk (0131 535 4133) SAC, West Mains Road, Edinburgh EH9 3JG.

Closing date for the return of applications is 9 July 2010

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Peter Hoebe <Peter.Hoebe@sac.ac.uk>

ETH Switzerland AquaticAdaptation

Eawag is the Swiss Federal Institute for Aquatic Science and Technology, a Swiss-based and internationally operating aquatic research institute within the ETH domain.

The Department of Aquatic Ecology seeks to recruit a : PhD student in Aquatic Ecosystems Ecology

The PhD student will be funded by a Swiss National Science Foundation grant, entitled “Responses of Aquatic Food Webs and Ecosystems to Global Environmental Change”.

The aim of the project is to understand how environmental change will affect the functioning of aquatic ecosystems. The project involves large-scale experiments that manipulate the ecological and evolutionary diversity of food webs under contrasting environmental conditions (e.g. temperature, inorganic nutrients, and dissolved organic matter). The project is broadly focused on aquatic food webs, so the student may work on microbial, phytoplankton, zooplankton, and fish communities. Ultimately, the research addresses fundamental links between the ecology and evolution of food webs and the physical environment and biogeochemistry of ecosystems.

We are looking for a self-directed and motivated student with a broad interest in ecology, evolution, and/or ecosystem science. Ideally, the student will be interested in fieldwork, microbial communities and food-web experiments.

Eawag is an international research institute, and is closely affiliated with top universities that grant PhD degrees, such as ETH-Zurich. The working language of the department is English. We offer a stimulating research environment in the Aquatic Ecology department, which has locations in Dübendorf (near Zurich) and

Kastanienbaum (near Lucerne). Located on the shores of Lake Lucerne, Eawag's Center for Ecology, Evolution & Biogeochemistry (CEEB) is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science. At both locations, the student will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science. The project will also involve collaborations between researchers at Eawag (Dr. Blake Matthews, Dr. Mark Gessner, and Dr. Helmut Bürgmann) and the University of Vienna (Dr. Christian Winter, and Dr. Gerh ard Herndl).

The starting date for the PhD student is flexible, but a starting date in 2010 is preferred. The PhD program at ETH-Zurich generally lasts three years. Applications should include a cover letter, a curriculum vita, and three references. Copies of prior publications or theses will also be considered if made available via PDF.

Please submit your application by 1 July 2010 as a single PDF file to Sandra Isenring, Eawag, Human Resources Department (recruiting@eawag.ch), indicating reference number 104402.

For further information: please visit Eawag's website (http://www.eawag.ch) contact Dr. Blake Matthews by email (blake.matthews@eawag.ch) or visit his website (http://homepages.eawag.ch/˜matthebl)

Blake.Matthews@eawag.ch

GoetheU Biodiversity

The Biodiversity and Climate Research Centre (BiK-F)has recently been founded by the Senckenberg Gesellschaft fuer Naturforschung,the Goethe-University Frankfurt am Main, and additional partners. It is fundedby the Federal State of Hesse through its Initiative for the Development ofScientific and Economic Excellence (LOEWE). The mission of the Centre is tocarry out internationally outstanding research on the interactions ofbiodiversity and climate change at the organism level. The Project Area C "Adaptation and Climate"invites applications for the position of a

PhD position Effector evolution in plant pathogens± Project C2.5 [Ref. #C39] TV-H E 13 (50%)

The main subject of the advertised position will be the elucidation ofevolutionary processes in the Hyaloperonosporaarabidopsidis species cluster, with focus on the evolution of effectorgenes during adaptation and radiation of downy mildews. The project willinvolve population genetics, genomics, and functional analyses.

The applicant should hold a diploma, masters orequivalent degree (e.g. BSc with honours) in biology, genetics, plant pathology, bioinformatics or a similar field of study. Experience in molecularbiology (PCR, molecular cloning) is a prerequisite. Knowledge in populationgenetics, plant pathology or molecular phylogenetics is an advantage. Advanced English language skills and an interest in joining amultidisciplinary research team are required. Knowledge of German is anadvantage, and at least the willingness to learn basic German is required.

Salary and benefits are according to a public serviceposition in Germany (TV-H E 13, 50%). The Research Centre BiK-F advocates gender equality.Women are therefore strongly encouraged to apply. Equally qualified severelyhandicapped applicants will be given preference. The contract shall begin 1st of July, 2010 and will berestricted to three years. The duty station will be Frankfurt am Main, Germany.The employer is the Senckenberg Gesellschaft fUEr Naturforschung. Please send your application by e-mail, mentioning the reference of this position (#C39) including a detailed CV, certificates, and 2references, before June 1st to: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific CoordinatorBiodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurtam Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de. For enquiries about the position and the contract conditions pleasewrite to Prof. Dr. B. Stribrny (e-mail: bernhard.stribrny@senckenberg.de)and for scientific enquiries to Prof. Dr. M. Thines (e-mail: marco.thines@senckenberg.de).

Frankfurt a. M., 17.03.2010 Prof. Dr. M. T^{1}rkay

Many thanks and best wishes, Marco

Prof. Dr. Marco Thines Biodiversity and Climate Research Centre (BiK-F) Gerog-Voigt-Str. 14-16 (visitors) Senckenberganlage 25 (mail) D-60325 Frankfurt Germany

Tel.: +49 6975421833

Marco Thines <Marco.Thines@senckenberg.de>

Groningen EvolutionaryGenetics

PhD position Evolutionary Genetics (1,0 fte)(210200)

Organisation The vacancy is at the Evolutionary Genetics group at the Centre for Ecological and Evolutionary Studies (CEES), Faculty of Mathematics and Natural Sciences, University of Groningen. Areas of research include speciation, evolution of reproductive and sex determination systems, and life-history evolution; main model organisms are the parasitic wasps Nasonia and Asobara, and the fruit fly Drosophila. The group provides a lively, internationally oriented, scientific environment with excellent facilities.

Job description The characterization of sex determining mechanisms has recently become feasible in a broader range of organisms due to advent of new molecular techniques, in particular the availability of whole genome sequences. To identify the mechanisms by which sex determining mechanisms can change requires further characterization of gene networks of a larger array of organisms in a phylogenetic context. Our research focuses on sex determination in haplodiploid organisms with the parasitic wasp Nasonia as model organism. In this PhD project we will investigate the genetic basis of sex determination in Asobara wasps, which are known to have multiple different forms of sex determination. We will develop molecular marker (microsatellite, SNP) maps to fine scale map sex loci using genetic crosses. We will use a functional genomics approach to identify sex determination genes using RNA sequencing and bioinformatic essays for candidate genes followed by functional and expression analyses (qPCR, RNAi).

Requirements We are looking for a masters or equivalent degree in biology with preferably a strong background in evolutionary and molecular genetics. The project is expected to be very demanding and asks for a creative mind. The candidate should have a strong interest in experimental molecular work on insects. Good proficiency of the English language is required. The candidate will be enrolled in Groningen Graduate School of Science, attend graduate courses within the Research School Ecology and Evolution and assist in teaching (10% of time).

Secundary The University of Groningen offers a salary of 2042 gross per month in the first year up to a maximum of 2612 gross per month in the final year. The full time appointment is temporary for 1.5 years with the perspective of prolongation with another 2.5 years. Objective of the temporary 4-year position is a number of research articles in peer-reviewed scientific journals, which together will form the basis of the thesis leading to the granting of the PhD degree (Dr) at the University of Groningen. After the first year, there will be an evaluation as to the feasibility of successful completion of the PhD thesis within the next three years.

The position is funded by a TOP grant of the Netherlands Organization for Scientific Research (NWO) and embedded in a research programme on haplodiploid sex determination that includes a postdoc project and technical support.

We would like to receive letters in Dutch or English, including the personal motivation for the position, a curriculum vitae along with names and addresses, including telephone/fax and e-mail addresses, of three referees.

For more information please contact: Prof. L.W. Beukeboom, l.w.beukeboom@rug.nl Dr L. van de Zande, louis.van.de.zande@rug.nl

Dr. Bart A. Pannebakker

Evolutionary Genetics Centre for Ecological and Evolutionary Studies University of Groningen P.O. Box 14 NL-9750 AA Haren The Netherlands Phone +31 50 363 8099 Fax +31 50 363 2348 Email b.a.pannebakker@rug.nl http://www.rug.nl/biologie/-onderzoek/onderzoekgroepen/evolutionarygenetics/-people/Pannebakker bartpannebakker@gmail.com

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ImperialCollege London NetworkBiology

*PhD Studentship in Network Biology Department of Computing, Imperial College London * *PhD Studentship: *Untaxed bursary of £15,200 per annum plus UK/EU fees. UK nationals are eligible. EU nationals are only eligible for the bursary if they meet the EPSRC requirement of having been in the UK for three years immediately prior to starting the PhD. Details can be found at http://www.epsrc.ac.uk/-PostgraduateTraining/StudentEligibility.htm

Fixed Term for 3 years, starting October 2010.

Imperial College is ranked in the top five universities of the world, according to the 2009 Times Higher Education World University Rankings. It has particular strength in Engineering, Natural Sciences, Life Sciences and Biomedicine, and was ranked the 6th in the world in technology, the 10th in the world in natural sciences, and 17th in the world in life sciences and biomedicine in the Times Higher Education World University Rankings, October 2009. The *Department of Computing *is one of the largest computing departments in the UK and is a world leader in academic research in computer science. The department has been awarded the top rating (5*) in each of the Research Assessment Exercises undertaken by the Higher Education funding Council for England (HEFCE). There are over sixty academic staff actively involved in research, creating a lively and stimulating atmosphere. The department also enjoys strong links with UK industry, which helps to ensure that its research and teaching is well informed and relevant to the needs of society. Imperial College London has active research in *systems biology *and related scientific disciplines. Over 60 academic appointments were made over the past decade at the interface between the life and physical sciences. The College also has substantial high performance computing resources.

We have a PhD studentship starting in October 2010 to work on topics at the intersection of computing, graph algorithms and systems biology. The position is for three years, and covers fees and a tax-free bursary with London weighting. An ideal candidate will have research interests in the following areas:

Large-scale data analysis and modeling

Systems biology

Network analysis and modeling

Graph algorithms

Parallel computing

The PhD studentship, under the supervision of Dr. Natas(a Prz(ulj, involves the development of new computational graph theoretic and modelling approaches applied to large-scale problems in systems and synthetic biology, proteomics, cancer informatics, and chemoinformatics. Analysis and modelling of large networked systems, such as protein-protein interaction and transcriptional regulation networks, will be performed, focusing on developing new methods for network alignment, network integration, as well as other techniques for deciphering large-scale systems biology data sets to improve biological understanding, get insights into disease and improve therapeutics. For more information about the project, see http://www.doc.ic.ac.uk/˜natasha/ . The project will interface with related programs and institutes at Imperial College, including the Institute of Systems and Synthetic Biology, the Centre for Bioinformatics, and the Centre for Integrative Systems Biology (CISBIC). Informal inquiries can be directed to: Dr. Natas(a Prz(ulj (natasha@imperial.ac.uk).

Applicants should have at least a distinction or first in a Masters level degree in computer science, or an equivalent degree in mathematics, physics, engineering, bioinformatics, or a related discipline. A good background in graph theory, mathematics, computing (knowledge of algorithms, C, C++, Linux, and a scripting language) would be advantageous. Some knowledge of biology and bioinformatics are desirable. Applicants must be fluent in spoken and written English. For further information on the PhD degree, see http://www3.imperial.ac.uk/computing/research/degrees . Applications *must *include the following:

A College application form, which can be obtained from http://www3.imperial.ac.uk/pgprospectus/applicationforms . A 2-3 page research statement that describes what you see as interesting research issues relating to this studentship and what relevant experience you have.

A detailed CV.

Transcripts of all degree results.

2 recent letters of reference.

To submit your application for this PhD studentship, please follow the

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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

INRA Nancy FungalPopulationGenomics

PhD position in Population Genomics of Fungi

I am looking for a highly motivated candidate to work on a population genetic/genomic project in the plant pathogenic species Melampsora larici-populina (responsible for the poplar rust). The aim of the PhD is to highlight the virulence factors of this fungal plant pathogen from a population genomic approach. Candidates should have a good background in evolutionary ecology and above all population genetics. Knowledge on host parasite interactions would be appreciated. Interest (but not necessarily good skills) in molecular biology (next generation sequencing) is required.

The proposed project stand at the core of the joint unit Tree-Microorganism interactions and lie at the interface of its two major teams “ecology and population biology of tree fungal pathogens (directed by B. Marçais) and ”eco-genomic“ (directed by F. Martin). The junior scientist will thus benefit from the complementary skills and resources of these two teams, including advanced population genetics knowledge, large and historical population sampling on one hand and, on the other hand, great genomic tool and molecular resources, including genome sequence and transcriptomic analyses performed on this model pathogen species.

The subject has been selected for application as "Young scientist contracts" which result from a partnership between INRA and graduate schools. These contracts have initial duration of 3 years (PhD) and can be renewed for 2 more years for a post doc project (including necessarily a period of time abroad). Young scientist contracts have very attractive remuneration conditions. Before obtaining his/her PhD, the doctoral student receives 2055? (gross) per month. After obtaining his/her PhD, the remuneration is 2373? (gross) per month. An annual bonus of 796? is paid half-yearly. More details on young scientist contracts can be found at http://www.international.inra.fr/join_us/positions/research_training_positions/young_scientist_contracts__1 Successful candidate will be selected by an examination committee of the graduate school RP2E (Nancy). All details on how to apply can be found at (French and English version underneath). http://www.rp2e.inpl-nancy.fr/index.php?id=5 The competitive examination is open to any nationality. Dead line for application is May 15th. Position will start in fall 2010.

Don't hesitate to contact me for any query (halkett@nancy.inra.fr).

Below is the abstract of the subject I propose. The field of population genomics has recently emerged at the cross between traditional population genetics and the development of high-throughput techniques, with the aim to decipher the strength of selection events on genome evolutions. Although not yet widely applied to plant pathology studies, these approaches seem particularly well suited to reveal the genetic bases of the adaptive potential of fungal plant pathogens. While the rapid pace of pathogen evolution (which result from intensive selection pressure through the massive deployment of resistant genes) presents a major impediment to sustainable agriculture, it also provides interesting opportunities to better understand the evolutionary biology of host-parasite interactions. Here we want to apply the population genomic toolboxes to decipher the evolution of virulence loci in the fungus responsible for the poplar rust (Melampsora larici-populina). Deepening into the genome's organisation, the project will successively try to (i) highlight genomic regions subjected to a selective sweep caused by a drastic selection event which was the overcoming of a major resistant gene, (ii) point out the genes (among these region) under positive selection, and putatively responsible for the gene for gene interaction and (iii) study the evolution, including recombination rate, of these genomic regions implied in fungal pathogenicity. This project would thus bring us fundamental knowledge on the genome evolution of pathogens, which would help designing sustainable strategies of crop protection.

Best regards,

Fabien Halkett

F. HALKETT halkett@nancy.inra.fr

UMR 1136 IAM (Trees-Microorganisms joint unit) INRA Nancy F-54280 Champenoux France Tel : +33 3 83 39 40 55 Fax : +33 3 83 39 40 69

halkett@nancy.inra.fr

IowaStateU ConservationGenetics

Ph.D. Graduate Assistantship, Conservation Genetics of Freshwater Mussels at Iowa State University

One graduate research assistantship is anticipated to be available to support a Ph.D. candidate interested in conservation genetics. The project involves laboratory and field components designed to improve our understanding of two federally protected freshwater mussel (Unionidae) species. Research goals are to understand the population structure across the respective species ranges and improve our knowledge of the age structure and growth rate within populations. The successful applicant will also be expected to develop and execute an original research project that compliments the described research. The position will be located at Iowa State University in the laboratory of Dr. Kevin J. Roe (http://www.public.iastate.edu/~kjroe/).

Applicants must be enthusiastic and capable of working independently. Prior experience with DNA extraction, PCR, microsatellites, DNA sequencing and/or freshwater mussels is preferred.

The position is expected to begin August 2010 (fall semester); admission for the spring semester (January 2011) is also acceptable. For more information and to apply, please email a curriculum vitae, a one-page statement of research interests and relevant experience, and the names and email addresses of three references to Dr. Kevin J. Roe (kjroe@iastate.edu).

Kevin Roe Natural Resource Ecology and Management 339 Science II Iowa State University Ames, IA 50011

515 294-8332

kjroe@iastate.edu

LeibnizInst EvolutionPathogenResistance

The Leibniz Institute of Marine Sciences (IFM-GEOMAR) is offering a

Scientist Position (PhD-candidate)

within the newly founded Emmy Noether group Evolutionary genetics of pathogen resistance in coastal ecosystems funded for a period of at least 36 months starting from July 2010.

Background: The consequences of climate change for the epidemiological spread of infectious disease are largely unexplored. Potential evolutionary responses to increasing selection pressure arising from interactions between disease agents and an altered environment have largely been neglected " especially in marine ecosystems. We are looking for a PhD student to work on the evolutionary ecology of host-parasite interactions in coastal ecosystems by investigating infection patterns of ubiquitous bacterial pathogens and evolutionary trajectories of target hosts from different key groups (fish, bivalves and crustaceans) within the Wadden Sea ecosystem. By combining molecular (gene expression, genome scans) and quantitative genetic tools (evolutionary potential of G matrices, GxGxE interactions) over a gradient of experimental systems ranging from field studies to mesocosms and laboratory experiments, we want to explore the evolutionary responses of different hosts to pathogen infection (mainly genus Vibrio) in changing environments. The project is a collaboration between the department of Evolutionary Ecology of Marine Fishes at IFM-GEOMAR, Kiel (http://www.ifm-geomar.de/-index.php?id=3D565&L=3D1) and the Alfred Wegener Institutes Wadden Sea station on the island of Sylt (http://www.awi.de/de/institut/standorte/sylt/). Most of the experimental work will be based on the island of Sylt, offering the unique opportunity to work in an ecosystem that recently claimed the status of world natural heritage site.

The group is a member of the DFG priority program SPP1399 Host-Parasite Coevolution and our collaborations with the Max Planck Institute for Evolutionary Biology (Pln, D), NIOZ (Texel, NL), and IPIMAR (Tavira, PT) offer a stimulating research environment for addressing questions on the ecology of host-parasite interactions.

Necessary qualifications include a diploma or master degree in evolutionary biology, ecology or related fields. Experience with molecular techniques and statistical analysis of large data sets is a definite plus.

The salary is in accordance with level 13 TV-L of the German tariffs for public employees.

Applications will be considered until June 30, 2010 or until the position is filled. Candidates should send a curriculum vitae, copies of diploma- or M.Sc.-certificates, list of publications, a summary of the diploma- or M.Sc.-thesis, and the names and addresses of two references to in a single pdf file to:

Dr. Mathias Wegner Email:mwegner (a) ifm-geomar.de

Further information can be obtained from http://-www.ifm-geomar.de/index.php?id=3Dmwegner&L=-3D1 The Leibniz Institute for Marine Sciences wishes to increase the number of female co-workers, and applications from women are particularly encouraged. Applications of handicapped persons will be favoured when all other qualifications are equal.

mazemiliano@mac.com

Munich HostParasitePredator Evolution

Reminder: PhD position in Evolutionary Ecology (trade-offs between host responses to parasites and predators)

A 3-year PhD position is available in the labs of Dr. Justyna Wolinska and PD Dr. Christian Laforsch (joint project) at the Ludwig-Maximilians-Universität (LMU) in Munich, to study the trade-offs between adaptive responses to parasites and predators in the context of inducible defences. While many studies have identified the benefits of predator-induced plasticity, little evidence exists for the associated costs. The proposed research will test the benefits and costs of inducible defences in the context of simultaneous exposure to parasites. We will use Daphnia (waterfleas) as the model host (for microparasites) and prey (for invertebrate and vertebrate predators).

The project is a combination of laboratory experiments (about 60% of the project), field work (20%) and molecular techniques (20%). The selected candidate will have the freedom to develop the project according to his/her own interests and strengths. The student will also take part in the PhD program of the LMU (including various courses).

Applicants should have a Master's or Diploma degree in biology. The working language is English. Experience in experimental design, statistics and using PCR-based molecular genetic methods would be advantageous.

Applicants should submit a single PDF file by e-mail (to both supervisors), containing the following items:

- cover letter with a brief summary of research background and professional motivation,

- CV,

- abstract of master/diploma thesis,

- contact information of two professional referees.

Application deadline: May 15. The position is available from 1st July 2010. If you have any specific questions (e.g. details of the project), feel free to email us: wolinska@bio.lmu.de or laforsch@zi.biologie.uni-muenchen.de.

See also: http://sci.bio.lmu.de/ecology/evol_e/people_wolinska_e.html http://sci.bio.lmu.de/ecology/evol_e/people_laforsch_e.html – Justyna Wolinska Ludwig-Maximilians-Universität, München Department Biologie II Evolutionsökologie Grosshaderner Str. 2 82152 Planegg-Martinsried, Germany

Phone: +49 (0)89 2180 74201 Fax: +49 (0)89 2180 74204 email: wolinska@bio.lmu.de http://www.biologie.uni-muenchen.de/ou/ecology/evol_e/people_wolinska_e.html justyna.wolinska@gmail.com

Poitiers France MicrobialDiversity

PhD position in Poitiers: microbial diversity associated with arthropods

The project will concern the characterization of the symbiotic communities of arthropods. Symbiosis constitutes a major evolutionary strength in the history of life [1]. If Wolbachia remains the most frequent endosymbiont in arthropods, recent studies show that the presence of other bacteria, the effects of which are still unknown, was probably underestimated [2]. Wolbachia are widespread (prevalence ˜62 %) in isopods and are involved in major host evolutionary changes [3]. Moreover Wolbachia induce an immunodepression in their hosts [4], so facilitating the establishment of opportunistic bacteria. Even if some pathogenic bacteria were described [5], the main part of the symbiotic community remains largely unknown in isopods.

The PhD project aims at a characterization of the microbes associated with Armadillidium vulgare and related species. This pill bug is one of the best studied organisms in the laboratory. Recent unpublished results show that endosymbionts (sex parasites or pathogenic bacteria) others than Wolbachia, are also present in this host. The project is part of EndoSymbArt and AdaWol ANR projects offering a stimulating research environment. It involves direct collaboration with members of the lab and with research groups in France. The project will start in October 2010. The PhD position will be will be granted (salary 1757 euros per month) by the CNRS (National Center for Scientific Research) (http://www2.cnrs.fr/DRH/doctorants-10/).

The successful applicant must hold a Biology M.S. degree or equivalent. A strong background in bacteria-invertebrates symbiotic interactions will be appreciated, as well as in molecular biology and DNA sequence handling. Skills in AFLP Amplified Fragment-Length Polymorphism, TGGE Temperature Gradient Gel Electrophoresis, FISH Fluorescent in situ Hybridization, Quantitative PCR constitute a plus. The application should be written in English and should include personal information/background, a detailed CV with a summary of research experiences, and at least one reference letter. Applications should be sent to: didier.bouchon@univ-poitiers.fr

Application deadline: 30/04/2010.

References [1] Moya, A., J. Pereto, R. G, Latorre A. 2008, Learning how to live together: genomic insights into prokaryoteâanimal symbioses, Nature Reviews Genetics 9:218-229. [2] Bouchon D, Cordaux R, GrÃve P. 2008 Feminizing Wolbachia and the evolution of sex detremination in isopods. in Insect symbiosis, K. Bourtzis and T. Miller (Ed.) 273-294. [3] Duron O, Bouchon D, Boutin S, Bellamy L, Zhou L, Engelstädter J, Hurst GD. 2008 The diversity of reproductive parasites among arthropods: Wolbachia do not walk alone. BMC Biology 24 :6-27. [4] C. Braquart-Varnier, M. Lachat, J. HerbiniÃre, M. Johnson, Y. Caubet, D. Bouchon D, M. Sicard. (2008). Wolbachia mediate variation of host immunocompetence. PLoS ONE 2008 Sep 26;3(9):e328 [5] Cordaux R, Paces-Fessy M, Raimond M, Michel-Salzat A, Zimmer M, Bouchon D. 2007 Molecular characterization and evolution of arthropod-pathogenic Rickettsiella bacteria. Appl Environ Microbiol. 73(15):5045-7.

– Pr. Didier Bouchon University of Poitiers UMR CNRS 6556 Ecology Evolution Symbiosis 40 avenue du Recteur Pineau F-86022 Poitiers cedex, France 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>

SouthDakotaStateU EvolutionaryGenetics

M.S. Graduate Assistantship Available in Evolutionary Genetics at South Dakota State University

One graduate assistantship is available to support a M.S. student interested in the genetic analysis of sickleweed (Falcaria vulgaris, Apiaceae) in North America. Sickleweed is a common weed native to Europe and western Asia. Little is known of its biology and ecological genetics in North America and its native range in Eurasia. During the past two decades, sickleweed has rapidly invaded 3240 ha of mixed grass prairie on the Fort Pierre National Grassland (FPNG) in central South Dakota. Research goals are to 1) study genetic diversity of sickleweed in North America and in its source populations in Eurasia, (2) determine the source and frequency of introduction and 3) combine genetic data with ecological data to understand the role of genetics in successful spread of this exotic species in North America.

The position will be located at South Dakota State University in the laboratory of Dr. Madhav Nepal. The project involves sample collections in the field and molecular work in the laboratory. Applicants must be enthusiastic, highly motivated and capable of working independently. Prior experience with DNA extraction, PCR and genotyping using molecular marker is a plus. The Start date is January 2011 (spring semester). To apply, please email a curriculum vitae, a one-page statement of relevant experience, and the names and email addresses of three references to: Dr. Madhav Nepal (Madhav.Nepal@sdstate.edu)

Madhav Nepal, Ph.D. Assistant Professor Division of Biology and Microbiology South Dakota State University, 57007 Brookings SD

Office : 224 West Hall PH: (608) 688-5971, FX: (605) 688-6677, EM: Madhav.Nepal@sdstate.edu

Madhav.Nepal@sdstate.edu

Spain Biodiversity

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

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

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

You must be proficient in Spanish language.

FINANCIAL SUPPORT.- The CSIC offers 5 full scholarships (6300

euros/student) and 5 for registration fees (1300 euros/student). The program finances additional full and registration scholarships for Latin American applicants.

HOW TO APPLY?.- The application period for studies starting in October 2010 is now open until 9-July-2010. Application to the CSIC fellowships is also open from 18-May to 25 June 2010.

You can find all the information and detailed instructions on how to apply at

http://www.masterenbiodiversidad.org/

Jesús Muñoz e-mail: jmunoz@rjb.csic.es Real Jardín

Botánico (CSIC) Plaza de Murillo 2 tlf. +34 91 420 3017 E-28014 Madrid fax. +34 91 420 0157 ESPAÑA (Spain)

http://www.masterenbiodiversidad.org http://www.rjb.csic.es/jardinbotanico/jardin/contenido.php?Pag=413 <http://www.rjb.csic.es/jardinbotanico/jardin/contenido.php?Pag=413&tipo=cie ntifico&codf> &tipo=cientifico&codf

KRAKEN research group (environmental modelling, data processing & analysis): < http://www.unex.es/unex/grupos/grupos/kraken > http://www.unex.es/unex/grupos/grupos/kraken SYNTHESYS: EU funds short visits to our institution: < http://www.synthesys.info/index.htm > http://www.synthesys.info/index.htm

Jesús Muñoz <jmunoz@rjb.csic.es>

Switzerland EvolutionaryGenomics

2 PhD-positions in evolutionary genomics are available in a collaborative project of the research groups of Dieter Ebert (University of Basel, Switzerland) and Christoph Haag (University of Fribourg, Switzerland).

We are looking for highly motivated candidates with interest in evolutionary genomics. A background in bio-informatics and genomics is helpful. The positions are funded to work on the evolution of (a)sexual reproduction (PhD projects). The suggested methodology includes genome scans, population surveys, SNP genotyping using microarrays, and comparative genomics. Previous experience with Daphnia is not required, but excellent written, verbal, and interpersonal skills, good work ethics, and the ability to think creatively and critically are desired. Starting dates are flexible, from August 2010 onwards. Positions are funded for 3 years. Successful candidates will take part in the Swiss doctoral school in Population Genomics.

One PhD student will be mostly located in Dieter Ebert's group working at Basel University, the other PhD student will be mainly located at Fribourg University. Details about the groups: http://evolution.unibas.ch/ http://www.unifr.ch/biol/ecology/haag/haag_lab_home.html Please send your application by E-mail to Dieter Ebert (dieter.ebert@unibas.ch). Applications should include a single pdf-file containing CV, a list of publications and a 1 page description of your research interests and motivation. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 7. June 2010 will be given full consideration. Interviews will be held in the first half of July 2010.

Contact information:

Prof. Dr. Dieter Ebert, University of Basel, Zoologisches Institut, Vesalgasse 1, CH-4051 Basel, Switzerland, Email: dieter.ebert@unibas.ch Phone: +41-(0)61-267 03 60 Fax +41-(0)61-267 03 62

Dr. Christoph Haag University of Fribourg Department of Biology Chemin du Musée 10 CH-1700 Fribourg, Switzerland Email: christoph.haag@unifr.ch Phone: +41-(0)26-300 88 71 Fax: +41-(0)26-300 96 98

UArizona OriginProtoGenome

Graduate PhD position to study the origin of the protogenome

In the laboratories of

Pierre Durand and Marc Weinberg in the Department of Molecular Medicine and Haematology, University of the Witwatersrand, Johannesburg, South Africa (pdurand@email.arizona.edu or marc.weinberg@wits.ac.za)

Richard Michod in the Department of Ecology and Evolutionary Biology, University of Arizona (michod@u.arizona.edu)

A funded position is available for a PhD student to study the origin of the proto-genome. This project builds on a conceptual scenario for the origin of the genome as an evolutionary transition (see references below). We aim to investigate the process by which selfish, autonomous biomolecules may form cooperative groups and ultimately a functionally integrated evolutionary unit. The successful candidate will work on developing a laboratory model system of ribozymes and/or selfish genetic elements to investigate changes in fitness components and life history trade-offs in individual, autonomous molecules that predispose to the formation of a new integrated whole (the proto-genome). The bulk of the project uses molecular biology techniques, but will also draw on evolutionary theory and ecology. This is a relatively new field and guidance and supervision will be provided.

This is a collaborative project. The successful candidate will be required to spend time in the laboratories of Pierre Durand and Marc Weinberg in the Department of Molecular Medicine and Haematology, University of the Witwatersrand, Johannesburg, South Africa and in Richard Michod's laboratory in the Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, USA. According to the student's situation and interests the successful candidate would apply to and enroll in either one of the associated graduate programs at the University of the Witwatersrand or the University of Arizona and the stipend would be determined by the current pay scales in those programs.

Interested applicants are encouraged to see the following:

1. For background concepts relevant to this project, see: PM Durand and RE Michod, Genomics in the light of evolutionary transitions. Evolution, 2010.In press. (doi:10.1111/j.1558-5646.2009.00907.x, https://wwwresearchgate.net/-publication/40023880_genomics_in_the_light_of_ev olutionary_transitions)

2. To provide applicants with an appreciation of the molecular biology approaches that may be used, see: MS Weinberg and JJ Rossi, Comparative single-turnover kinetic analyses of trans-cleaving hammerhead ribozymes with naturally derived non-conserved sequence motifs. FEBS Letters 2005.

3. To provide applicants with an appreciation for the evolutionary and ecological approaches that will be applied to investigate the origin of the proto-genome as an evolutionary transition in individuality, see: RE Michod, Evolution of individuality during the transition from unicellular to multicellular life. PNAS, 2007.

We are seeking a self-motivated candidate with a molecular biology background, who can work independently, as well as part of a team. The position is open to individuals from all countries with either a MSc or BS / BSc (Hon) (with work experience and/or outstanding results) and a desire to make a contribution in this area of research. Funding and additional scholarships may be available dependant upon the candidate's background and expertise. Informal enquiries are welcome to any of the investigators above. To apply, please send a detailed CV with the contact details for three references and a cover letter explaining why you think you are suited for this project to the Principal Investigator: Dr. Pierre Durand at pdurand@email.arizona.edu. A provisional starting date will be early 2011. The position will remain open until a suitable candidate is found.

Rick Michod <michod@u.arizona.edu>

UBath EvolutionaryGenetics

PhD opportunity in evolutionary genetics

There is an opportunity for a PhD project in the Kover lab to look at predictability of responses to selection at the molecular level. We are looking for someone interested in evolutionary questions and confortable with bioinformatics tools. The project is interdisciplinary in nature and would be carried in colaboration with Lawrence Hurst's group. However, there is enough flexibility to taylor to student's interest.

"Paula X. Kover" <p.x.kover@bath.ac.uk>

UBern PopulationGenomics

PHD POSITION IN POPULATION GENOMICS

The CMPG lab (http://cmpg.iee.unibe.ch) is looking for a highly motivated student to work on the detection of multi-locus adaptive events having occurred in the recent history of human populations.

These investigations will be done by a combination of bioinformatics, phylogenetics, and population genetics analyses. Using available information on gene interactions and polymorphisms in humans and primates, this project should enable us to better understand concerted adaptive evolution and epistatic interactions between genes scattered over the genome. The project will be partly supervised by Prof. Marc Robinson-Rechavi from the Evolutionary Bioinformatics Group in Lausanne (http://bioinfo.unil.ch/)

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

The CMPG lab is well equipped with computational tools including a 64 node Linux cluster, and access to the much larger Ubelix cluster of the University (1000+ CPUs). Our lab is also affiliated to the doctoral program in Ecology and Evolution (http://www.unil.ch/-ee), the Swiss NSF ProDoc program in Population Genomics, and the Swiss Institute of Bioinformatics (http://www.isb-sib.ch), which all provide access to stimulating and helpful doctoral training and courses.

The position will start, for 3 years, on 1st September 2010. Gross salary follows the Swiss NSF scale and is around CHF 40,000.- per year.

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

Application deadline is May 1st 2010

– 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: laurent.excoffier@iee.unibe.ch (NEW) http://cmpg.iee.unibe.ch/ (NEW)

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>

UCollegeLondon SexualSel Complexity

UCL 4-year Studentships in Biodiversity, Ecology and Evolution

Two 4-year Studentships are offered at UCL as part of the Darwin School for Biodiversity, Ecology and Evolution. This is a new collaborative venture between UCL, Imperial College, the Institute of Zoology, the Natural History Museum and the Royal Botanic Gardens Kew. Students will have access to the resources, facilities and collections of these institutions. In the first year of study, students will be enrolled in the UCL Systems Biology MRes programme. This provides a research-intensive programme of taught courses and hands-on training in the principles of systems biology, advanced biological modelling, quantitative approaches and research skills along with two research projects. For further details see: http://www.ucl.ac.uk/systems-biology/graduate-training. Each student will then progress to one of the two PhD projects:

1) Identifying genes involved in sexual selection.

Supervisors: Prof Andrew Pomiankowski & Dr Kevin Fowler

Our aim is to improve understanding of the genetic basis of female sexual preferences. Research will be undertaken using the stalk-eyed fly Diasemopsis meigenii to uncover the number of genes involved, their effect sizes and linkage patterns. The student will map the genes for the male ornamental trait (eyespan), and uncover the nature of any genetic covariance with female preference. The student will also map genes for male fertility and ejaculate properties (sperm and accessory gland proteins) as these are thought to be important in determining the benefits of mate choice. The genetic analyses will be carried out using QTL (quantitative trait locus) mapping on a SNP map of the D. meigenii genome. The student will work closely with a postdoctoral fellow and research technician employed on our NERC grant addressing these topics, and with other members of the stalk-eyed fly group with diverse interests in reproductive biology and sexual selection. There will be opportunities for field work associated with this Studentship to better understand the mating behaviour of this and allied stalk-eyed fly species. Further information: see http://www.ucl.ac.uk/stalkie/ or contact: a.pomiankowski@ucl.ac.uk.

2) Comparative genomics to study the evolution of loss of complexity.

Supervisor: Prof Max Telford

While organisms have generally increased in complexity through evolutionary time, many instances are known in which characteristics have been lost in different lineages. The project will use bioinformatic approaches to study newly available genome sequence data from two evolutionarily pivotal animals, the priapulid worm Priapulus caudatus and the deuterostome Xenoturbella bocki. Both fruitflies and nematodes have lost a significant proportion of genes present in other animal groups. This may be related to changes in morphology and also to the evolution of the rapid developmental programs seen in these species. Priapulus is an Ecdysozoan related to arthropods and nematodes, yet has been shown to have a slowly evolving genome compared to these taxa. Comparisons of the conservatively evolving Priapulus genome with those of model organisms may give an insight into the link between morphological evolution and changes in the tempo of genome evolution. In a similar vein, Xenoturbell a is a deuterostome related to echinoderms and vertebrates yet it has lost typical deuterostome characters such as gill slits and a through gut. Genome comparisons will shed light on the genetic basis for such differences. The project will be co-supervised by Prof Jürg Bähler. Further information: contact: m.telford@ucl.ac.uk.

How to apply

Expressions of interest with a covering letter, CV, and names and contact details of two referees should be sent as soon as possible to Prof Pomiankowski (a.pomiankowski@ucl.ac.uk) or Prof Telford (m.telford@ucl.ac.uk) as appropriate. In addition, a formal application should be submitted to UCL admissions: see http://www.ucl.ac.uk/admission/graduate-study/application-admission/apply-online/ . Closing date for applications is 30/07/10. Studentships will start in Sept. 2010 and provide a stipend and tuition fees for 4 years of study. Studentships are available to all UK/EU applicants who satisfy the requirements of 'home/EU' student status. For further details see: http://www.ukcisa.org.uk/student/info_sheets/-tuition_fees_ewni.php# . ucbhpom@ucl.ac.uk

UEdinburgh PlantTaxonomy

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

Royal Botanic Gardens Edinburgh/ University of Edinburgh

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

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

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

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

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

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

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

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

MSc course Director, Dr Louis Ronse De Craene Royal Botanic Garden Edinburgh Tel +44 (0)131 248 2804 Email: l.ronsedecraene@rbge.ac.uk Postgraduate Secretary, The University of Edinburgh

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UGoettingen InsectFungusMolEvolution

Institute of Zoology, University of Goettingen, Germany:

PhD position - Insect-fungus molecular ecology

Deadline for application: 15th June 2010. The preferred starting date: August 2010.

We are looking for a creative and highly motivated person with strong interest in working at the interface of evolutionary ecology and molecular biology. The project is part of a larger research program where we seek to understand the ecological and evolutionary dynamics of fungal secondary metabolism in the decomposer food web. As a link between molecular and organismal research at the University of Goettingen, the project aims at disentangling the mechanisms underlying cross-talk and cross responses in soil fungus-fungivore interactions. The candidate will work on the induced chemical response in the Folsomia candida-Aspergillus model fungus-fungivore system by means of molecular genetic techniques (e.g., gene expression profiling) and biochemical analyses of secondary metabolites. The project is embedded in a cooperative network comprising the fungal molecular genetics group led by Gerhard Braus, the mycotoxin research group led by Petr Karlovsky in Goettingen, and the fungal genomics group of Nancy P. Keller at the University of Wisconsin, USA.

Applicants must have a master/diploma degree in Biology or a related discipline. Substantial experience in molecular genetics/genomics (e.g., microarray studies, quantitative PCR techniques), preferentially of fungi, is mandatory. In addition to enthusiasm and reliability, good English and social skills are essential to work effectively in the multi-disciplinary team. Experience with work on /Aspergillus/ and/or fungal secondary metabolites would be an advantage.

Goettingen is a medium-sized, old but vivid town in the center of Germany http://en.wikipedia.org/wiki/Goettingen, close to the Harz mountains. The Georg-August-University Goettingen has a long and influential academic tradition in Europe and provides excellent research conditions across many disciplines, including four Max-Planck Institutes. Given the excellent connection to the Intercity Express high speed network big cities, such as Berlin, Hamburg, Munich, or Cologne can be reached within a few hours.

The term of the position will be for a period of three years. Gross salary: ~29,000 Euros per annum (0.65 TV-L E13).

If you interested in this project, do not hesitate to contact Marko Rohlfs (rohlfs@zoologie.uni-kiel.de) for further details. If you want to apply, please send your CV, a letter of motivation including relevant experience, and contact details of two referents as a single pdf or word file to Marko Rohlfs. Women are especially encouraged to apply. Severely handicapped people will be preferentially considered in case of equivalent qualifications.

Relevant publications:

Kempken F, Rohlfs M (2010) Fungal secondary metabolites – a chemical defense strategy against antagonistic animals? Fungal Ecology (doi:10.1016/j.funeco.2009.08.001)

Rohlfs M, Albert M, Keller NP, Kempken F (2007) Secondary metabolites protect mould from fungivory. Biology Letters 3: 523-525

Wölfle S, Trienens M, Rohlfs M (2009) Experimental evolution of resistance against a competing fungus in Drosophila. Oecologia 161: 781-790

– PD Dr. Marko Rohlfs Institute of Zoology and Anthropology University of Goettingen Berliner Str. 28 37073 Goettingen, Germany

Marko Rohlfs <rohlfs@zoologie.uni-kiel.de>

UGuelph MolecularEvolution

The College of Biological Science at the University of Guelph is offering support to enable the recruitment of several exceptional PhD students, including in the areas of areas of evolutionary biology, biodiversity, and genomics. Suitable candidates are sought who can be put forward in an application for this funding. Possible positions include:

1. Genome size evolution / evolution of transposable elements. 2. Arctic biodiversity using DNA barcoding. 3. Applied DNA barcoding, such as in food safety or forensic/economic applications. 4. DNA barcoding of parasites, pathogens, and vectors of disease.

Supervisors will depend on the topic of interest, but will include some combination of Drs. Ryan Gregory, Sarah Adamowicz, and Robert Hanner in the Department of Integrative Biology and the Biodiversity Institute of Ontario.

Please note the following important details:

- The positions are open only to Canadian students, and are only at the PhD level (not MSc). - Funding for one or more of these positions must be applied for through the College of Biological Science once a suitable candidate is identified to be put forward; it is not guaranteed that one or more applications will be successful. - Successful applicants must be able to begin studies no later than Fall 2011. - Applicants must have at least an A average to be eligible. - Holders of major scholarships (NSERC, OGS) are not eligible.

If you are interested and meet all of the above requirements, simply send an email to rgregory@uoguelph.ca to discuss potential research projects in more detail.

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

http://www.gregorylab.org/web/ rgregory@uoguelph.ca

UHawaii Hilo FungalEvolution

Scholarship in the Tropical Conservation Biology and Environmental Science (TCBES) M.S. Program at the University of Hawai-i

Join a team of researchers examining the diversity and dynamics of fungal community structure in native Hawaiian forests across both elevational and successional gradients. Building upon previous work done on the Hawaiian Islands documenting the diversity of fleshy macrofungi using traditional sampling methods, this project is adding a molecular component through the collection of environmental isolates, construction of cloning libraries, and metagenomic analysis. Results of this project will provide a much broader picture of both the taxonomic and genetic fungal diversity present in native Hawaiian forests, including both macro- and microscopic taxa. Additionally, the span of this project across both spatial and temporal gradients will allow the investigation of not only changes in species composition and function, but also how such changes may play a role in fungal speciation and that of any associated plant species. The graduate scholar will receive training in field and molecular methods, and will contribute to the overall project while conducting thesis research.

The successful applicant will receive $22,000 annual salary, will enroll in the TCBES Program, and will join a vibrant research community in evolutionary biology 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://tcbes.uhh.hawaii.edu Brian A. Perry, Ph.D. Assistant Professor Department of Biology University of Hawai-i at Hilo 200 W. Kawili St. Hilo, HI 96720 (808) 974-7363 baperry@hawaii.edu www2.hawaii.edu/~baperry

baperry@hawaii.edu

UHawaii Hilo PlantSpeciation

PLEASE CIRCULATE

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/ I am looking for an enthusiastic and energetic M.S. student to join me and my group to study the mechanisms of speciation in

Hawaiian Metrosideros (‘Ohi‘a), a group of trees that appears to represent multiple stages of the speciation process. The graduate scholar will develop a research project with me that is aligned with the broader research goals of our program. Our program involves molecular, field, and greenhouse studies to examine patterns of reproductive isolation and neutral and expressed genetic variation among habitat-associated varieties and species. The graduate scholar will receive training in field and molecular methods and contribute to the broader program. S/he will also receive training through participation in the TCBES Program, which includes 40-50 students (15-20 in each cohort), 30 on-campus faculty, and 50 affiliate faculty from outside institutions.

A Bachelor’s degree and strong interest in evolution required. Bachelor’s degree in biology, with courses or experience in ecology, evolutionary biology, or genetics preferred.

The graduate scholar will receive $22,000 annual salary, will enroll in the TCBES Program in August 2010, 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 inquiries ASAP to Dr. Elizabeth Stacy (estacy@hawaii.edu; www2.hawaii.edu/˜estacy/).

Elizabeth Stacy Assistant Professor Department of Biology TCBES Graduate Program University of Hawai‘i at Hilo 200 West Kawili Street Hilo, HI 96720 Phone: 808-933-3153 Fax: 808-974-7693

estacy@hawaii.edu

UIdaho MolecularPlantSystematics

M.S. position in molecular plant systematics at the University of Idaho

The Tank lab (http://phylodiversity.net/dtank) at the University of Idaho is seeking to fill a position for a M.S. student to pursue research in molecular plant systematics to begin August 2010. While receiving graduate training in molecular plant systematics, the student will act as a herbarium assistant in the Stillinger Herbarium (http://www.uidaho.edu/herbarium) helping to coordinate a large digitization project focused on imaging and databasing Idaho vascular plant collections.

Applicants should have a strong interest in plant systematics and be working towards a career or further degree involving collections based research, phylogenetics, taxonomy, and/or evolutionary biology.

Applications should include: 1) a cover letter indicating specific interest in this position, 2) a general statement of research interests and experience, and 3) a CV, including names and contact information for at least three references. Interested applicants should send materials to Dr. David Tank (dtank@uidaho.edu).

The student selected for this position will be required to successfully enroll as a graduate student in the College of Natural Resources at the University of Idaho. For information about policies and entrance requirements pertaining to university admission see: http://www.uidaho.edu/cogs/admissions .

David C. Tank, Assistant Professor Director, Stillinger Herbarium College of Natural Resources University of Idaho PO Box 441133 Moscow, Idaho 83844-1133

208.885.7033 (office) 208.885.8012 (lab) 208.885.6564 (fax) dtank@uidaho.edu http://www.phylodiversity.net/dtank/ http://www.uidaho.edu/herbarium.aspx dtank@uidaho.edu

UIdaho PlasmidHostRangeEvolution

PhD student opportunity at the University of Idaho

A Research Assistantship is available for a Ph.D. student to work on mathematical models and simulations of plasmid host range evolution, and on statistical analyses of data obtained from experimental plasmid evolution studies. The student will work under the direction of Dr. Zaid Abdo (Mathematics, Statistics, Bioinformatics and Computational Biology) and in close collaboration with Dr. Eva Top (Biological Sciences, Bioinformatics and Computational Biology). This joint experimental-theoretical project is funded by the National Institutes of Health, and is highly interdisciplinary. The successful candidate will be enrolled in the Bioinformatics and Computational Biology program at the University of Idaho (http://www.bcb.uidaho.edu/default.aspx?pid=

85454). The PhD student will also be part of the Initiative for Bioinformatics and Evolutionary Studies (IBEST) group (http://www.ibest.uidaho.edu/ibest/index.html), a very dynamic and collaborative interdisciplinary research group with excellent research resources.

Qualifications: Student should be highly motivated, and have a strong background in statistics and mathematical biology. The successful candidate should have a serious desire to learn about microbial population biology, and preference will be given to candidates who have both a strong quantitative and experimental background.

The stipend pays US$21,000 per year and tuition, fees, and health insurance are covered as well. In addition, funds are available to attend conferences. Moscow, the home of the University of Idaho, is a city of 22,000 people, nestled between Moscow Mountain and the beautiful rolling hills of the Palouse. With a small town friendliness and safety, Moscow is referred to as the "Heart of the Arts" - with an annual international Jazz Festival, live music on the town, the Rendezvous in the Park, and summer theatre. Moscow is also a great place for those who love the outdoors, with beautiful rivers, lakes, and diverse mountains within short driving distance. The University of Idaho and Washington State University, just eight miles apart, share a large number of cross-listed courses and many collaborative programs and research activities. Moscow is 80 miles from Spokane, Washington, and an hour?s flight from Seattle.

For more information about the project and graduate school requirements at the University of Idaho please contact Dr. Zaid Abdo (zabdo@uidaho.edu) or Dr. Eva Top (evatop@uidaho.edu). For more information on the plasmid research, see http://people.ibest.uidaho.edu/~etop/research.html HOW TO APPLY: For preliminary screening, email a statement of background and interests, TOEFL scores (for foreign applicants), GRE scores (if you have them), and a copy of transcripts of academic courses taken to Dr. Zaid Abdo (zabdo@uidaho.edu). Starting date is flexible.

zabdo@uidaho.edu

ULausanne EvolutionaryGenomics

PHD IN FUNCTIONAL EVOLUTIONARY GENOMICS

Center for Integrative Genomics, University of Lausanne, Switzerland

A PhD student position (~4 years) is available in the evolutionary genomics group of Henrik Kaessmann in the framework of major new projects funded by the European Research Council.

We are seeking talented and highly motivated applicants (preferably with some experience/background in molecular evolution), who have strong programming skills (or the willingness and drive to acquire them) and an interest in evolutionary genome analyses using bioinformatics approaches. A MSc degree or equivalent is required.

Our group has been interested in a range of topics related to the functional evolution of genomes from primates (e.g., emergence of new genes and their functions) and other mammals (e.g., the origin and evolution of mammalian sex chromosomes). In the framework of a new major line of projects funded by the European Research Council, a large amount of qualitative and quantitative transcriptome data is being produced for a unique collection of tissues from representative mammals by the wet lab unit of the group using next generation sequencing technologies (RNA-Seq). The PhD student will perform integrated evolutionary/bioinformatics analyses based on these data and available mammalian genomes. The specific project will be developed together with the candidate.

The language of the institute is English, and its members form an international group that is rapidly expanding. The institute is located in Lausanne, a beautiful city at Lake Geneva.

For more information on the group and our institute more generally, please refer to our website: http://www.unil.ch/cig/page7858_en.html Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann (Henrik.Kaessmann@unil.ch).

– Henrik Kaessmann, Ph.D. Associate Professor Center for Integrative Genomics University of Lausanne, Switzerland E-mail: Henrik.Kaessmann@unil.ch Phone: +41 (0)21 692 3960

Some recent publications from the lab:

Henrichsen, C., Vinckenbosch, N., Zöllner, S., Chaignat, E., Pradervand, S., Frédéric Schütz, Ruedi, M., *Kaessmann, H. and *Reymond, A. (2009) Segmental copy number variation shapes tissue transcriptomes. Nature Genet. 41: 429-9.

Potrzebowski, L., Vinckenbosch, N., Marques, A. C., Chalmel, F., Jegou, B. & Kaessmann, H. (2008) Chro-

mosomal Gene Movements Reflect the Recent Origin and Biology of Therian Sex Chromosomes. PLoS Biol. 6: e80.

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Henrik.Kaessmann@unil.ch

UlmU BatVirusDynamics

PhD Position in Evolutionary Ecology (Coronaviruses in European and African Bats)

A 3-year PhD student position is available at the Institute of Experimental Ecology at Ulm University, Prof. Dr. Elisabeth Kalko, in close collaboration with Prof. Dr. Christian Drosten (Bonn University; joint project), to study ecological correlates of emergence and dynamics of novel coronaviruses in Chiroptera (bats) in Europe and Africa. The research funded by the German Research Foundation (DFG) will test a range of hypotheses integrating virology and ecology.

Involving a combination of analytical and field work in both Germany and West Africa (Ghana), the project combines molecular, endocrine and behavioural techniques. The selected candidate will conduct ecological research as part of an established international team of virologists and ecologists at a well-known West African research institute providing attractive field infrastructure and will be based at Ulm.

Applicants should have completed a MS degree or equivalent in ecology or a related discipline and speak English fluently. Experience in experimental design, statistics and ecological methods is an asset, in particular previous experience with capture, handling, tracking or obtaining samples from birds or bats in tropical environments. Knowledge of Africa and publications from previous work would he highly regarded. The selected candidate needs to be willing to repeatedly spend several months at a time in tropical settings under difficult conditions. This requires organizational skills and the ability to live and work independently.

Please submit a single PDF file by e-mail, containing (a) a cover letter addressing the selection criteria with a brief summary of background and motivation, (b) CV including publications and language certificates if applicable, (c) abstract of MS thesis and (d) contact information of two professional referees. Applications will be reviewed from

1 June 2010 and continue until position is filled. The position is available from 1 July 2010 and requires an EU residency and work permit. Please send your application to elisabeth.kalko@uni-ulm.de.

For further information, please refer to: http://www.uni-ulm.de/nawi/bio3.html http://www.virology-bonn.de/drupal6/?q=node/5 http://www.kccr-ghana.org/ * Dr. Stefan M. Klose Institute of Experimental Ecology (Bio III) University of Ulm Albert Einstein Allee 11 89069 Ulm, Germany Fon +49.621.60.28386, +49.731.50.22661 Mobile +49.176.63102147, Fax +49.621.60.6628386 stefan.klose@uni-ulm.de http://tinyurl.com/sklose * Recently worked on: Klose, SM, Welbergen, AJ, Kalko EKV (2009) Testosterone is associated with ability to maintain harems in free-living grey- headed flying-foxes (Biology Letters) http://tinyurl.com/ffharems "Stefan Klose (Univ Ulm, Bio 3)*" <stefan.klose@uni-ulm.de>

UMunich PlantEvolution

Ph.D. position in plant evolutionary biology

I am looking for a Ph.D. candidate (3 yrs) interested in the evolution of plant reproductive traits, sexual systems, or biogeography. Current research topics in our group can be found at http://www.sysbot.biologie.uni-muenchen.de/en/people/renner/. The student would we employed according to German TV-L 13 and would be part of Munich University's graduate program in Evolution, Ecology, and Systematics: http://www.eeslmu.de/ . German language skills are not needed, but writing skills, good work ethics, and the ability to think creatively and critically are desired. Munich has a large and active research community in evolutionary biology and phylogenetics, and the city offers excellent infrastructure and beautiful surroundings.

The closing date for applications is June 15, 2010, or when the position is filled. Please send your application, together with a full CV, copies of recent-most educational certificates, and the names of two referees to Susanne Renner (renner@lrz.uni-muenchen.de).

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

UOttawa EvolutionaryFungalGenomics

University of Ottawa - Evolutionary Fungal Genomics

Three research projects are currently available in the field of evolutionary fungal genomics for highly motivated graduate students. The research will be carried out in a newly established, CIFAR (Canadian Institute for Advanced Research) affiliated laboratory led by Dr. Nicolas Corradi in the Department of Biology of the University of Ottawa, Canada. (http://www2.cifar.ca/research/integrated-microbial-biodiversity-program/program-members-imb/?i=394).

The projects will focus on the genomics of two evolutionary unrelated groups of fungi: the Arbuscular Mycorrhizal Fungi (AMF) and the Microsporidia. Two graduate thesis projects will involve the study of AMF genomics in a broad sense, while one graduate student position is open to study the complete genome sequence of a recently described microsporidian parasite.

Applicants for the PhD position on AMF genomics should have some experience in general molecular biology (PCR, cloning, DNA sequencing) and inverted microscopy. Previous experience with either “in vitro” culturing of AMF, bioinformatics software (e.g. Consed, Augustus, Artemis), programming (BioPerl) or with high-throughput DNA sequencing technologies will represent strong assets for the final selection of candidates. For the graduate project on Microsporidia genomics, an applicant with some experience with general molecular biology (PCR, cloning, DNA sequencing) and at least one of the following bioinformatics software (e.g. Consed, Artemis, Velvet) will be preferred. Knowledge of programming (BioPerl) is not necessary for this position but will represent a strong asset for the final selection of the candidate.

Enquiries about specific graduate projects can be sent to Dr. Nicolas Corradi (ncorradi@uottawa.ca). Complete application packages, including a CV (with a list of publications, if applicable), a brief (1-page) statement of research interests, and the names and e-mail addresses of 3 referees should be sent to ncorradi@uottawa.ca. Evaluation of applications will start by July 1st, 2010 and continue until suitable candidates are found.

Relevant papers:

AMF Genomics: Corradi N., Ruffner, B., Croll D., Colard A. and I.R. Sanders. 2009. High molecular diversity at the copper-zinc superoxide dismutase gene among and within species of arbuscular mycorrhizal fungi. Applied and Environmental Microbiology. 75: 1970-1978 Corradi, N., Croll, D., Colard, A., Kuhn, G., Ehinger, M. and I.R. Sanders. 2007. Gene copy number polymorphisms in an arbuscular mycorrhizal fungal population. Applied and Environmental Microbiology 73, 312-319. Corradi, N. and I.R.Sanders, 2006. Evolution of the P-type II ATPase gene family in the fungi and presence of structural genomic changes among isolates of Glomus intraradices. BMC Evolutionary Biology, 6. 21.

Microsporidia Genomics: Corradi N., Pombert, J.F., Farinelli, L., Didier, E., and P.J. Keeling. Submitted. How to make the smallest nuclear genome even smaller: lessons from the microsporidium Encephalitozoon intestinalis. Corradi N., Haag K.L., Pombert J.F. Ebert D. and P.J. Keeling. 2009. Draft genome sequence of the Daphnia pathogen Octosporea bayeri: insights into the gene content, structure and evolution of a large microsporidian genome and a model for host-parasite interactions. Genome Biology 10: R106 Lee,S.C., Corradi, N., Byrnes, E.J., Torres-Martinez, S., Dietrich, F.S., Keeling P.J. and J. Heitman. 2008. Microsporidia evolved from ancestral sexual fungi. Current Biology. 18: 1675-1679

ncorradi@uottawa.ca

UOxford SocialEvolution

Graduate Research Assistant - Evolutionary Social Ecology - University of Oxford Grade 6 Starting salary £25,751 - 30,747 p.a.

A Graduate Research Assistant position is available, for

2 years and 9 months, from 1 October 2010, to work on a project studying social networks in birds from an ecological and evolutionary perspective. The post is funded as part of an ERC Advanced Investigator grant of euro 2.5M over five years to Prof Ben Sheldon. The post will be based in the Edward Grey Institute, Department of Zoology, University of Oxford. The main duties of the post-holder will be to carry out fieldwork around Oxford to collect data on social behaviour and social relationships in wild birds. The post- holder will participate in experiments testing a range of hypotheses about the causes and consequences of social structure with an emphasis on dispersal. This is an exceptional opportunity to participate in a major research project, for which extensive pilot data are already available, and for which funding is guaranteed at a very high level for the duration of the project.

The successful candidate will have a BSc in biology or a related subject, and demonstrate skill and enthusiasm for biological research. Experience of fieldwork under arduous conditions, and of working as part of a multi-disciplinary team are desirable, as are fieldwork skills involving birds.

The post is based in a dynamic and expanding research-active institute, of c. 45 people, fully integrated within the Department of Zoology. Further details about the institute available at: http://www.zoo.ox.ac.uk/egi/- Informal inquiries (with CV) to Prof Ben Sheldon (ben.sheldon@zoo.ox.ac.uk); start date 1 October 2010.

Further particulars and application forms can be downloaded from http://www.zoo.ox.ac.uk/jobs or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS (tel: 01865 271190); email: recruit@zoo.ox.ac.uk. Applications, together with CV and contact details of three referees and a cover letter explaining how the candidate meets the selection criteria, as outlined in the further particulars, should be sent to the above address quoting reference number AT10017. The closing date for applications is 14th June 2010. Interviews will take place by mid July.

ben.sheldon@zoo.ox.ac.uk

UPlymouth ConservationGenetics

NERC PhD Studentship

We are seeking an independent and motivated graduate to fill a NERC studentship starting in October 2010 investigating genetic diversity, rarity and fitness in bumblebee (Bombus spp.) populations.

The project will be supervised by Dr Mairi Knight, Dr Jon Ellis, Dr Richard Billington (School of Biomedical and Biological Sciences, University of Plymouth, UK), and Dr Mark Brown (School of Biological Sciences, Royal Holloway, University of London, UK).

Project Description

There is growing recognition of the urgency with which we need to address the issue of pollinator declines, alongside general concern over the relevance and usefulness of our current approaches to measuring population viability and health in a conservation context. The studentship will sit alongside and build on an existing project, taking a comparative, multi-disciplinary approach to assessing whether measures of neutral genetic diversity and population size are relevant as proxies for population viability, specifically quantifying how they relate to direct measures of fitness in bumblebee (Bombus) populations. The overarching aim of the project is to develop tools that are fit for the purpose of active population monitoring and management while at the same time directly testing widely adopted but increasingly queried theoretical assumptions linking rarity, genetic diversity, and fitness.

The project offers a rich opportunity for a student to develop a significant breadth and depth of key skills in the biological sciences, including field sampling, genotyping and genetic analysis, immunological and biochemical assays, and parasites/pathogen screening. The successful candidate would be based in Plymouth but would also spend some time developing specific skills under the supervision of Dr Mark Brown at Royal Holloway, University of London.

Qualifications and experience required Candidates should have a demonstrable enthusiasm for this general field of study and hold a minimum of an upper second class degree in a relevant subject (e.g. Biology, Ecology, Genetics). We welcome applications from candidates with a relevant MSc or MRes. No previous knowledge of the study organism or experience in field sampling, biochemical assays, molecular ecology or pest and pathogen screening is strictly essential although experience in any of these areas, particularly standard laboratory techniques, would be an advantage. A full UK driver's licence would also be beneficial.

Further Information

The personal maintenance stipend for NERC studentships for 2010/11 will be approximately £13,590 per annum (non-taxable). The position is open to UK citizens and EU citizens who have been resident or studied in the UK for 3 years. For full eligibility requirements see http://www.nerc.ac.uk/funding/available/-postgrad/eligibility.asp. For further information or an informal discussion on the project please contact Dr Mairi Knight (mairi.knight@plymouth.ac.uk). General information on the supervisors' research profiles can be found on the University of Plymouth and Royal Holloway websites: http://www.plymouth.ac.uk/schools/-bio and http://www.rhul.ac.uk/Biological-Sciences/ . Application procedure

Please submit a covering letter with your application explaining your suitability for the post. For further details on how to apply, please visit www.plymouth.ac.uk/pghowtoapply or contact Catherine Johnson (email: catherine.johnson@plymouth.ac.uk). Completed applications can be returned to: Catherine Johnson, Graduate School Research Office, Faculty of Science & Technology, Rm A504 Portland Square, Plymouth, PL4 8AA.

The closing date for applications is Friday 18 June 2010 and interviews are expected to be held in the week commencing 28 June 2010.

Applicants who have not received an invitation to interview by the end of June should consider that their application has been unsuccessful on this occasion.

mairi.knight@plymouth.ac.uk

UQuebecRimouski CrustaceanGeneFlow

NSERC-funded Ph.D. position on gene flow in crustaceans at the Université du Québec à Rimouski

Following the opening of the Bering Strait some 7.4 to 4.8 million years ago, many Pacific taxa invaded the Arctic and North Atlantic Oceans. The subsequent closing of the Bering strait has allowed independent evolution of the Pacific and Atlantic populations and establishment of vicariant taxa in many organisms. With the projected opening of the northwest passage through climate changes, there will be opportunities for new genetic exchanges among the three oceans. This Ph.D. studentship will examine these questions in a selected number of crustacean taxa using mitochondrial and nuclear makers. Levels of cryptic diversity prior to re-opening of the Arctic and expected levels based on past and contemporary gene flow will be assessed. This project is part of the Canadian Marine Biodiversity Network CHONe.

Applicants should email a covering letter and CV to France Dufresne (France_dufresne@uqar.qc.ca). The CV should include: 1. Contact details (including e-mail addresses) for the applicant and 2 referees who would be available to provide references.

France_Dufresne@UQAR.QC.CA

UYork EvolutionaryEcology

NERC PhD studentship project Risks of pharmaceuticals to wild birds Supervisors: Dr Kathryn Arnold (ka619@york.ac.uk), Dr Alistair Boxall (abab500@york.ac.uk), & Dr Piran White (pclw1@york.ac.uk)

Pollutants have long been shown to influence fitness-related traits in wild animals. Emerging but under studied risks are those posed by pharmaceuticals and personal care products (PPCPs) is the environment. These compounds can enter the environment via animal excretory products, or via wastewater and treated and untreated sewage, and may end up in freshwater or terrestrial ecosystems. Some fat-soluble PPCPs can accumulate in animal tissues, and recent research has shown that certain substances such as Prozac can affect the reproductive hormones in certain aquatic animals. They also have the potential to bioaccumulate through the food chain, but the extent of this and its possible effects are unknown.

This project will consider the risk of veterinary drugs to wild birds, using toxicological and ecological field and modelling approaches. It will focus on: (a) uptake into food items; b) uptake into the animals themselves; (c) effects of exposure on fitness related traits; and (d) risks to individuals and populations. The student will have the opportunity to develop expertise in field ecology, ecotoxicology and biological modelling.

Informal enquiries can be made to Dr Kathryn Arnold ka619@york.ac.uk

For more information on the application procedure check the following University of York website: http://www.york.ac.uk/graduatestudy/applying/ .Applications should be submitted to the Graduate Schools Office by May 31st, 2010. Please include with your application: (i) a full CV and (ii) a brief covering letter explaining why you are interested in the project and indicate which project you are applying for as well as the name of the supervisor (s). Interviews are planned for the second week of June 2010.

For further information on the application process, contact: The Graduate Schools Office, University of York, Heslington, York YO10 5DD, UK E-mail: graduate@york.ac.uk (postal applicants and all other general enquiries) Qualifications: For the NERC studentship candidates should have a good first degree (minimum 2:1) in any of the following disciplines: geography, environmental science, chemistry, maths or subjects relevant to the project they are applying for. An appropriate Masters degree will be an advantage. Applications from individuals with applied or business experience is welcome. Generally only UK residents are eligible for NERC funding. To check: http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp Dr Kathryn Arnold

Environment Department, University of York, YORK YO10 5DD, UK

tel +44 (0) 1904 434067

ka619@york.ac.uk

http://www.york.ac.uk/depts/eeem/people/arnold/arnold.htm Kathryn Arnold <ka619@york.ac.uk>

Vienna PopulationGenetics

just a quick reminder-the deadline for applications (25.5.2010) is approaching...

PhD positions in Population Genetics

Over the past years, Vienna has developed into one of the leading centres of population genetics. The Vienna Graduate School of Population Genetics has been founded to provide a training opportunity for PhD students that builds on this outstanding on site expertise.

We invite applications from highly motivated and outstanding students with a background in one of the following disciplines: bioinformatics, statistics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply.

Available topics include: - The role of population subdivision in maintaining genetic variation and inducing divergence - Evolutionary genetics of aging in the D. simulans clade - Statistical methods for detecting various types of selection in genetic data - New algorithm and models to analyze population genetic massive parallel sequence data - Population genetic estimators from NGS data - Population genetics of interspecific adaptation and differentiation - Probabilistic models for the population genetics of molecular evolution - Investigating the molecular basis of morphological evolution within and between species - The genetics of two closely related species of Aquilegia - Measuring gene flow by massively parallel sequencing - Admixture mapping with Bayesian probabilistic models for genome wide population genetic data

Applications need to be received by 21.5.2010 and include CV, motivation letter, two letters of recommendation and an indication of the two preferred topics in a single pdf.

More information about the about the Vienna Graduate School of Population Genetics, the training program and the application procedure can be found at www.popgen-vienna.at . Christian Schlötterer Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://i122server.vu-wien.ac.at/pop Vienna Graduate School of Population Genetics http://www.popgen-vienna.at VetCore Illumina Sequencing Service http://i122server.vu-wien.ac.at/pop/seq/VetCore2.htm schlotc@gmail.com

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Vienna TheoreticalEvolutionaryBiology

PhD-position in theoretical evolutionary biology, Vienna

A 3-year PhD-position in theoretical evolutionary biology is available in the Mathematics and BioSciences Group at the University of Vienna (see www.mabs.at). The successful applicant will work with Michael Kopp on a recently funded project aimed at studying the genetic basis of adaptation to changing environments. Other project partners include Joachim Hermisson, Reinhard Bürger (both University of Vienna) and Thomas Lenormand (CNRS Montpellier).

The project will be based on the “moving optimum model” of adaptation to gradually changing environments (see recent Genetics papers at www.mabs.at:kopp/publications.html). This model shall be extended by including adaptation from standing genetic variation and evolution of multiple correlated traits, using a combination of methods from mathematical population genetics and computer simulations. As part of the project, the student will have the opportunity to spend several months in Montpellier to work with T. Lenormand.

Applicants should be either biologists with good knowledge of mathematics or applied mathematicians/physicists/computer scientists with a strong interest in evolutionary biology. Previous experience in population genetics will be an asset. Knowledge of German is not required.

Informal inquiries as well as formal applications (including a statement of research interests, a CV and contact information for two academic references, in a single PDF file) should be addressed to michael.kopp@univie.ac.at. Review of applications will start June 15 and continue until the position is filled. The ideal starting date is October 2010, but this is flexible and can be negotiated.

Vienna is one of the most attractive cities worldwide, and its scientific community provides a vibrant and stimulating environment with a unique depth of expertise in different areas of both theoretical and empirical evolutionary biology (see www.evolvienna.at). The monthly gross salary is around 1850 Euros.

– Dr. Michael Kopp Postdoctoral researcher Mathematics and Biosciences Group Max F. Perutz Laboratories University of Vienna

Dr. Bohr-Gasse 9 (postal address) VBC 5, room 1722 (physical address) A-1030 Wien Phone: ++43 (0) 1 4277 24052 Mobile: ++43 (0) 664 60277 24052 Fax: ++43 (0) 1 4277 24098 Email: michael.kopp@univie.ac.at www.mabs.at michael.kopp@univie.ac.at

Jobs

Cincinnati EPA ResTech PopulationGenetics

The Ecological Exposure Research Division (EERD) of the National Exposure Research Laboratory (NERL), Office of Research and Development (ORD), U.S. Environmental Protection Agency (EPA), located in Cincinnati Ohio, is seeking an individual, at least 18 years of age who is either a student (in good standing enrolled in a degree program, not necessarily carrying a full course load, but pursuing a degree at a recognized educational institution) or recent graduate (graduated with a degree from a college or university with the past two years) to provide services under a contractual agreement to provide technical laboratory support for research projects focusing on any of the following projects: (1) use of population genetics approaches to reconstruct histories, spread and other facets related to aquatic invasive species; (2) development of molecular techniques to inventory and quantify organisms collected from stream, river, lake, and other samples; (3) population genetic studies of aquatic organisms subjected to one or more environmental stressors. Work involved with the tasks may include, but is not limited to: (1) tissue and sample collection and organization; (2) DNA extractions; (3) PCR amplification and purification; (4) molecular cloning; (5) microsatellite genotyping; (6) DNA sequencing; (7) analysis of genotype and DNA sequence data; and (8) other general laboratory and field duties necessary to carry out research (e.g., sample collection and transport, routine equipment maintenance).

The student/recent graduate contractor should ideally possess skills/experience in specific molecular biology laboratory work, such as DNA extraction and PCR chemistry and also general laboratory practices, including health and safety, as well as having completed a B.S. degree in Biology, or a related sub-discipline such as Genetics, Molecular Biology, Biochemistry, Environmental Sciences, Zoology or Botany, within the past 24 months.

This work is projected to begin as soon as possible, depending upon the availability of the selected student contractor, and represents a not-to-exceed estimate of 1880 hours of effort for one year, with an option to continue an additional year. The hourly rate is commensurate with the minimum required level of education and experience, as follows: $22.01 per hour.

U.S. citizens are eligible to participate in this program. Non-U.S. citizens may be eligible to participate, depending on their immigration status and the applicable regulations of the United States Citizenship and Immigration Service (USCIS). All non-US citizens must submit, as part of their proposal package, evidence of their immigration status that allows them to work in the United States. EPA ORD employees, their spouses, and children are NOT eligible to participate in this program and receive these contracts.

To see further details and to apply for the position go to: http://www.epa.gov/oamrtpnc/q1000145/index.htm . This job posting is currently scheduled to close May 7, however the application period may be extended depending on the number of qualified applicants responding by that date.

martinson.john@epa.gov

ColoradoStateU NaturalSciencesDean

Position Description Dean of the College of Natural Sciences, Colorado State University

Colorado State University (CSU) seeks a visionary leader to serve as dean of the College of Natural Sciences (CNS). The dean is the chief administrative and academic officer with responsibility for leadership in coordinating and overseeing the Colleges programs, budgets and related activities including resident instruction, research, outreach and international activities. The dean is responsible for annual appropriated budget allocations of $25 million for resident instruction as well as oversight of annual research budgets of approximately $25 million. The dean reports directly to the Provost/Academic Vice President. The College of Natural Sciences is one of eight colleges within Colorado State University. The CNS has eight departments: Biochemistry and Molecular Biology, Biology, Chemistry, Computer Science, Mathematics, Physics, Psychology and Statistics.

Colorado State University, Fort Collins, is a Carnegie Doctoral/Research University-Extensive land-grant institution enrolling approximately 25,000 students from 49 states and 82 countries. Fort Collins, located 60 miles north of Denver at the base of the Front Range of the Rocky Mountains, is a rapidly growing community with a population of approximately 150,000. Fort Collins enjoys a temperate, semi-arid climate and rich cultural and recreational opportunities.

The search committee will accept confidential applications and nominations until the position is filled. For full consideration, a complete application must be received electronically by July 15, 2010. To view the complete job description, please go to http://www.natsci.colostate.edu/employment/Dean/. Questions or nominations should be directed to Patsy Harlan at patsy.harlan@colostate.edu.

Colorado State University is an EO/AA employer and conducts background checks on all final candidates.

Lisa Angeloni

Lisa Angeloni <angeloni@lamar.colostate.edu>

DukeU LaboratoryHelp

Job for a recent college grad...

Full-time teaching/prep positions in the Biology 102L “Genetics and Evolution” course at Duke University

Position description: Work full time (40 hours/week) as a teaching assistant and laboratory prep assistant in the introductory biology program for the 2010-2011 academic year. The position has two main components, teaching and behind-the-scenes laboratory preparation.

Teaching component: The primary teaching responsibility of the position is to lead laboratory sections of up to 12 students in the Biology Departmentâs new genetics and evolution Gateway course, Biology102L. Each Biology 102L section meets weekly for 2.5 hours for a combined hands-on laboratory/problem-based learning session. Additional teaching responsibilities include (a) attending and taking notes at all course lectures including the weekly large discussion section, (b) grading weekly student written assignments and occasional oral presentations, (c) helping with the preparation and grading of mid-semester hourly and final exams, and (d) assisting students during office hours and otherwise mentoring students as beginning biologists.

Teaching assistants should plan to return to Durham early the week of August 23, 2010, and are expected to participate in a teacher-training workshop before the fall semester begins. TAs also attend weekly prep sessions during the semester on Monday afternoons.

Prep component: The second set of duties associated with the position is to assist in the preparatory work for the teaching labs in Biology 101L, 102L, and the laboratory diversity course, Biology 106L, as determined by the Lab Administrator. Responsibilities include setting up and putting away equipment and specimens for laboratory exercises, maintaining supplies in lab rooms between sections, cleaning glassware, assisting with field collection of live specimens, and helping to care for a diverse collection of invertebrate animals in salt-water aquaria. The lab prep workload is likely to require evening (until 10 PM) and/or early morning (8 AM) work.

Salary: The projected salary for the position is $17,500. Employment begins on August 23, 2010 and ends May 9, 2011 with payment made in 9 equal amounts on the 25th of each month starting in September and ending in May. Full-time teaching/prep employees are eligible for health plans made available by the University.

Qualifications: Applicants should have a strong, varied background in biology, especially genetics and evolution, with a superior science GPA. A very important attribute is a high level of energy and an enthusiasm for teaching genetics and evolution. Prior enrollment in Biology 25L, 118, and 116, or the equivalent, is highly desirable; experience tending Drosophila is a plus. Teaching assistants in Biology 102L are expected to be actively engaged with their students in all aspects of the course and to serve as role models and mentors. Because they are a vital part of the introductory biology teaching team both in the classroom and behind the scenes, full-time assistants must be willing to commit themselves fully to the responsibilities of the position described above and as determined by the faculty members in charge of the Gateway course.

Interviews and Application Process: Formal interviews are planned to begin after May 3, 2010. Hiring decisions will be made on a rolling basis thereafter, continuing as necessary.

Interested applicants should provide (a) a cover letter, (b) a transcript, and (c) a resume with the names of two references (preferably at Duke for Duke students or alumni) to Julie Noor. These may be emailed to jkfnoor@duke.edu, delivered to Julie Noorâs office (070 BioSci.) or to her mailbox in the Department of Biology, or mailed to her at the Department of Biology, Box 90338, Duke University, Durham, NC 27708-0338. To be assured of consideration, applications should be submitted by May 3, 2010.

For more information contact Julie Noor by phone at 919-613-8224 or e-mail at jkfnoor@duke.edu

noor@duke.edu

Mexico FieldTech MosquitoEvolution

A field technician is needed for a project in Tapachula, Mexico from June through August, 2010. This project is looking at larval ecology of the mosquito Aedes aegypti. Aedes aegypti is a vector of Dengue Fever. These mosquitoes develop as larvae in containers of water in and around peoples' houses. In order to design more efficient approaches for controlling Ae. aegypti it is critical to understand the factors that regulate the larval population within water-filled containers. These studies focus on understanding the impact of density and competition on the population. Field work involves collecting buckets from people's houses to use for the experiments, counting larvae everyday, identifying larval instars and identifying adult mosquitoes. We are looking for a person that has the following skills: pays close attention to detail, experience with microscopes, willing to work long hours, tolerant of mosquitoes, and able to be lead a 2 person team. Knowledge of Spanish is preferable but not required for application.

Lodging and Food will be covered, Air transportation is negotiable.

For more information on the project please visit the following website and click on people, bios and projects: Rachael Katz

http://www4.ncsu.edu/˜fgould/index1.html To Apply: Please send a cover letter, resume, and references to rskatz@ncsu.edu

"Rachael S. Katz" <rachael_katz@ncsu.edu>

MichiganStateU Director with EvolBiol experience

Office of the Vice President for Research and Graduate Studies

Fixed-term, 12-month basis, 100% time

Minimum salary is $75,000

Duties: Managing Director of a new NSF Science and Technology Center being established, to operate August 1, 2010 - July 31, 2021, and headquartered at Michigan State University. Position reports to the Director of the BEACON Center. The administrative team to be managed includes an administrative assistant, education director, diversity director, bookkeeper, knowledge transfer manager, K-12 outreach manager, and one or more information technologists. Managing Director duties include working with Center faculty and staff to:

1) assist the director and the center's Executive Committee in formulating center policies and planning of center activities (research, education, outreach)

2) administer the process for allocation of funds to projects, on an annual basis, in coordination with all of the partner institutions

3) prepare reports to the National Science Foundation documenting all Center activities and their outcomes, including financial, scientific, educational, and outreach

4) coordinate with partner universities to oversee their conduct of Center-funded projects

5) coordinate with other staff to organize the meetings, conferences and workshops sponsored by the Center, and to prepare for site visits to the Center by its External Advisory Committee and by the National Science Foundation

6) prepare renewal proposals for the Center's NSF funding, and assist Center faculty and staff in preparation of new proposals for additional center-related activities

7) participate in one or more of the center's research, education, or outreach projects, including, ideally, ones initiated by the successful candidate for this position

Qualifications: Ph.D. in a natural science or an engineering discipline, including computer science, or related area. Qualifications other than degree: substantial experience in conduct of funded research projects, as a PI, co-PI, or research associate; preparation of research proposals and authorship of professional articles, preferably including content related to evolutionary biology and/or computational evolution. Experience managing a group of researchers is preferred.

Applications: Due June 15, 2010. Position to begin August 1, 2010. Late submissions will be considered if a suitable candidate pool is not identified by the deadline. MSU is an equal-opportunity employer. MSU is committed to achieving excellence through cultural diversity. The university actively encourages applications and/or nominations of women, persons of color, veterans and persons with disabilities. Cover letter, resume, names of three references and 2-page statement describing interest in the position to goodman@egr.msu.edu.

All interested parties are to apply to goodman@egr.msu.edu

j.dunican@jobtarget.com

MichiganStateU ResAssist MammalianGeneticStructure

Research Assistant I - Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI

*** Please apply online at http://www.hr.msu.edu/-hiring/msujobs.htm ****

Posting Number: 3852 Department of Fisheries and Wildlife Position type: Research Position title: Research Assistant I

Position Summary: The Department seeks a highly motivated individual to join the Scribner lab as a full time Research Assistant I beginning in the summer of 2010. The successful applicant will contribute to projects in the area of mammalian landscape genetics that employ molecular, remote censusing, and field-based approaches to understand the importance of land-use and land-cover on spatial genetic structure of mammalian species in Michigan. The Scribner lab is housed in the Natural Resources Building on the Michigan State University campus; a collaborative research group with interests in evolutionary ecology, behavioral ecology, and resource conservation.

Additional Information: Responsibilities will include but are not restricted to: DNA extraction and quantification, PCR, microsatellite and mtDNA sequencing, data base management, coordination of molecular and ecological data bases, general lab organization and maintenance. Opportunities for field research exist.

Basic Qualifications: Applications should have an interest in ecological genetics including applications of landscape and phylogeographic theory to studies of population and individual-based analyses of spatial genetic structure. The position requires an independent, highly organized and motivated individual with experience with generation of molecular data and integration and analyses of genetic and ecological data bases. Educational requirements include knowledge equivalent to that which normally would be acquired by completing a B.A., B.S. or M.S. degree in zoology, molecular biology, microbiology, genetics, or related fields; one to three years of related and progressively more responsible or expansive work experience, including knowledge and skills in: DNA sequencing, microsatellite and/or SNP genotyping, and PCR, and experience in areas of curation, manipulation, and analysis of molecular genetic databases and operation of laboratory equipment, including automated sequencing/genotyping platforms; knowledge of computer operation, database management, and use of word processing software and software associated with genotyping and sequencing data; knowledge of safe laboratory practices and safety regulations; or an equivalent combination of education and experience; possession of a valid vehicle operator's license.

Required Applicant Documents: Resume/CV Cover Letter References

Contacts: Sarah Wescott, Administrative Asst. Human Resources Office Michigan State University Tel: (517)-884-0211 Email: kovachsa@msu.edu

Kim Scribner, Professor Department of Fisheries & Wildlife and Department of Zoology 13 Natural Resources Building Michigan State University East Lansing, Michigan 48824-1222 tel: (517)-353-3288 (office) (517)-432-4935 (lab) fax: (517)-432-1699 email: scribne3@msu.edu website: http://www.fw.msu.edu/-~scribne3/ scribne3@msu.edu

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Munich EvolutionProgramCoordinator

The EES-LMU Graduate Program in Evolution, Ecology and Systematics at the University of Munich (LMU) is looking for a

Coordinator (full time)

for our Master and Ph.D. programs, our summer school, and our seminar series. The coordinator will also be the local organizer of a joint Erasmus Mundus Master Program (MEME) that is a collaboration with the Universities of Groningen, Uppsala, and Montpellier (with Harvard University as an external partner). 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. The official language of the programs is English, but knowledge of German is also desirable. Experience with teaching, administration or curriculum coordination is an advantage.

The novel, research-oriented EES-LMU Master program started in fall 2007, mainly with international students. Currently about 20 students are enrolled, and we expect this number to increase in the future. The EES-LMU Ph.D. program started in 2008 and currently has about 30 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, and the Bavarian Natural History Collections are involved. The MEME program will welcome its first Master students in fall 2010, with up to 32 students spread over the 4 partner universities. The coordinator functions as an interface between university administration, international partners, instructors, and students, and he/she could also be involved in teaching.

For more information on the programs, please see the websites:

http://www.eeslmu.de/eeswiki http://www.evobio.eu/ 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 evolution, ecology and systematics. The initial appointment will be for 2 years, with the possibility of extension pending funding, and will be paid at TVöD 13 according to the German salary scale. The application deadline is May 28, 2010. Interviews will be held in early June. Informal inquiries and applications including a letter of motivation, CV, and contact information of two references should be sent (preferably by email as a single pdf file) to:

Prof. John Parsch Department of Biology II University of Munich Grosshaderner Str. 2 82152 Planegg-Martinsried Germany parsch@bio.lmu.de

parsch@zi.biologie.uni-muenchen.de

MuseumKoenig Bonn Herpetology

The Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn (http://www.zfmk.de), seeks to fill the position of a researcher in the Department of Vertebrates (successor of Prof. Wolfgang Böhme). The position is expected to be available by December 2010. Potential candidates will hold a PhD in zoology or related areas, have their research focus on systematics of reptiles and/or amphibians, and present a substantial publication record in taxonomic, phylogenetic and other biosystematic research. The candidate is expected to work in these fields from a sound theoretical basis and be able to apply an array of appropriate modern methods. He/she should be able to combine collection-based work with modern phylogenetic and/or ecological approaches. The candidate is also expected to integrate into ongoing research projects at the ZFMK and teaching programmes in the University of Bonn and to be successful in raising external funds.

The successful candidate will be active in research projects and will be responsible as a curator for caring, managing and further increasing and developing the substantial, internationally important amphibian and reptile collections in the ZFMK. He/she will also be involved in the self-administration of the institute and may eventually serve as the head of the vertebrate department. The candidate is also expected to demonstrate commitment to community engaement in his/her field of research.

The successful candidate will be employed for an initial period of five years, after which he/she will obtain tenure depending on his/her performance. According to German law, applications by women and by disabled scientists will be given priority in case of superior or equal qualifications. Depending on occupational qualifications and experience, salary corresponds to grade TV-L/13 - 15 in the German Public Service scheme.

The ZFMK is a fellow institute of the "Wissenschaftsgemeinschaft Gottfried Wilhelm Leibniz" (WGL Science Community) and works in close cooperation with the University of Bonn. It comprises internationally important scientific collections, libraries, electron microscopy,and bioacoustic, histological and molecular laboratories.

Interested applicants should submit a CV, complete publication record, a statement of teaching experience and research funding, certificates of university degrees, and selected publications in hard copies to the following address:

Prof. Dr. J.W. Wägele, Director, Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, D-53113 Bonn, Germany, by August 31 2010. E-mail inquiries: <w.waegele.zfmk@uni-bonn.de>.

Prof. Dr. J. Wolfgang Waegele Direktor Zoologisches Forschungsmuseum Alexander Koenig und Lehrstuhl für Spezielle Zoologie Rheinische Friedrich-Wilhelms-Universität Bonn Adenauerallee 160 53113 Bonn, Germany

w.waegele.zfmk@uni-bonn.de

Tel.: 0049 (0) 228 9122 200 Fax: 0049 (0) 2289122 202 http://www.zfmk.de

Werden Sie Mitglied der Alexander Koenig Gesellschaft! (http://www.zfmk.de/web/Foerderer/-Freunde/index.de.html)

"W. Waegele" <w.waegele.zfmk@uni-bonn.de>

NewYorkU ResTech PhenotypicVariation

The Rockman Lab at NYU seeks a research technician to support its research into the genetic basis of phenotypic variation (http://homepages.nyu.edu/~mr176).

The technician will be responsible for routine laboratory operations, including ordering supplies, maintaining inventories, preparing media and reagents, and managing our frozen strain collection. In addition, the technician will have a major role in experimental analysis of phenotypic traits (behavioral, morphological, cellular, and molecular) in our research organisms, Caenorhabditis nematodes. There is also space for development of independent projects.

Applicants should be capable, organized, responsible, and motivated, with experience in experimental biology. Worm experience is not essential. The start date is negotiable; our preference is for a start between May 31 and July 23.

Our laboratory is part of the Department of Biology and Center for Genomics and Systems Biology at New York University, located in the heart of Greenwich Village in Manhattan. The collaborative and collegial research environment is ideal for work in evolutionary functional genomics. New York University is an equal opportunity employer.

Applicants should send a CV outlining their qualifications to mrockman@nyu.edu .

Matthew Rockman Department of Biology and Center for Genomics & Systems Biology New York University 100 Washington Square East, Rm 1009 New York, NY 10003 (212) 998 8490

mrockman@nyu.edu

PurdueU ResTech TurtlePopulationGenetics

Description: This is a three-month technician job that is part of a study of the population genetics of eastern box turtles. The technician will help search for eastern box turtles in the wild across Indiana and help with various laboratory duties at Purdue when weather permits. Duties will include 1.) travelling independently or with a grad student around Indiana and conducting visual surveys for eastern box turtles, 2.) collecting morphological data and taking a tissue sample from each individual, 3.) entering data, 4.) independently performing various laboratory procedures such as DNA extraction and PCR. Note housing is provided only when traveling; applicant responsible for housing while doing laboratory work.

Qualifications: the successful applicant will be energetic, willing to work outdoors in inclement weather and exposed to insects, thorns, storms, etc. Experience in wildlife, biology or related field is preferred. Experience with simple GPS data, turtle locating, and genetics laboratory experience are also preferred. A drivers license and a good driving record are required. Submit 1.) a cover letter describing why you are the best candidate for the job, 2.) a CV and 3.) the names and contact information for three references to Steve Kimble at skimble@purdue.edu.

Steve Kimble PhD student, Department of Forestry and Natural Resources Purdue University skimble@purdue.edu sjkimble@gmail.com 205.337.4843 http://web.ics.purdue.edu/~rodw/Steve%20Kimble.htm steve kimble <sjkimble@gmail.com>

UArizona iPlant ProgrammerAnalyst

iPlant Tree of Life Engagement Team Analyst

The iPlant Tree of Life (iPToL) project (http://iptol.iplantcollaborative.org) is seeking an engagement team analyst (ETA) to work at the BIO5 Institute at the University of Arizona in Tucson. The ETA serves as a liaison between scientific working groups the iPlant software development team. This involves active discussion with the scientists, research into appropriate supporting technologies, and the judicious application of technical judgment to convert working group conversation into practical design requirements.

The primary responsibilities of the iPToL Engagement Team Analyst include:

- Translation of working group discussions into formal software requirements - Tool research and evaluation, prototype software development - Attending working group meetings and leading technical discussions - Working with scientific collaborators to develop workflows and narratives - Performing related duties as assigned by the iPToL Scientific Lead and Project Manager

REQUIRED QUALIFICATIONS - Advanced degree (MS or Ph.D) in a life science discipline (biology, genetics, biochemistry, etc.). Candidates with a degree in another natural science, computer science, information technology or a related discipline will also be considered with a demonstrated track record of research experience in the life sciences; - 2-3 years work experience conducting computational biology research and/or collaborative scientific software development (academic, government, or industry); - interest in science and technology and ability to rapidly adapt to new technologies; - excellent oral presentation and communications skills; - advanced ability to work independently under established deadlines and as part of a team; - ability to travel as required to partner/collaborator institutions, relevant conferences, etc.

PREFERRED QUALIFICATIONS - A research background in evolutionary biology or phylogenetics - experience in projects involving advanced computing and information technologies used in life science research in academia, government laboratories, and/or industry; - strong programming skills - proven ability to promote and support the use of high-performance computing, visualization, networking, and massive data storage systems to scientists to expand their research impact.

To apply to this position, please visit http://tinyurl.com/iptol-eta Sheldon McKay, PhD Engagement Team Scientific Lead, iPlant Collaborative BIO5 Institute, University of Arizona Email: mckays@email.arizona.edu Google Voice: (203) 701-9204

sheldon.mckay@gmail.com

UBern Zambia CichlidBreeding

Short title: Swizerland/Zambia_Field assistant cooperative breeding African cichlids_UnivBern

"2 field assistant to study cooperative breeding African cichlids, Lake Tanganyika (Zambia)

The project investigates the influences of personalities on helping behavior and fitness prospects in the highly social, cooperatively breeding cichlid Neolamprologus pulcher. It is part of an ongoing project which has been launched in 2009 attempting to follow permanently marked individuals over several years. The field assistants will be involved in catching, marking and testing individuals and carrying out behavioral observations under water using Psion PDAs and Observer software of marked fish in their natural group. We search for 2 field assistants for the field season of the University of Bern in autumn 2010. The field work will last 3 months and takes place near Mpulungu, Zambia, starting end of August /beginning of September. Candidates must hold a SCUBA diving certificate (PADI Open Water Diver or equivalent) and should have diving experience (diving depth: 8-12m). The field team will have 3 members and support from local authorities. Experience in conducting behavioral observations is considered an asset. Accommodation at the field site is remote and very basic, but beautifully located on the shore of Lake Tanganyika. Fieldwork and diving is physically demanding. All expenses for travel, accommodation and medical precaution are covered, but no salary can be paid.

Candidates send a statement of scientific interests and their CV to: markus.zoettl@iee.unibe.ch

Further information about the working group and our institute: http://behav.zoology.unibe.ch/ Contact: Markus Zöttl Institute of Ecology and Evolution University of Bern Wohlenstrasse 50A 3032 Hinterkappelen Switzerland Tel: +41 31 631 9158"

Thank you very much, Markus

PhD candidate Institute of Ecology and Evolution University of Bern Wohlenstrasse 50A 3032 Hinterkappelen Switzerland

Tel: +41 31 631 9158

"Zöttl, Markus (IEE)" <markus.zoettl@iee.unibe.ch>

UCaliforniaSanDiego DrosophilaEvolution

Project Scientist Position

Division of Biological Sciences at the University of California, San Diego invites applications for a new Project Scientist position with a strong preference for the rank of Assistant Project Scientist. Applicants must have a Ph.D. and several years of postdoctoral training in Drosophila biology. The area of scholarship is open, but we are interested in candidates with substantial experience in genetics and/or evolution. The successful candidate must have strong written and oral communication skills as they will manage the Drosophila Species Stock Center and be responsible for developing genetic resources for the Center. Level of appointment will be commensurate with qualifications and experience. Salary will be based upon University of California pay scale.

Complete applications received by May 21, 2010 will be assured of consideration. A complete application will consist of a curriculum vita, including a full list of publications, synopsis of professional goals, research interests and three letters of recommendation (mailed directly from referee) to:

Therese Markow Laboratory Search Committee

Attention: Dan Angeles, Mail Code 0346-A

Division of Biological Sciences

University of California, San Diego

9500 Gilman Drive, La Jolla, CA 92093-0346

or dangeles@ucsd.edu with the Reference-candidate name on the subject line.

UCSD is an equal opportunity-affirmative action employer with a strong institutional commitment to the achievement of diversity among its faculty and staff, and applicants are also invited to summarize their own contributions to diversity.

Therese Ann Markow, Professor Amylin Chair in Life Sciences Section of Ecology Behavior and Evolution Division of Biological Sciences Muir Biology Building 2215 9500 Gilman Drive University of California at San Diego La Jolla, CA 92093-0116

Email: tmarkow at ucsd.edu Phone: (858) 246 0095 Laboratory: (858) 246 0402 FAX:(858) 534-7108

http://biology.ucsd.edu/labs/markow/ http://stockcenter.ucsd.edu Therese Markow <tmarkow@ucsd.edu>

UCapeTown AvianEvolution

Opportunity to join the University of Cape Town

Position: Senior Lecturer - Percy FitzPatrick Institute of African Ornithology, Department of Zoology (Ref. 2205).

We invite applications for the above permanent position in the Percy FitzPatrick Institute of African Ornithology, a world-renowned, national Centre of Excellence in ornithological research with a strong emphasis on postgraduate supervision.

The Institute is seeking a person with strengths in modern approaches to avian conservation or avian evolutionary/behavioural ecology and with competence in biostatistics. Applicants must have a PhD, with at least five years postdoctoral experience, a sound publication record in ornithology and experience in postgraduate supervision.

The successful candidate will be expected to work as part of a research team, but to pursue his/her own research, publish research findings in journals of high international standing, recruit and supervise postgraduate students, and attract research funding. The annual remuneration package, including benefits, is R433 117 (w.e.f. 1 July 2010: R446 898). Closing date: 30 June 2010

To view the full advertisements and application requirements, please visit www.uct.ac.za and click on Vacancies.

UCT is committed to the pursuit of excellence, diversity and redress. Our Employment Equity Policy is available at http://hr.uct.ac.za/policies/ee.php .

Jacqueline.Bishop@uct.ac.za

UdelosAndes PopulationGenetics

Job announcement (versión en español abajo):

*UNIVERSITY OF LOS ANDES: Population Geneticist *

The Department of Biological Sciences at the Universidad de los Andes in Bogotá, Colombia, seeks to fill a full time position in Population Genetics at the Assistant or Associate Professor level. The successful applicant will be based in the Institute of Population Genetics and Phylogeography. The applicant must possess a Ph.D., preferably with postdoctoral experience and a successful track record of scientific productivity. Applicants with additional expertise in molecular population genetics, coalescent theory, genomics or computational biology are especially encouraged to apply.

The successful candidate will be expected to teach an undergraduate course in genetics, along with graduate courses in his or her area of expertise, advise undergraduate, masters and doctoral students in the Department of Biological Sciences.

The Biological Sciences Department at the Universidad de los Andes is among the top biology programs in Latin America, and hosts 26 full-time professors. Internationally recognized research programs include speciation genetics, microbial genomics, phylogeography, bioinformatics, evolutionary ecology, human genetics, and molecular systematics. The Institute houses a molecular genetics laboratory and the Department offers a centralized DNA sequencing facility. The Biology faculty is young and growing rapidly, with five new hires in the last year. For more information visit: http://cienciasbiologicas.uniandes.edu.co/ Interested candidates should send (preferably as a single PDF) a curriculum vitae, a 1-page description of her or his research program, and a brief teaching statement describing experience and philosophy to the search committee (Comité de Contrataciones Profesorales) at the following email address: ccontbio@uniandes.edu.co

Deadline for receipt of material is: July 31, 2010. Preferred candidates will then be asked to submit letters of recommendation and copies of recent publications.

For additional information, please contact: Andrew J. Crawford, Assistant Professor Instituto de Genética de Poblaciones y Filogeografía, Departamento de Ciencias Biológicas, Universidad de los Andes Email: aj.crawford244@uniandes.edu.co Web: http://dna.ac * * *UNIVERSIDAD DE LOS ANDES: **Genética poblacional*

El Departamento de Ciencias Biológicas de la Universidad de los Andes en Bogotá, Colombia, busca candidatos para una plaza de profesor asistente / asociado en Genética de Poblaciones. El candidato seleccionado estará vinculado al Instituto de Genética y Filogeografía. Los candidatos deben poseer título de doctorado, preferiblemente con experiencia postdoctoral, y contar con una amplia producción científica. Estamos especialmente interesados en candidatos con conocimiento en genética molecular de poblaciones, teoría de coalescencia, genómica o biología computacional.

El candidato seleccionado deberá impartir un curso de pregrado en genética, conjuntamente con cursos de posgrado en su área de especialidad y la supervisión de estudiantes de pregrado, maestría y doctorado en el Departamento de Ciencias Biológicas.

El Departamento de Ciencias Biológicas de la Universidad de los Andes ofrece uno de los mejores programas en Biología y Microbiología de América Latina y en él trabajan 26 profesores investigadores de tiempo completo. Cuenta con múltiples programas de investigación reconocidos a nivel internacional, como genética de la especiación, genómica microbiana, filogeografía, bioinformática, ecología evolutiva, genética humana y sistemática molecular. El Instituto cuenta con un laboratorio de genética molecular y el Departamento dispone de una unidad de secuenciación centralizada. El Departamento ofrece un ambiente joven, dinámico y vibrante con un crecimiento rápido. El último año se contrataron cinco nuevos investigadores. Para mayor información, visite: http://cienciasbiologicas.uniandes.edu.co/ Los candidatos interesados deben enviar un curriculum vitae, una descripción de su línea de investigación (una página), y una declaración breve de su experiencia y filosofía docente (preferiblemente en un solo documento PDF) al Comité de Contrataciones Profesorales por el siguiente correo electrónico: ccontbio@uniandes.edu.co

La fecha límite para la entrega de documentos es el 31 de julio de 2010. A los candidatos seleccionados se les solicitarán cartas de recomendación y copias de sus publicaciones recientes.

Si necesita información adicional, por favor no dude en contactar a: Andrew J. Crawford, Profesor Asistente Instituto de Genética de Poblaciones y Filogeografía,

— / —

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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UKansasLawrence ResTech HydrozoanSystematics

Research Assistant/Technician: Hydrozoan systematics and evolutionary development A staff research assistant position in the fields of systematics and evolutionary development is available in the Cartwright lab (http://www.people.ku.edu/˜pcart/index.html) in the Department of Ecology and Evolutionary Biology at the University of Kansas in Lawrence, KS. This lab investigates the evolution of the marine invertebrate group, Hydrozoa, by investigating their phylogenetic relationships and comparative development. The research assistant will directly contribute to both lab management and the lab research program. The position is for 1-2 years, available immediately but start date is negotiable. Salary range $30,000–$35,000/year, depending on experience.

Responsibilities include:

Assisting in the daily operation of the lab including ordering supplies and preparation of reagents. (25%) Supervising undergraduate employees. (10%) Maintaining aquaria with live cultures of hydrozoans. (10%) Molecular biology laboratory procedures: DNA and RNA extraction, PCR, RT-PCR, cloning, library construction, in-situ hybridization. (50%) Involvement in the lab research program by working as a team member and contributing to the intellectual environment. (5

Required qualifications:

A Bachelors degree in biological sciences or closely related field from an accredited 4-year institution. 1 year of professional experience in molecular lab research. Molecular laboratory experience outside of classroom laboratories, such as lab internships, independent undergraduate research, or graduate work in a lab, may be substituted for professional experience. Ability to work independently, and with attention to lab protocols, detail and organizational requirements as demonstrated by professional experience or independent student research as described in letter of application. Enthusiasm for research in systematics, evolutionary development or invertebrate biology as demonstrated through professional or independent laboratory experience, or class work and described in letter of application. Preferred qualifications: Professional laboratory research experience in molecular phylogenetics and/or evolutionary development. Lab, museum collection, or field experience in invertebrate biology. Familiarity with bioinformatics and a computer programming language such as PERL or Python.

For complete position description and application instructions visit https://jobs.ku.edu, position #00208310. Questions can be directed to Dr. Paulyn Carwright email: pcart@ku.edu Review begins 5/15/10 EOAA employer

pcart@ku.edu

UKansas ResTech DrosophilaVariation

An NIH-funded Research Technician position is available in Stuart Macdonald's lab in the Department of Molecular Biosciences at the University of Kansas. The Macdonald lab explores the genetic basis of complex phenotypic variation within and between species using Drosophila as a model system. We seek an enthusiastic individual to supervise and carry out large-scale genetics/genomics projects, and to oversee various lab activities. The responsibilities of the technician will include maintaining and using a large panel of Drosophila strains, and helping with quantitative genetic experiments. The successful candidate should be motivated, organized, and careful, and should have excellent oral and written communication skills. Salary will be commensurate with experience and will include benefits.

Required qualifications are a Bachelors degree in biology or a related field, and demonstrable experience conducting research in a (broadly- defined) genetics or molecular biology laboratory. Preference will be given to candidates with significant experience in the laboratory (including troubleshooting and optimizing protocols). Prior experience with Drosophila is not essential, but would be an asset.

The position is open and review of applications will begin on May 21 and continue until the position is filled. Informal inquires are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at https://jobs.ku.edu (position number 00206283). Attach a cover letter (describing your interest in the position and any relevant expertise), a full CV, and complete contact information for 3 referees. EO/AA Employer.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 1030 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu web: http://web.ku.edu/-sjmac/ sjmac@ku.edu

ULouvian TeachingAssistant

Dear all,

below is an offer for a teaching position offered in Belgium (Universite catholique de Louvain). As knowledge of French is a prerequisite for this position, the rest of the message is in French. My apologies for those who are therefore not concerned. Nicolas

L'université catholique de Louvain annonce la vacance d'un poste d'assistant en biologie quantitative / conservation de la biodiversite. Ce poste, d'une duree de 6 ans, vise a la realisation d'une these de doctorat tout en assurant +-250h d'enseignement de travaux partiques par an.

Notre equipe de recherche "Quantitative Conservation Biology" mene des recherches en dynamique et viabilite des (meta)populations dans un cadre de conservation de la biodiversite. Notre site web (http://-www.uclouvain.be/quant-cons-biol) detaille nos projets de recherche actuels.

Le detail du poste (ref 00001328) est disponible ici: http://wwwsapsme.sipr.ucl.ac.be/HR/-RFC?sap-language=3DF&_FUNCTION=-3DZ_WWW_HR_DISPLAY_POS_DESCRIPT&POSITION=-00001328&FACULTE=SC Les candidatures doivent etre soumises au plus tard pour le 28 mai: http://-www.uclouvain.be/11617 Si les aspects quantitatifs de l'ecologie et de la conservation de la biodiversite vous attirent, si realiser une these de doctorat dans notre equipe de recherche tout en assurant une activite d'enseignement vous interesse, prenez contact des que possible avec moi.

Prof. Nicolas Schtickzelle Research Associate (FNRS) & Lecturer Head of Quantitative Conservation Biology group

Universite catholique de Louvain Earth and Life Institute Biodiversity Research Centre Croix du Sud 4 B-1348 Louvain-la-Neuve Belgium

phone : +32 10 47 20 52 fax : +32 10 47 34 90 office: building Carnoy, room C.157

nicolas.schtickzelle@uclouvain.be http://-www.uclouvain.be/quant-cons-biol nicolas.schtickzelle@uclouvain.be

USDA Montana EvolutionInvasivePlants

Interdisciplinary: Research Evolutionist/Entomologist, GS-0408/0414-12/13

Salary Range of $68,809.00 - 106,369.00 per year

The United States Department of Agriculture, Agricultural Research Service, Northern Plains Agricultural Research Laboratory, Pest Management Research Unit in Sidney, Montana is seeking a permanent full-time Research Ecologist/ Entomologist as a lead investigator in classical biological control of invasive plants of the Northern Great Plains. The research focuses on plant and insect ecology; plant-herbivore interactions; characterization of ecological factors affecting biological control agents (insects or other arthropods) and invasive weeds; host-specificity and efficacy studies of potential biological control agents; non-target effects of biocontrol on ecological communities; post-release efficacy studies; and long-term monitoring. For details and to apply, see http://www.usajobs.opm.gov/ .Reference Job Announcement Number —-ARS-X10W-0124A. Applications must be postmarked by May 28, 2010. U.S. citizenship is required. This announcement has been amended to extend the closing date to May 28, 2010. USDA/ARS is an equal opportunity employer and provider.

"Gaskin, John" <John.Gaskin@ARS.USDA.GOV>

UTexas ResTech FishHostParasite Coevolution

Dear Brian, While the ideal candidate for my advertised position would have experience with parasitology, this is not a requirement. Furthermore, the research program is very much an evolutionary project and my lab is an evolutionary ecology lab. Consequently, I view evolutionary biologists as my focal audience for this job advertisement. I would therefore appreciate it if you would post the following (revised) job description with the subject line: Job: Research Technician: host-parasite coevolution in fish, University of Texas / HHMI

Position Title: Research Technician 1

Employer: Howard Hughes Medical Institute

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

Classification: Full-time

Starting Salary: $30,000 to $35,000 annually depending on qualifications, plus benefits.

Start date: Earliest possible start date is May 15 2010, later start dates are possible.

Duration: Renewable annually depending on performance, with an expected duration of three years.

Job summary:

The Bolnick lab in the Section of Integrative Biology at the University of Texas at Austin, is seeking a highly motivated research technician to assist with a study of geographic mosaic coevolution between fish and their macroparasites. Research will focus on documenting geographic variation in parasite communities of the threespine stickleback and corresponding variation in stickleback immunogenetics. For more information on the Bolnick lab, visit:

https://webspace.utexas.edu/dib73/Bolnicklab/-Bolnicklab.html 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, measurements of fish morphology and diet, DNA extraction, PCR, and next-gen sequencing. Training will be provided as needed. The technician will have the opportunity to assist with periodic field work on Vancouver Island, Canada, to obtain specimens. The technician may also assist with daily management of the laboratory, including purchasing, equipment maintenance, database management, and animal care.

Minimum qualifications:

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

Preferred qualifications:

Experience with one or more of the following: fish parasitology, morphometrics, immunology, DNA sequencing, and/or population genetic analyses of DNA sequence data. Ideal candidates would have 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 field research is also a plus.

To apply:

Applications will be reviewed as they are received, and the position will remain open until filled. The application should include:

1) a letter of application with a description of past research experience and education (degree, institution, GPA, courses taken)

2) a curriculum vitae

3) the names of three references

The application may be sent via email as a pdf file (preferred) or word file to:

danbolnick@mail.utexas.edu

Or, applications may be sent via mail to:

Dr. Daniel Bolnick

Section of Integrative Biology

One University Station C0930

University of Texas at Austin

Austin TX 78712, USA

HHMI is an Equal Opportunity Employer.

Dr. Daniel I. Bolnick

Early Career Scientist Howard Hughes Medical Institute

Associate 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 https://webspace.utexas.edu/dib73/TheBolnickLab/Home.html Dan Bolnick <danbolnick@mail.utexas.edu>

UZurich ResAssist Bioinformatician

Research assistant (Computer scientist/bioinformatician) - University of Zürich

A research assistant position is available for a computer scientist/bioinformatician at the University of Zürich.

We are interested in bacterial-plasmid coevolution, and approach this through mathematical and computational modelling, as well as genome-wide analyses to investigate the role of horizontal gene transfer in bacterial evolution. The successful candidate will be involved in analysing bacterial sequence data and/or developing complex simulations of bacterial evolution. Involvement in the respective project(s) will depend on the skills and interests of the successful candidate.

We are looking for a highly motivated individual with a strong computational background. The candidate should have excellent programming skills and a background in computer science, bioinformatics, statistics or related disciplines and have a diploma/MSc degree.

The successful applicant will be supervised by Dr Daniel Rankin (http://www.socialgenes.org/people/rankin.html), a theoretical evolutionary biologist interested in a wide range of topics, from social evolution to the link between evolution and ecology. The position will be based in the Computational Biology and Bioinformatics Group, led by Professor Andreas Wagner (http://www.bioc.uzh.ch/wagner/). The group is very international and consists of a very diverse range of individuals who work on a wide range of interesting evolutionary topics.

The candidate should have a diploma/MSc degree and have excellent programming skills and a background in computer science, bioinformatics, biology, statistics or related disciplines. Previous research experience, and willingness to gain some experience in evolutionary biology will be seen as an advantage. The successful candidate will be encouraged to be involved in the publication process, and those that want to pursue a PhD will be encouraged to apply for their own funding.

Zurich is located less than one hour from the Alps, and is a small but vibrant city that is regarded to have one of the best standards of living in the world. There is a large international community and is well connected to all major European cities. The working language of the group is English, and knowledge German is very helpful but not necessary.

To apply, please send an eâmail with the applicant's CV and cover letter (explaining the experience and motivation for applying for the job), along with the contact details of at least 2 potential referees, in a single pdf file to d.rankin@access.uzh.ch. Please mention âResearch assistant position" in the subject of the eâmail.

Deadline for applications is Friday 21st May 2010. The position, funded by the Swiss NSF, is available to start immediately and will be between 12 and 18 months.

Further information: Dr Daniel Rankin (http://www.socialgenes.org/) Eâmail: d.rankin@access.uzh.ch, Tel: +41 44 63 56143

d.rankin@socialgenes.org

WoodsHole ResAssist MarineMicrobeDiversity

Position Title: Research Assistant II/III V Marine Microbes

Description: The Marine Biological Laboratory in Woods Hole, MA is seeking applicants for a full-time Research Assistant position with the Josephine Bay Paul Center. The successful applicant will contribute to the project, which will explore diversity of marine microbes and the influence of changing chemical environments on microbial population structures.

Duties: Duties include but are not limited to the preparation and massively-high throughput pyrosequencing of tag libraries from marine microbial populations.

Education and Experience: Bachelors or Masters degree with training in molecular biology and bioinformatics. Must have several years of laboratory experience. Candidate is expected to be familiar with modern nucleic acid sequencing and analysis technologies, including library construction and operation of capillary sequencers and robotics platforms.

Special Instructions to Applicants:

Required Applicant Documents -Resume/CV -Cover Letter -References (3)

Please submit three items: (i) a cover letter describing your research goals and your specific motivation to join our lab, (ii) a CV, and (iii) contact information for three references, including your Ph.D. supervisor by completing an application using the MBL website: http://www.mbl.edu/hr/employment.html .

Posting Number: 0000312

Deadline: Until a suitable candidate is found.

The MBL is an Equal Opportunity/Affirmative Action Employer/Non- smoking workplace.

"Katie K. Newhall" <knewhall@mbl.edu>

YaleU 2yearLectureship SystematicBotany

Two-Year Systematic Botany Lecturer Position Department of Ecology & Evolutionary Biology Yale University

A full-time, nine-month lecturer position in the Yale University Department of Ecology & Evolutionary Biology is available for a Ph.D. with expertise in systematic botany. Position is available for academic years 2010-11 and 2011-12.

Duties will include: - in Spring semester, teaching an undergraduate biology major's course in Plant Diversity and Evolution, a concurrrent undergraduate Lab in Plant Diversity and Evolution. - in Fall semester, teaching a comprehensive undergraduate course on the Diversity of Life for majors and nonmajors, and an undergraduate biology seminar on a topic to be chosen. - supervising or advising undergraduate research projects.

The required qualifications are: - a Ph.D. in biology with research experience in plant phylogenetics, anatomy, or diversity. - previous college teaching experience with demonstrable effectiveness - broad familiarity with organismal diversity - professional competence in systematic botany

The primary responsibilities of the position are those involved in the teaching mission. Applicants with active research interests in botanical or fungal systematics may be offered the opportunity to join the research group of Professor Michael Donoghue, where they may be eligible to earn an additional 3 months of summer salary. Any such arrangement is secondary to the primary teaching obligations.

Salary and benefits will be for a full-time, nine-month lecturer ($52,000).

Applicants please send a CV, names of three references, statement of teaching experience, statement of research experience and goals to: Ms. Marcia Rynaski (marcia.rynaksi@yale.edu), Department of Ecology and Evolutionary Biology, Yale University, P. O. Box 208106, New Haven, CT 06520; phone: (203) 432-3891.

Applications will be accepted until position is filled.

Richard O. Prum William Robertson Coe Professor of Ornithology Chair, Department of Ecology & Evolutionary Biology

phone- (203) 432-9423 website- http://www.yale.edu/eeb/prum/ Richard Prum <richard.prum@yale.edu>

Other

454 sequencing facilities

Hello all,

I am interested in sequencing the mitochondrial genome (454) for a number of species and am looking for a company in Canada that can do this. The McGill/Genome Canada group was recommended but when I contacted them they indicated that they were not taking any new projects. Are there any other Canadian (or further abroad) institutions or companies that offer 454 sequencing - and could be recommended. Thanks

Stephen

Stephen D. Petersen Visiting Fellow, Fisheries & Oceans Canada 501 University Crescent Winnipeg, Manitoba, R3T 2N6

Stephen Petersen <alertstephen@gmail.com>

Alignment format conversions

Dear colleagues,

We have developed a open web-based tool (ALTER) to transform between different alignment formats. The originality of ALTER lies in the fact that it focuses on the specifications of popular programs rather than on conversion among canonical formats, which often encompass different variations under the same name. ALTER is available at:

http://sing.ei.uvigo.es/ALTER/ Further detaisl are explained in: Glez-Peña D, Gómez-Blanco D, Reboiro-Jato M, Fdez-Riverola F, Posada D. 2010. ALTER: program-oriented conversion of DNA and protein alignments. Nucleic Acids Research (Web server issue): 1-5

http://dx.doi.org/10.1093/nar/gkq321 Hope ALTER is useful for some of you. Suggestions are welcome (see the feedback button at the web site). Best,

D

– David Posada Facultad de Biología Campus Universitario 36310 Vigo Spain

Phone: +34 986 812038 Cell: +34 647 343300 Fax: +34 986 812556 Email: dposada@uvigo.es Web: darwin.uvigo.es

dposada@uvigo.es

Ancient DNA lab film

Dear evoldir community,

for a non-profit, internet based, film project about evolutionary biology, I am looking for some footage of an ancient DNA clean lab. On my wish list are someone cutting a piece of bone, powderizing the bone and doing some wet lab things that look like a pcr. All of this, of course, while wearing the white suits that are used in clean labs.

Does anyone have such material? Or, could someone help me to get the material? It is most important that the material can be used under a creative commons license. The movie will be published on the internet and especially teachers and museums will be allowed to download the movie and use it however they want. I could pay for the material.

The editor of the movie is based in London, so if you are in or near London, that may make things easier, because I could send someone with a camera to your lab. The footage doesn't need to come from inside a real clean lab, as long as it really looks like one!

For the other movies of this project, see http://www.evolution-of-life.com We now have 6 movies online, in German, French and English.

Best wishes & many thanks, Pleuni Pennings

–

Pleuni S. Pennings, PhD

University of Munich (LMU) from June 15th, 2010:Organismic and Evolutionary Biology, Harvard, Boston Mail: pleuni@dds.nl My website: http://www.eeslmu.de/eeswiki/Pleuni_Pennings My movie project: http://www.evolution-of-life.com Pleuni Pennings <pennings@lmu.de>

Anemone samples

Hello,

I am studying the phylogeogoraphy of Anemone multifida (cut leaf anemone), a flowering plant native to North America and Chile. I am currently studying in Alberta, and it would be fantastic to get specimens from places such as: Colorado, Montana, Wyoming, Utah, Idaho, North and South Dakota, Manitoba, Saskatchewan, Northwest Territories, Yukon, BC and Quebec. Please let me know if you would be willing to stuff some leaves in a bag with silica gel – we will gladly cover any costs.

Thanks!

Jamie McEwen

– Jamie McEwen, BSc Dept. of Biology, University of Calgary jrmcewen@ucalgary.ca (403) 220-7907 https://webdisk.ucalgary.ca/ ˜ jrmcewen/web/index.html jamie.r.mcewen@gmail.com

Atelerix samples

I am a PhD student studying African hedgehogs. I am looking for contacts in order to obtain geo-referenced tissue samples of Somali and South African hedgehogs (Atelerix sclateri and A. frontalis, respectively; links to distribution maps from IUCN can be found below) as well as North African hedgehog (A. algirus) from the Balearic Islands. If anyone travels to or works in these regions or has contacts who do, I would be extremely grateful to receive your help; tissue samples can easily be collected from roadkill. I would also be happy to receive samples of other hedgehogs from Africa as well (A. algirus, A. albiventris, Paraechinus aethiopicus).

Distribution maps A. frontalis: http://www.iucnredlist.org/apps/redlist/details/2274/0/rangemap A. sclateri: http://www.iucnredlist.org/apps/redlist/details/2275/0/rangemap Please contact me for more information or with any possible leads. Many thanks for your help,

Dianna Steiner

Doctoral Student University of Porto, Portugal/CIBIO (Research Centre of Biodiversity and Genetic Resources/Centro de Investigação em Biodiversidade e Recursos Genéticos)

http://cibio.up.pt Campus Agrário de Vairão R. Padre Armando Quintas 4485-661 Vairão, Portugal

e-mail: dianna.steiner@mail.icav.up.pt

tel: +351 25 266 0411 mobile: +351 91 258 9262

Dianna Steiner <dianna.steiner@mail.icav.up.pt>

BBSRC and NERC funding

This will only be of interest to those applying for research funds in the UK. It is worth knowing that it is now the policy, and might have been for sometime, not to allow grants rejected by the BBSRC, to be submitted to NERC, unless they are substantially changed. I have just had a grant pulled at the 11th hour because of this ruling.

Adam Eyre-Walker

a.c.eyre-walker@sussex.ac.uk

BroodParasiticBirds Website

We would like to announce www.indigobirds.com, a website devoted to collecting and disseminating information about the brood parasitic indigobirds (see “Background” below). This multimedia website summarizes research on these fascinating birds, along with locality records, range maps, pictures, and song recordings. One of the primary objectives of the site is to increase knowledge about these birds by collecting notes, photographs, and especially recordings of indigobird songs from the public, students, birders, and both amateur and professional ornithologists.

Because indigobird species are morphologically similar and difficult to identify in the field, the distributions of these birds are poorly known. Indigobird males, however, convey critical information in their songs; by mimicking their host species, males provide an unambiguous indication of the species that raised them. Thus, we are particularly interested in gathering geo-referenced sound or video recordings of indigobirds throughout Africa. If you have or would like to collect indigobird recordings, please email us at indigos@bu.edu. We will do our best to identify the indigobird species you’ve recorded and use the information to improve our database of indigobird distributions on the website.

We hope that the website will be a reference for biologists, students, and bird enthusiasts, and invite suggestions on how we can improve its content.

Regards,

Jeffrey DaCosta Michael Sorenson Boston University www.indigobirds.com indigos@bu.edu

Background: Indigobirds (10 of 19 species in the genus Vidua) are African parasitic finches that reproduce only by laying their eggs in the nests of other species, mainly firefinches (genus Lagonosticta). Most indigobirds parasitize a single host species, which is evidenced in two remarkable traits. First, young indigobirds mimic the species-specific and elaborate mouth patterns of their respective hosts. Second, adult male indigobirds include songs of their host species in their own repertoire. Experiments with captive birds have demonstrated that this mimicry of host song results from a behavioral imprinting process in which both male and female indigobirds learn the songs of the host species. As a result individuals mainly mate with other individuals that have been reared by the same host species, and females parasitize nests belonging to the same species that raised them. This remarkable social behavior results in the cohesion of indigobird species but also provides a mechanism for rapid sympatric speciation (i.e., speciation without geographic isolation). sympatric speciation (i.e., speciation without geographic isolation).

Convert nucleotide MSA into protein alignment

Dear colleagues,

Does anyone know a program that can translate a full multiple sequence nucleotide alignment directly into the (aligned) amino acid sequences without doing it sequence by sequence?

It would be an enormous time saver!

Best wishes,

Birgit

NOTE NEW PHONE NO!

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

+44 1223 588049 bhmm2@cam.ac.uk

DalhousieU VolPosition PlantReproduction

Hello,

I am a phd student at Dalhousie University. I am seeking volunteer(s) to help with a study of the reproductive biology of a flowering plant. The study will be conducted in the eastern section of Algonquin Park (Ontario) this summer. The position involves camping from Mon-Fri in the eastern section of Algonquin park from July 15-Oct. Volunteers are expected to commit to a minimum of 5 days during this period. Volunteers are welcome to help out for longer periods of time!! Transportation from Ottawa to the field site and return will be provided. Food and camping equipment can also be provided.

Please email maggie at mbartkow@dal.ca for more information.

Cheers, Maggie

– Magdalena Bartkowska, M.Sc. Biology Department Dalhousie University phone:494-8005

mbartkow@dal.ca

Dsimulans samples

we are starting a project on Drosophila simulans population genomics. We are interested in knowning whether anybody in the community has and is willing to share D.simulans populations. We are specifically interested in recently caught Drosophila simulans from specific populations (severallines collected in the same population).

Thanks a lot!

Josefa

Josefa Gonzalez Life Science Research Associate Department of Biology 371 Serra St Stanford University Stanford, CA 94305-5020 http://www.stanford.edu/~jgonzalp (650) 736 2249

“jgonzalp@stanford.edu” <jgonzalp@stanford.edu>

Evolution 3Dvideos

Hello everyone,

I disturb you, just to comment that, with the aim of spreading in an “extra-scientific” area, some aspects of the work we have done in our lab of Ecology and evolution (University of Vigo), we have conducting several informative 3D video. If anyone is interested, can see the video on the web:

http://webs.uvigo.es/plantecology/divulgacion.en.html If anyone is interested, can also download high definition version freely accessing Youtube:

Lizards as seed dispersers in island ecosystems: http://www.youtube.com/watch?v=zPsNAaL8K68&feature=channel Biological Invasions and Zebra mussel (Dreissena polymorpha): http://www.youtube.com/watch?v=biUpmQ9fz7g&feature=channel I hope you enjoy it.

Luis Navarro

–

Luis Navarro phone 1: (+34) 986 812619 Depto. Biologia Vegetal phone 2: (+34) 647 343097 Facultad de Ciencias fax: (+34) 986 812556 As Lagoas-Marcosende email: lnavarro@uvigo.es Universidad de Vigo http://webs.uvigo.es/lnavarro 36200-Vigo http://webs.uvigo.es/plantecology Spain

Luis Navarro <lnavarro@uvigo.es>

Evolution Body Shape

Dear colleagues

We have recently launched a global study on the evolution of male and female body shape at www (dot) bodylab (dot) biz. This is an exciting project that makes use of new developments in computer generated imagery to independently manipulate over twenty different body measurements. We recognise that there may be much more to human attractiveness than a small number of measures can capture, and we are trying to understand how all the traits that make up a body combine to influence attractiveness.

Studying this many traits requires samples of thousands of raters, and hence we launched bodyLab (dot) biz - a web platform for our study. Starting in April 2010 with populations of 120 male and 120 female models based on measurements of real people, we aim to “breed” from the most attractive individuals, using the power of natural selection to shape our virtual population of human bodies.

A secondary aim of our project is to demonstrate the power of natural selection and the relevance of evolutionary biology to the general public - worldwide. We provide participants with feedback on their rating statistics, alert users to updates to our male and female populations, and provide information on the progress of our study via FaceBook and Twitter. Our interactive site will encourage lasting interest from our participants and fellow researchers, and we invite other research groups who wish to propose collaborations or who can help us enhance the experience for visitors to bodyLab.

Please visit our site, rate the bodies, and spread the word to your friends and colleagues. Many thanks,

Rob Brooks www.eerc.unsw.edu.au Participate in our new global study on the evolution of attractiveness www (dot) bodylab (dot) biz

rob.brooks@unsw.edu.au

Evolution Textbook Recommendations answers

Hi, All:

About two months ago I solicited recommendations on textbooks in evolutionary biology that might fit a niche somewhere intermediate to the breadth and detail of Futuyma’s ’Evolution, 2nd edn.’ and considerably more elementary texts like Kardong’s “An Introduction to Biological Evolution”. My apologies for the delay in posting the promised summary - the response was a bit greater than I’d anticipated (a good problem to have) and, quite frankly, teaching duties overwhelmed me until the semester came to a merciful end.

Great thanks to all those who took the time to provide feedback, all quite useful. I have organized the responses below save for one which will not be posted as per the respondent’s request. Freeman and Herron’s “Evolutionary Analysis” was the overwhelming favorite with ~30 favorable nods. Of the other texts given more than one positive review - Sterns&Hoekstra’s “Evolution: An Introduction”, Ridley’s “Evolution, 3rd edn”, and Zimmer’s “The Tangled Bank” - Stearns & Hoekstra received the most at 6 or 7. I think reading the invidual comments is worthwhile - many (although certainly not all) provide more specific details as to why they like a particular text.

I also received a pdf of a review of the Zimmer book. I do not know if the EvolDir can handle attachments but I will try to send it as an attachment in a separate message.

I have organized all of the rather lengthy set of responses below with the following organization [Note: the book title in the first 1 or 2 posts favoring that text is bolded]: My original post; A few that are more general and mention several possibilities without arguing in favor of any of them (including a link to a site that lists more possibilities than are mentioned here); Comments in favor of Freeman & Herron; Comments in favor of Stearns & Hoekstra; Comments in favor of Zimmer; Comments in favor of Ridley; Comments on miscellaneous other texts.

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

The available choices are summarized here:

http://www.evolverzone.com/?tag=books-textbooks Plus, you might consider Carl Zimmer's The Tangled Bank, which is not as basic as Kardong's book.

I've taught evolution at the undergrad and grad levels now for 17 years and have tried multiple textbooks. I agree that Kardong and several others (including the nicely produced new textbook by Carl Zimmer) are too basic for a majors course at a 4-year undergrad college. I think the best ones are Futuyma, Ridley, Strickberger, Freeman & Herron, and the interesting new textbook from Cold Spring Harbor by Barton et al.

*****

I have taught using Futuyma, Ridley and Freeman & Herron. I have not yet tried using Strickberger nor Barton et al. The one that worked best with my particular course was Futuyma. This is because I like to use the textbook as a "reference" for the course. I want the students to know that the textbook does not run the course–I do. The textbook is ONE of the resources in the course. A good reference text will provide more depth and different examples than what I provide in class. Furthermore, such a textbook should provide citations to the actual literature, so that students can use the textbook as a springboard for developing their own library research projects. In this respect, Futuyma's text is the best.

*****

I agree that Futuyma's textbook is dense, but it is very well-organized, well-written, focuses on the main mechanisms, and provides references. It would be great if publishers also provided cool things like simulators (e.g. for testing students' hypotheses about population genetics), good problem sets, etc. I think most publishers focus too much on making the textbook the center of the course. But it's only one tool in the arsenal.

(That said, I might try Barton et al. next year, just for variety...)

*****

I am in the same boat. Using Futuyma and skipping a little less than 1/3. Several people have suggested Freeman's Evolutionary Analysis. I have been tempted by the Hoekstra and Stearns book, because of its emphasis on theory. I would like to hear what you find out.

*****

Scott Freeman's book is pretty standard these days, I think you'd find

it meets your criteria. I was a graduate evolutionary biology student

and I found it useful and informative, and not too basic.

— / —

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

ExtractingDNA from CambialTissue

Hi,

I'm seeking advice on extracting DNA from cambial tissue for microsatellite analysis. Please shoot me an e-mail (shmi.narayan at gmail dot com) if you would be willing to share expertise or suggest relevant papers.

Thanks!

Lakshmi Narayan Graduate Student UC Berkeley

shmi.narayan@gmail.com

GeneMapper availability

Dear all,

Does anyone know if there is somewhere where one can purchase the GeneMapper software for a reasonable price? Applied Biosystems is selling it (GeneMapper v4.1 full) for $1,000 dlls !!!

Peak Scanner is no longer freely available, and its performance is, anyhow, of lower quality compared to GeneMapper.

I appreciate any suggestions, Ella

Ella Vázquez Domínguez Instituto de Ecología, UNAM Ap. Postal 70-275, Ciudad Universitaria México DF 04510 México Tel +52 55 5622 9015

ella@miranda.ecologia.unam.mx

Invasive species survey

Dear Colleagues, I would like to draw your attention to the world's largest collaborative project on invasive species. The Global Garlic Mustard Field Survey is just entering its second field season and we already have demographic data and seed collections from 65 populations – more than any published study on invasive species. This year we are hoping to double that number and we are particularly keen to have more North American contributors.

The project is an international collaboration aimed at obtaining much-needed data on the abundance and distribution of /Alliaria petiolata/ (Garlic Mustard). It involves a very basic sampling protocol that standardizes sampling across sites, making it ideal for incorporation into field courses, nature surveys, and long-term monitoring and management efforts. The estimated duration of sampling for a team of two people is 2-4 hours per population.

For academics who substantially contribute to this endeavor, we anticipate the possibility of authorship on manuscripts resulting from the work. Our plan for the future includes development of teaching modules and expanding to similar surveys for other key invasive species. The sampling protocol and additional information are available at the following website: www.GarlicMustard.org < http://www.garlicmustard.org/ >. Please contact us directly if would like to participate or if you have any questions or concerns.

Dr. Robert Colautti Biology Department Duke University rob.colautti@duke.edu <mailto:rob.colautti@duke.edu>

Dr. Oliver Bossdorf Biology Department University of Bern bossdorf@ips.unibe.ch <mailto:bossdorf@ips.unibe.ch>

Dr. Steven Franks Biology Department Fordham University franks@fordham.edu <mailto:franks@fordham.edu>

rob.colautti@duke.edu

Knome sequencing program

I wanted to pass along Knome's announcement that we're giving away sequencing (30x mean coverage) and discovery-supportive data analysis services for a total of six human exomes, to be distributed among the three research groups who submit the most compelling, feasible proposals on what pair of human exomes they would sequence and why. We'd love to hear from imaginative human evolutionary geneticists on what questions they might study here. The deadline for application submissions is 15 June 2010. Please see the attached announcement sheet for more information on the awards.

Thanks for spreading the word, if it's appropriate, and all best!

Nathan

– Nathaniel Pearson, PhD Director of Research Knome, Inc. 1 Main St, Suite 530 Cambridge, MA 02142 USA

Tel. 617.250.8460 Fax 617.250.8610

Nathaniel Pearson <npearson@knome.com>

MEDUSA error in R

Dear colleagues,

I'm trying to run MEDUSA in R but I get an error message that I don't understand when trying to summarize the results, and I can't get pass through it. Can anyone help?

I have my pruned phylogenetic tree and a table of species richness that seems to be read ok in R.

Phylogenetic tree with 14 tips and 13 internal nodes.

Tip labels: Da, Dv, Do, Dc, Dq, Dl, ...

Rooted; includes branch lengths. > sps_richness V1 V2

```
1 Da 7 2 Dv 13 3 Do 6 4 Dc 3 5 Dq 10 6 Dl 3 . . .
```

I then run Medusa and it seems to me that it works ok:

```
> medusa.out <- runMedusa(medusa.tree, sps_richness, estimateExtinction = T, modelLimit = 20, cutAtStem = T, startR = 0.05, startE = 0.01) 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 > medusa.out [,1] [,2] [,3] [,4] [,5] [1,] 0 -70.11320 2 144.2264 144.748136 [2,] 11 -67.25890 5 144.5178 147.374937 [3,] 14 -65.23652 8 146.4730 154.473034 [4,] 9 -64.23225 11 150.4645 168.064505 [5,] 20 -63.65072 14 155.3014 190.301442 [6,] 4 -63.18208 17 160.3642 228.364160 [7,] 1 -62.80783 20 165.6157 305.615664 [8,] 6 -62.35120 23 170.7024 538.702396 [9,] 19 -61.82863 26 175.6573 Inf [10,] 7 -61.34799 29 180.6960 -399.304029 [11,] 27 -60.79912 32 185.5982 -166.401763 [12,] 10 -59.97216 35 189.9443 -90.055671 [13,] 17 -58.54577 38 193.0915 -53.908454 [14,] 16 -57.96749 41 197.9350 -31.665023 [15,] 2 -57.50421 44 203.0084 -16.991584 [16,] 8 -55.54274 47 205.0855 -9.771653 [17,] 3 -55.25354 50 210.5071 -1.992927 [18,] 5 -54.80782 53 215.6156 3.615631 [19,] 21 -54.21820 56 220.4364 7.636404 [20,] 12 -54.09977 59 226.1995 11.654093 [21,] 13 -53.06485 62 230.1297 13.129693
```

Then I try to summarise by running summaryMedusa and I get the wretched error message:

```
> summaryMedusa(medusa.tree, sps_richness, medusa.out, cutoff = 4, plotTree = TRUE, useCorrection = FALSE, cutAtStem = TRUE) Error en z[i + sum(interior), ] <- c(anc, dec, startTime, endTime, sr, : número de items para para sustituir no es un múltiplo de la longitud del reemplazo
```

(Sorry it is in Spanish, but it translates to “Error in z[i + sum(interior),] <- c(anc, dec, startTime, endTime, sr, : number of items to shift are not a multiple of the length of the shift”)

Any idea of what it means and how I can get Medusa to run? Thank you very much in advance.

Ramiro

Dr. Ramiro Morales-Hojas Molecular Evolution lab IBMC-Instituto de Biologia Molecular e Celular Rua do Campo Alegre 823 4150-180 Porto Portugal

Tel.: +351 226 074 900 extension 1612

rmhojas@ibmc.up.pt

MEDUSA error in R answers

Dear all,

I had some interest by other members of evoldir to know the answer to my question regarding the error running MEDUSA in R. Fortunately I had a couple of very useful comments and am able to run it now. Here are the two comments:

Hi Ramiro,

I was having this same problem, and I found that it has to do with the table layout. In runMedusa, it inserts a column of tip ages (which in your case would be all zeros), but in summaryMedusa it does not insert this same column but the program expects that column in order to run. Its a simple enough problem to fix. I just inserted a column of zeros, but when I mentioned this problem to Luke Harmon, he provided scripts that fixed the issue. I've attached his scripts to this email. Just load these into R and that should fix the problem.

Good luck!

cheers, Elizabeth

Hi Ramiro,

This is a bug in the current version of Medusa. Expect a new version soon. In the meantime, you can source the attached files and things should work.

Luke

Thanks a lot for the replies and hope that it helps other people.

Cheers,

Ramiro

Dr. Ramiro Morales-Hojas Molecular Evolution lab IBMC-Instituto de Biologia Molecular e Celular Rua do Campo Alegre 823 4150-180 Porto Portugal

Tel.: +351 226 074 900 extension 1612 rmhojas@ibmc.up.pt

rmhojas@ibmc.up.pt

Mendels manuscript

Mendels's original manuscript “Versuche über Planzen-Hybride” has been found!

The original handwritten document has been found and is in excellent condition. There is a chance that the document will again be lost to the scientific community. The document is being held by the law firm: Wahlert in

Stuttgart, Germany. Please contact them and let them know that this document must be preserved. The German government is trying to determine if it should be listed as a German cultural treasure, but the law firm may be not cooperating. Thanks for your help!

Tel. +49 711 1876-277 Fax. +49 711 1876-103 horst.teller@wahlert-law.com

William Taeusch <taeusch@gmail.com>

NESCent CallCourseProposals

Call for Evolutionary Courses and Course Proposals at NESCent

What courses would you like to see offered to the evolution community?

The National Evolutionary Synthesis Center (NESCent) is expanding its course offerings and would like your suggestions.

NESCent welcomes ideas and proposals for postgraduate-level short courses (1-2 weeks) on topics of relevance to synthetic evolutionary science. Do you have a bright idea? Please let us know.

We are seeking course proposals in two phases:

Phase 1 (April 22 - May 15) - Solicitation of course ideas from the evolutionary biology community

NESCent is soliciting ideas for short courses from the community at large. Ideas should be a paragraph or two, and include the following: A description of the topic, the intended audience, evidence for demand and uniqueness, and (optionally) nominations for instructors. This is your opportunity to tell us what new courses you would like to see, and our effort to identify the courses most in demand from the evolutionary biology community.

Topic suggestions can be submitted via email to eog@nescent.org (Deadline May 15).

All ideas will be posted online MAY 15. The evolutionary biology community will be encouraged to vote for topics of particular interest through the end of May.

The most successful topics will be solicited for full course proposals in Phase 2 (see below), and nominated instructors will be notified of the opportunity to apply for consideration.

Phase 2 (Deadline July 10) - Solicitation of full course proposals

Full-length proposals from those interested in being instructors are accepted in the second phase. These may address the topics specifically listed in the call, but need not be restricted to those topics. Note that anyone can submit a full proposal at this point, even if it has not been submitted and voted upon in Phase 1.

For a list of current and previous courses offered at NESCent see http://www.nescent.org/courses/ . For additional details contact the NESCent Education and Outreach group at eog@nescent.org.

Jory Weintraub <jory@unc.edu>

Next Generation InHouse Computing 2

Dear All

Further to Jackie Lighten's round robin query regarding Linux boxes and second generation sequencing bioinformatics pasted below, I just wanted to contribute a further bit of info that may save the community some frustration, or stimulate feedback that may help people out.

Central to 454 Roche's genomic/transcriptomic sequence assembly is the Newbler assembly suite. The last time I checked (admnittedly a while ago), 454 were permitting downloads of their Off Instrument Application, so that users could analyse their own data from .sff files etc. Check with your 454 Roche representative to establish if this is still the case.

The rub is, when I last tried, I could only install the Off Instrument Application on to a Red Hat distribution of Linux and they were only supporting the installation of the software on to Red Hat (includes yearly subscription fee). I tried Ubuntu plus a couple of others, but with no success.

Thus, if you have need a for the Newbler suite and the above still holds, you may want to choose the Linux distribution carefully before setting up your bioinformatics toolkit.

Establishing virtual machines via VMWare gives you a great deal of flexibility in your choice of Linux distributions.

If anyone has any feedback on the above, it would be good to hear from you?

All the best

Si Creer

Simon Creer Senior Research Fellow Molecular Ecology and Fisheries Genetics Lab Environment Centre Wales Building School of Biological Sciences Bangor University Bangor Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk Tel: +1248 382302 Fax: +1248 371644 Home Page: http://biology.bangor.ac.uk/ ˜ bssa0d/ “Creer,Simon” <s.creer@bangor.ac.uk>

Nucleotide to protein translations answers

Dear colleagues,

Thank you very much for your many replies! There are a number of top hits and a few programs only mentioned once or twice. Most are free to download as well.

Top hits are old favourites:

MEGA (Windows) http://www.megasoftware.net BioEdit (Windows) http://www.mbio.ncsu.edu/BioEdit/bioedit.html Se-Al (Mac) http://tree.bio.ed.ac.uk/software/seal/ Others:

TranslatorX (online) http://translatorx.co.uk MacClade (Mac, not free) http://macclade.org/macclade.html Mesquite (all platforms) http://mesquiteproject.org/mesquite/mesquite.html Seaview (all platforms) http://pbil.univ-lyon1.fr/software/seaview.html DAMBE (all platforms) http://dambe.bio.uottawa.ca/dambe.asp TransAlign.pl http://www.molekularesystematik.uni-oldenburg.de/33997.html Geneious (not free) http://www.geneious.com DNAsp (all platforms) http://www2.ub.es/dnasp/download.html t-coffee (all platforms or online) http://www.ebi.ac.uk/Tools/t-coffee/index.html Proseq (Windos, Linux) http://dps.plants.ox.ac.uk/sequencing/proseq.htm Mbetoolbox (all platforms) http://www.bioinformatics.org/mbetoolbox/ FAST (soon to be released by David Ardell)

NB: I used BioEdit as I have already used it for manual alignment editing (I just didn’t see the toggle function to protein!).

Just a word of warning: the toggle function Ctl+A to select all sequences and Ctl+G or Ctr+T to toggle to protein view (and back) will not save the protein view! You need to use the dropdown menu <sequence> and select the permanent translation option. And when you do this, it will ’correct’ your protein for those nasty frameshifts and premature STOP codons and not tell you about it! It just inserts an ’X’ for the missing residue! So you need to check your alignment carefully to find those with problems.

Thanks again everyone!

Happy translating,

Birgit

NOTE NEW PHONE NO!

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

+44 1223 588049

bhmm2@cam.ac.uk

Outsource amplification sequencing

Dear EvolDir list members,

For my PhD project, I wish to generate DNA sequence data for phylogenetic analysis of an Afrotropical butterfly genus (Cymothoe). Unfortunately, time does not allow me to generate all the data myself. Therefore, I am considering outsourcing the amplification and sequencing of 3-5 nuclear regions for about 30-50 specimens.

I have heard of possibilities for outsourcing sequencing in Korea. But I have no idea about pricing and whether it is also possible to outsource amplification.

Does anyone have experience with outsourcing this kind of labwork? I’d be very interested in any experiences (good or bad), price indications and/or recommendations you may have.

Thanks in advance!

Robin

robin.vanvelzen@wur.nl

Robin van Velzen PhD student Netherlands Centre for Biodiversity Naturalis (section NHN) Biosystematics Group Wageningen University

Wageningen Campus, Radix building 107, Room W4.Aa.095 Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands PO Box 647, 6700 AP Wageningen, The Netherlands Tel. +31 (0)317 483425 http://www.bis.wur.nl Robin.vanVelzen@wur.nl

Outsource amplification sequencing answers

Dear all,

I have received many emails with suggestions and recommendations regarding my question about outsourcing DNA amplification and sequencing and wish to thank everyone who has been so kind to reply to my request!

Please find below a summary of the suggestions and recommendations:

Many people pointed out that the 'Korea' option implies using services offered by Macrogen (www.macrogen.com) that currently also has an office in The Netherlands. Their sequencing services are highly recommended by most, and are cheap (5-7 USD per sample) but they don't offer PCR amplification.

Another recommendation is Functional Biosciences Inc in Wisconsin, USA (http://www.functionalbio.com) that offers pcr amplification and direct sequencing plates of DNA for 5-600 USD.

A recommended European option is Genoscreen from France (http://www.genoscreen.fr/index_eng.htm) who can do various things, including tailor-made analyses.

The Nevada Genomics Centre in the USA (http://www.ag.unr.edu/genomics/) offers various services including extraction, amplification and sequencing and are recommended for their responsiveness and fast work.

I also received several kind emails directly from labs offering PCR amplification and sequencing services: Genetic Marker Services (http://geneticmarkerservices.com/) from the UK Central Analytical Facility at Stellenbosch University in South Africa (http://academic.sun.ac.za/saf/) Georgia Genomics Facility in the USA (http://dna.uga.edu/) Fragment Analysis & DNA Sequencing Services (FADSS) in British Columbia, Canada (http://web.ubc.ca/okanagan/ikbarberschool/research/analytical/fadss.htm l)

I hope the above list is of help for people considering outsourcing their labwork, and does not qualify as advertising (I am sure there are many more companies out there).

All the best,

Robin

Robin van Velzen PhD student Netherlands Centre for Biodiversity Naturalis (section NHN) Biosystematics Group Wageningen University

Wageningen Campus, Radix building 107, Room W4.Aa.095 Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands PO Box 647, 6700 AP Wageningen, The Netherlands Tel. +31 (0)317 483425 http://www.bis.wur.nl ——my original post——

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Robin.vanVelzen@wur.nl

Problems with SAMOVA software

Dear Evoldir members,

I am having difficulty running the SAMOVA 1.0 software and was wondering if anyone had come across the problem before and knows of a solution. The program requires two input files, one a Arlequin file, and the other a file specifying the geographical locations of the sampled populations. Examples of both types of file come with the software but when I load the example files or my own, I always receive the same error message (see below) and the software crashes.

Reading Project: Reading general settings in input file ... 1 <ERROR # 1> from function "Project::open()" : unable to read Profile Settings Error opening project... proj_AMO.arp Error during run of

If anyone can help solve this problem I would be most grateful to hear from you.

Best wishes Sean Fitzpatrick

Sean Michael Fitzpatrick <sfitzpatrick10@qub.ac.uk>

Samples to the UK

Hi there,

I have a quick note for EvolDir. I recently tried to have samples of * Drosophila* sent by Fedex to the UK from the US, through Stansted airport. The samples were denied entry to the UK. Fedex told me that the reason for this is that DEFRA/Customs have a new rule as of 12 months ago that *Drosophila *samples are not allowed to go through Stanstead airport due to handling restrictions. The exact details are unclear but it means you can't use Fedex to mail samples from the US as they operate mainly out of Stansted in the UK. If you do mail samples from the US make sure to go with a courier that operates through either Heathrow, Gatwick or Manchester as these airports are cleared to receive and process *Drosophila* samples. This could extend to other biological samples - but I'm not sure on this.

Regards,

Gilbert Smith.

– Gilbert Smith School of Biology Dyers Brae House University of St Andrews St Andrews, Fife Scotland KY16 9TH

Tel: (44) 1334 463371

Gilbert Smith <gs70@st-andrews.ac.uk>

ShortCourses YouWouldLike

What Short Courses Would You Like To See Offered to the Evolution Community?

Let your voice be heard! NESCent (The National Evolutionary Synthesis Center) is expanding its course offerings and would like community feedback on potential new short courses (1-2 weeks in duration) to offer.

As a result of our recent call for suggestions, we received several great ideas for new courses. Your feedback will help us determine which ideas to solicit for full proposals.

To see the ideas and provide your input, please go to https://spreadsheets.google.com/viewform?formkey=-dGFpaTkwZGJidzBmZEhLZHRuY1dfdEE6MQ by May 31st, 2010. At that time, we will issue a call for full proposals, which will be due by July 10th, 2010.

If you have questions, please contact Jory Weintraub (jory@nescent.org).

Thank you for your input!

Jory

jory@nescent.org

Jory Weintraub <jory@unc.edu>

ShortCourses YouWouldLike 2

Last Chance to Voice Your Opinion: What Short Courses Would You Like To See Offered to the Evolution Community?

Let your voice be heard! NESCent (The National Evolutionary Synthesis Center) is expanding its course offerings and would like community feedback on potential new short courses (1-2 weeks in duration) to offer.

As a result of our recent call for suggestions, we received several great ideas for new courses. Your feedback will help us determine which ideas to solicit for full proposals.

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If you have questions, please contact Jory Weintraub (jory@nescent.org).

Thank you for your input!

Jory Weintraub <jory@unc.edu>

Software CANGS for 454 data

Update of CANGS, a user-friendly utility of processing and analyzing 454 G-FLX data in biodiversity studies

new features:

1) poly N tails are removed from the 3' ends of the reads before trimming adapter B 2) barcodes of different length are accepted 3) filtering of reads with ambiguous bases has been made optional 4) We introduced a new option to filter for sequencing errors. Rather than conditioning on a minimum count in the data set, we condition on the occurrence in independent data sets.

CANGS is available at: http://i122server.vu-wien.ac.at/pop/software.html In addition to these new features, CANGS provides the following options: - removal of PCR primers - quality filtering of sequences - generates input files for further downstream analyses (e.g.: rarefaction) - links 454 sequences with a taxonomic name from GenBank (various options are provided)

Christian Schlötterer Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://i122server.vu-wien.ac.at/pop Vienna Graduate School of Population Genetics http://www.popgen-vienna.at VetCore Illumina Sequencing Service http://i122server.vu-wien.ac.at/pop/seq/VetCore2.htm schlotc@gmail.com

Software Phobos update

Dear Community,

Phobos is a widely used tandem repeat search program, for which an updated version is now available from my web page.

http://www.ruhr-uni-bochum.de/spezzoo/cm/cm_phobos.htm Particularly interesting for population genetic studies is the integration of Phobos in tools to design flanking primers (see below).

The power of Phobos in a genome comparison context, can be seen in our recent paper: “Genome-wide analysis of tandem repeats in Daphnia pulex - a comparative approach” which can be viewed here: http://www.biomedcentral.com/1471-2164/11/277 Phobos is free for academic users.

Some of the most important features are:

- search modes for perfect and imperfect tandem repeats.

* perfect repeats can be detected in the pattern size range from 1 to several thousand bp in complete genomes

* imperfect repeats The pattern size range is only limited by the computational power. For the comparative analysis mentioned above, we used the pattern size range of 1-50 bp.

- Phobos uses an exact, in particular non-probabilistic search algorithm.

- Phobos is fast. Detecting imperfect microsatellites (1-6bp) in the complete genome of homo sapiens takes less than 30 minutes (mismatch and gap penalty of -6) on a modern computer.

- Phobos comes as a version with GUI and a command-line version.

- The main feature of Phobos is the high precision with which it finds tandem repeats. This makes Phobos an ideal tool also for a statistical analysis of tandem repeats in genomic libraries and complete genomes.

Since the first announcement on evoldir in January 2008, Phobos has become much more efficient and many new features have been added. For example:

- new output formats requested by users.

- it is now possibility to design flanking primers for tandem repeats, by using one of the following approaches:

* STAMP: Is an open source primer design pipeline for tandem repeats build on the powerful Staden package. (Can also be downloaded from my web page.)

* Geneious plugin: This is a plugin for the Geneious software.

Project status: (current Phobos version 3.3.11)

Phobos has been tested extensively by us and the community of several hundred users. Since its release, only few bugs have been detected and removed. For the current version no problems are know. We use Phobos in our lab, from population genetics analyses to genome comparison.

Best regards,

Dr. Christoph Mayer Department of Animal Ecology, Evolution and Biodiversity, NDEF 05/751 Ruhr-Universitaet Bochum 44780 Bochum Germany

Email: cm@tp4.rub.de Web.: www.ruhr-uni-bochum.de/spezzoo/cm Tel.: 0234 32 25072

Christoph Mayer <cm@tp4.ruhr-uni-bochum.de>

cm@tp4.rub.de

Software TranslatorX

Dear Colleagues.

I hope you will not mind us bringing this FREE website to your attention.

http://www.translatorx.co.uk/ TranslatorX is a tool to align protein-coding nucleotide sequences based on the corresponding amino acid alignments. Given a set of nucleotide sequences, TranslatorX translates them to amino acids using the appropriate genetic code, aligns those amino acid sequences and, from the resulting alignment, determines the optimal alignment of nucleotide sequences. Because a different genetic code can be set for each taxon, the software is particularly useful for comparative studies of mitochondrial genomes.

Further capabilities of the software are described on the website or in this publication:

Abascal F, Zardoya R, Telford MJ (2010) TranslatorX: multiple alignment of nucleotide sequences guided by amino acid translations. Nucleic Acids Res. doi:10.1093/nar/gkq291

We hope you find it useful.

Best wishes

Federico Abascal, Rafael Zardoya and Max Telford.

Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html TranslatorX: multiple alignment of nucleotide sequences guided by amino acid translations

http://www.translatorx.co.uk/ Telford & Littlewood: Animal Evolution. OUP http://ukcatalogue.oup.com/product/9780199570300.do Files and software for downloading:

Mrimpatient: If you cant wait to see latest result of MrBayes analysis.

Xstem and Ystem: Software for 2y structure data in rRNA phylogenetic analyses.

MtZoa and MtHydro : new amino acid substitution matrices

Hacked version of MrBayes using these matrices

http://web.mac.com/maxtelford/iWeb/Work/Downloads.html Xenoturbella You Tube video http://uk.youtube.com/watch?v=3DyJXNcoxL2Xs The Linnean Society of London http://www.linnean.org/ m.telford@ucl.ac.uk

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SouthAfrica Volunteers MouseEvolution

Volunteers needed as field assistants for the project:

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

July/August to December 2010

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to evolution, ecology and behavior before starting an MsC or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o‘ clock), and stops its activity with dusk (19 o‘ clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers are also expected to help with maintenance of the research station (water pump, solar power, etc.)

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1000 (around 105 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 130 Euro) per month applies. Students must buy their own food etc in Springbok (costs of about R 2000 or 210 Euro/month). Including extras, you should expect costs of about 300 - 400 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for volunteers for the period July / August to December 2010. The volunteer project is ongoing, i.e. positions will also be available in 2011. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@ieu.uzh.ch.

More information under www.stripedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin

Research Assistant, Department of Animal Behavior,

University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland.

Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences,

University of the Witwatersrand, South Africa.

WORKING AS A FIELD ASSISTANT IN GOEGAP NATURE RESERVE

A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

Blue skies without a single cloud for six weeks rocky mountains with little vegetation yellow, orange and pink fields of flowers in whatever direction you look small mammals, lizards and birds in our front yard and Mountain Zebras, Springbok and Ostrich right next door...

This was my time at the Succulent Karoo Research Station in Goegap Nature Reserve in South Africa! During six weeks from the beginning of July until the middle of August I've been living here, studying mice, experiencing nature like never before and being part of a small community where there was always something to laugh and joke about!

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I improved quickly shaking the mice out of the traps, weighing them and checking the number of the ear tag. Other duties like cleaning the cages of the mice in the captive colony, washing the dirt from probably several months out of the traps, painting the new Wendy House and putting in a floor

— / —

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

StazioneZoologica Italy

Dear EvolDir community the Stazione Zoologica of Anton Dohrn Naples might be suppressed by the Italian Government. We need of your help. If you wish that the Stazione Zoologica remains as an autonomous scientific Institution, please fill the form at http://www.szn.it/SZNWeb/showpage/1?_languageId_=2 Please contact as many colleagues as you can

Gabriele Procaccini Stazione Zoologica Anton Dohrn of Naples

pro@szn.it

Tajikistan collaboration

A coleopterologists >>cry for help<< from Tajikistan:

I recently was in Dushanbe, Tajikistan, for research. In this context, I had a longer conversation (in Russian) with Prof. Abdusalaya Kh. Kadyrov.

He is close to retirement and spent most of his professional life on a large (some thousands of specimens) collection of the following families of beetles from most parts of southwestern Tajikistan (as well as other parts of Tajikistan and Central Asia).

Cerambycidae Buprestidae Elateridae Staphylinidae Scarabaeidae

He believes that this collection contains several (many?!) new species and is unique in its geographic context. During the time of the civil war in the 1990ies, and because of currently miserable scientific circumstances in Tajikistan (as well as because of no knowledge of English), Kadyrov lost his few previous contacts to some international colleagues. He would like to re-initiate collaborations with specialists who will publish with him on his collections, and can at best visit him and the collection in Dushanbe. In the case of co-authorships, he is also ready to share parts of his material, BUT NOT TO SELL IT, ONLY!

A MAJOR LIMITATION is that neither Prof. Kadyrov nor his doctoral student can speak English. Contact and further collaboration need to be in Russian or Tajik (a modern variety of Farsi/Persian).

Email him through his doctoral student, Dilshoda Yakubova:

yadsh@yandex.ru or dilios@mail.ru

His address is: Tajikskii Nationalnyi Universitet Biologicheski Fakultet, Kafedra Zoologii Dushanbe, Tajikistan

His home telephone: 0092 2 36 62 62

Best regards, Matthias Stoeck

PS: I personally would like to add that I am only the messenger who would like to help...I cannot/will not take responsibility for any future outcomes, be them positive or negative.

Matthias Stöck University of Lausanne Department of Ecology and Evolution (DEE) UNIL, Biophore, CH-1015 Lausanne Switzerland http://www.unil.ch/dee/-page40038.html email: matthias.stoeck@unil.ch

Matthias Stoeck <matthias.stoeck@unil.ch>

Warbler Paternity data

I don't think this message got through the first time, so I'm trying again. If you've received it twice, I apologize. I am a graduate student at UC Riverside and I'm seeking data on rates of extra-pair paternity in species of wood warbler (Family Parulidae) as part of a comparative analysis. Any unpublished information about 1) the percentage of nests that contain extra-pair young and 2)the total percentage of extra-pair young in warbler species would be greatly appreciated. Anyone who can provide me with such information will be gratefully acknowledged and cited. My email is anne.jacobs at ucr.edu

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Webserver GrassPortal grassPhylogenetics

GrassPortal (www.grassportal.org) will allow users to access and visualize information on the name and description, geographical distribution, ecological characteristics and evolutionary relationships for all the worlds grass species. GrassPortal will integrate and link these data within a web interface, providing research and educational users with tools for interacting, discovering and extracting information.

We are currently recruiting potential users and would like participants to take part in our user evaluation survey and in so doing also have the option to become early users of the beta-version of the portal before it goes publicly online. The online survey provides a number of different scenarios for the use of GrassPortal and then asks a number of questions of the user that will help us to decide on the ultimate structure and content of GrassPortal. This is a very important part of the portal design as it will tell us what users actually do and dont want from GrassPortal.

If you are interested in participating, please email Vernon Visser for further details (vernon@grassportal.org).

Vernon Visser

Post-doctoral Research Associate Dept. of Animal and Plant Sciences Alfred Denny Building The University of Sheffield Western Bank S10 2TN United Kingdom Tel: +44 777 496 2894

Vernon Visser <vervis@gmail.com>

PostDocs

AarhusU CancerMolecularEvolution

I have a post doc opening, which I would appreciate if you could post. It is in cancer genomics, but the group also works in molecular evolution and I would thus appreciate to target this audience as well.

Best, Jakob Skou Pedersen

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Post-doctoral position in cancer genomics at Aarhus University, Denmark

A post-doctoral position (three years) is available in the bioinformatics group at the Department of Molecular Medicine (MOMA), Aarhus University Hospital, Skejby, Denmark, to study the function of ncRNAs in cancer and the potential clinical applications. The successful applicant will both be responsible for individual projects and participate in large collaborations involving Danish biotech companies. Overall, the research will focus on the analysis of large collections of clinical samples from several types of cancer tumors, which will be characterized using various functional genomics techniques, including NGS and ncRNA micro-array expression profiling. The aim is to identify and characterize ncRNAs that are dys-regulated in cancer using integrated bioinformatical analysis of these data sets.

The ideal applicant holds a Ph.D. degree in bioinformatics or a related discipline with relevant publications in genomics. Demonstrated experience in large-scale data analysis using statistical or machine-learning methods is required. Experience with analysis of micro-array data or next generation sequencing data is highly desirable.

The Department of Molecular Medicine offers a stimulating interdisciplinary research environment with strong clinical ties, focusing on translational cancer research. The department has long experience with cancer genomics and houses a next generation sequencing facility (see http://www.mdl.dk/ for further information). The bioinformatics group, headed by associate professor Jakob Skou Pedersen, is devoted to the study of non-coding RNAs in gene- regulation and cancer development. The work includes both the development of sound statistical methods and their application in genomics data analysis.

Currently, the monthly postdoc salary begins around 4800 including supplements and pension. Non-Danish and Danish applicants may be eligible for tax reductions, if they have not lived in Denmark the last 3 years.

For more information on the position, contact ass. prof. Jakob Skou Pedersen (e-mail: jakob.skou@ki.au.dk; phone: +45 89492 9412).

For a full description and application guidelines see http://jobsys.au.dk/en/sun/academic-positions/ . Jakob Skou Pedersen <jsp@binf.ku.dk>

BiKF Germany Biodiversity

The Biodiversity and Climate Research Centre (BiK-F) is a new interdisciplinary institute with the mission to carry out internationally outstanding research on the interactions of biodiversity and climate change on the organism level. It has been founded by Senckenberg Gesellschaft fuer Naturforschung, the Goethe-University Frankfurt am Main, and others partners. The Centre is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). It provides a new, dynamic research environment that integrates a variety of disciplines from both natural and social sciences. The Project Area D “Ecological Genomics” invites applications for the position of a

Postdoctoral Researcher Biodiversity of arctic vertebrates

The successful candidate will have a PhD in genetics, evolutionary biology, molecular biology, molecular ecology or related fields and a strong, independent research record. Good laboratory experience, sequence analysis, teamwork skills, supervision of PhD students and introduction of techniques to new lab members are expected. Familiarity with next generation sequencing is an advantage. Furthermore, good written and oral communication skills in English, the willingness to write research-funding proposals and to learn some German are essential for a rewarding research.

The main work will be to establish molecular techniques, sequencing strategies, and analytical methods to link evolutionary processes in vertebrates (preferably arctic mammals) with environmental changes. This research will be done in collaboration with a lab manager and graduate/undergraduate students that will be involved in the project. Frankfurt is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities. Supervising an own PhD student is negotiable.

Salary and benefits are according to a public service position in Germany (TV-H E 13). The Research Centre BiK-F advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

Target start date is September 01, 2010. The position will be offered for 3 years, with the possibility of an extension pending performance and availability of funds. The duty station will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Naturforschung.

Please send your application by e-mail attachment, mentioning the reference of this position (#D17) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2 referees and a copy of your thesis and other relevant exams before June 20th to:

Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de. For enquiries about the position and the contract conditions please write to Prof. Dr. A. Janke (ajanke@senckenberg.de).

recruiting <recruiting@senckenberg.de>

ClemsonU PopulationGenomics

A National Science Foundation funded Post-Doctoral Research Position is available in the Department of

Biological Sciences at Clemson University. The Postdoc will work collaboratively with the senior scientist and graduate students on genomic approaches to population genetics, evolution, and adaptation. The successful candidate will be involved with data collection and analysis of large sequence data sets, some gathered with "next-generation" methods plus others collected with Sanger-sequencing. The projects require laboratory skills for preparing high quality genomic DNA for PCR and sequencing, bioinformatics skills for de novo assembly and alignment and annotation of orthologous sequences, and/or experience with population genetic analyses. In addition to the primary research responsibilities, duties will include assisting and mentoring graduate students, preparation of manuscripts for publication, and the organization and curation of large sequence datasets. Applicants are required to have a Ph.D. in biological sciences or related field.

Applicants should make initial inquiries to clemsongenomicspostdoc@gmail.com , followed by electronic transfer of their CV, a letter of intent describing candidate's motivation, qualifications, skills, and experience relevant to this position, plus contact information for three references. Applications will be reviewed starting 10 May 2010 and until the position is filled.

ErasmusMC Rotterdam HumanPopulationGenetics

"The Department of Forensic Molecular Biology (FMB) of the Erasmus University Medical Centre Rotterdam (Erasmus MC) in the Netherlands (http://www.erasmusmc.nl/fmb/research/) offers a research position for a young postdoctoral scientists to work with genome-wide SNP population data for various purposes. Salary is competitive and will be according to experience. Tentative starting date is November 2010. The position is planned for 2 years with possible extension. Suitable PhD students who will have their degree by the end of 2010 are also encouraged to apply.

We are looking for a highly motivated person interested on developing his/her scientific skills in the interdisciplinary department of FMB consisting of international members (working language is English). The FMB is a well established department within the Erasmus MC, with an over the average of the Eramsus MC scientific production. The main FMB research focus is to study various human biological aspects in order to develop new molecular tools for future application in forensics. These include among others finding genetic markers associated to visible traits and bio-geographic markers. However, research focuses not only on identifying biomarkers but moreover on understanding the biological processes that create marker values.

The successful candidate will be involved in different projects related to the analysis of population data currently obtained with genome-wide SNP microarrays by FMB and its collaborators; furthermore, he/she will collaborate with other departments at Erasmus MC and our worldwide study partners. Main research will be based on quantifying the amount of population differentiation, ascertaining suitable markers for detecting population differentiation and developing new algorithms for predicting population ancestry from the data. In addition the candidate may be involved in the various ongoing projects to identify the genetic basis of human visible traits and their predictions. He/she must have a strong background in theoretical population genetics, preferentially human, and/or in bioinformatics. Programming skills on either C++, Java or R are essential, as well as knowledge to create and manage large databases. Previous experience with analyzing dense SNP microarray data would be highly desirable.

Erasmus MC is situated in Rotterdam, the second largest city of the Netherlands. Rotterdam is a cosmopolitan city with a large number of immigrants from all around the world; it is situated South-West of the Netherlands and it is well connected by road, sea and airplane to all Europe.

Send CV, publication list, 3 reference addresses, motivation letter to: Prof. M. Kayser, m.kayser@erasmusmc.nl till 4 weeks after appearance of this advert, for more information: Dr. Oscar Lao, o.laogrueso@erasmusmc.nl"

Thank you very much in advance for all your help.

Best regards,

Oscar Lao

Oscar Lao <o.laogrueso@erasmusmc.nl>

ETH Zurich TheoreticalEvolution

The Evolutionary Ecology group of ETH Zürich & EAWAG is offering a

Postdoc Position in Theoretical Evolutionary Ecology

We are seeking a postdoc to work on the topic of symbiont-mediated coevolution. There is increasing evidence that microbial endosymbionts play a crucial role in host-parasite coevolution. Symbionts have been shown to protect their hosts against parasites or to alter the specificity of host-parasite interactions. These aspects are not captured by existing models of host-parasite coevolution. The goal of this project is to develop new models that incorporate effects of symbionts on the reciprocal selection between hosts and parasites to achieve a conceptual understanding of the coevolutionary dynamics in such systems. A convenient experimental system to test predictions from these models is available in the group (aphids, their bacterial symbionts and aphid parasitoids).

This position is funded by the Swiss National Science Foundation and is available for 2 years. The successful candidate will be working in the Evolutionary Ecology group led by Christoph Vorburger (http://www.evec.ethz.ch). This group is associated with the Institute of Integrative Biology at ETH Zürich, Switzerland (http://www.ibz.ethz.ch), as well as the Department of Aquatic Ecology at EAWAG, the Swiss Federal Institute of Aquatic Science and Technology (http://www.eawag.ch). These institutions offer an excellent work environment and ample opportunities for collaboration, particularly with the Theoretical Biology group of Prof. Sebastian Bonhoeffer (http://www.tb.ethz.ch) and the host-parasite group of Prof. Jukka Jokela (http://homepages.eawag.ch/~jokelaju/).

A PhD is required for this position. Candidates should have experience using mathematical modeling and computer simulation to study ecological and evolutionary problems. The expected starting date for this position is 1 October 2010, but this can be negotiated.

Please send a letter of application, curriculum vitae, publication list, and the names and contact details of three academic references as a single PDF file to Sandra Isenring, Human Resources, recruiting@eawag.ch, indicating reference number 104403. Deadline for applications is July 15, 2010. For enquiries about this position please contact Christoph Vorburger (christoph.vorburger@eawag.ch).

We are looking forward to your application.

Christoph Vorburger SNF Förderungsprofessor für Evolutionäre Ökologie Institut für Integrative Biologie ETH Zürich & EAWAG Überlandstrasse 133 Postfach 611 8600 Dübendorf SWITZERLAND

office: BU-G13 phone: +41 44 823 5196 fax: +41 44 823 5028 christoph.vorburger@eawag.ch vorburgc@ethz.ch www.evec.ethz.ch

Christoph.Vorburger@eawag.ch

Finland 2 MolecularSystematics

Two postdoctoral positions are available in the newly funded project “Diversification of plant-feeding insects over millions of years: what is the role of dramatic climate changes?” (funding from the Kone Foundation) headed by Niklas Wahlberg (University of Turku, Finland) and Tommi Nyman (University of Eastern Finland). A strong background in molecular systematics is required for both positions. The positions are available for one year starting in September 2010, with a possibility to extend for a second and third year. Salary will be 2100euro per month (non-negotiable) paid as a tax free stipend up to 18,800euro per year, with 6400euro per year subject to taxes (in practice, about 1900euro per month net income). One postdoc will work in Turku, Finland, the other in Joensuu, Finland, with active interaction planned between research groups.

The postdoc in Turku will work in the research group of Niklas Wahlberg (http://nymphalidae.utu.fi), expanding the work on Nymphalidae butterflies to other lepidopteran groups (Geometridae and Noctuoidea). The major focus of this postdoc will be to generate new molecular data for geometrid moths, assist in generating molecular data for noctuids, and take responsibility in analyzing resulting data using phylogenetic methods. The candidate should particularly be familiar with methods used to analyze changes in rates of diversification over evolutionary time (e.g., with algorithms in programs such as SymmeTree and Medusa). Interested persons should send their CV, a statement of why they are interested, and contact information of two references to Niklas Wahlberg (niklas.wahlberg@utu.fi) by the 31 July 2010.

The postdoc in Joensuu will work in the research group of Tommi Nyman (www.joensuu.fi/biologia/nyman), and focus on the diversification history of sawflies (the mostly herbivorous basal grade of Hymenoptera). The first task of this postdoc will be to increase the number of easily amplifiable nuclear genes to be used for phylogenetic and timing of diversification analyses. The candidate should be familiar with whole-genome databases, publicly available EST libraries, primer design, and lab practices when developing new markers. The candidate will be expected to generate new molecular data for sawflies, and to take responsibility for analyzing the resulting data using phylogenetic methods. Interested persons should send their CV, a statement of why they are interested, and contact information of two references to Tommi Nyman (tommi.nyman@uef.fi) by the 31 July 2010.

The project will facilitate numerous comparative analyses that will shed light on common patterns in the evolutionary radiations of two species-rich and ecologically important insect herbivore taxa. Both research groups are young, dynamic, and innovative; a perfect opportunity to take advantage of a robust background knowledge to find something new and exciting for science in a collegial atmosphere!

– Niklas Wahlberg Academy Research Fellow Laboratory of Genetics Department of Biology University of Turku 20014 Turku FINLAND

Phone: +358 2 333 5569 Fax: +358 2 333 6680 Skype: niklas_w2

Nymphalidae Systematics Group: http://nymphalidae.utu.fi niklas.wahlberg@utu.fi

France Microme PathwayCuration

European MICROME project Post Doctoral Position in France.

- Context: GENOSCOPE is both the French National Genome Centre, now part of the Genomic Institute of the Commissariat à l'Energie Atomique (CEA), as well as an independent research institute dedicated to high-throughput studies in biology, bioinformatics and systems biology. One of our research areas is that of prokaryote metabolism, including the study of bacterial communities, the search for novel enzymatic functions, metabolic reprogramming, and modelling. CEA is involved in the European MICROME project which began in December 2009 (http://www.microme.eu). This project aims to extend the scope of microbial genome annotation from functional assignment at the gene level, to the systematic generation of pathway assemblies and genome-scale metabolic models. Microme will provide a robust, scalable infrastructure integrating a curated repository of reference pathways with genome-scale constraint-based models and downstream applications in comparative genomics and biotechnology.

- Functions and responsabilities: CEA is seeking to recruit a scientific curator for a demanding role in the assignment of functional Gene-Protein-Reaction (GPR) annotation, as well as the curation of metabolic pathways from reference organisms. In the first phase of the project Microme will be populated with reference data available from existing resources. Following this, all metabolic pathways of 4 reference bacterial genomes will be checked, corrected and completed as necessary. The curator will contribute to this work as well as to the expert curation of reference pathways across the full spectrum of species covered by Microme. He or she will work closely with other members of the MICROME consortium (of which there are 14), particularly with the Swiss-Prot group at the Swiss Institute of Bioinformatics (SIB) and with partners at the European Bioinformatics Institute (EBI).

- Qualifications and experience: A university degree in life sciences and a broad knowledge in biochemistry and/or enzymology, and/or molecular biology are the minimum requirements. A higher degree (such as MSc/PhD) and/or relevant post-graduate experience are highly desirable. Previous experience in database curation is advantageous but not essential.Experience in using biological databases and sequence analysis tools is desirable. The successful candidate must be detail-oriented and must be able to quickly and accurately interpret scientific literature. The position requires excellent communication and organizational skills in order to interact well under time pressure within a team of software developers and biologists and with external partners.

- Job conditions: This position is offered in the context of a European project for an initial period of one year, which may be renewed twice. Depending on the background and experience of the successful candidate, the monthly salary will be between 2400 to 2900 euros.

Interested candidates should send a letter of motivation, and a CV to: cmedigue@genoscope.cns.fr anne.morgat@isb-sib.ch The closing date is 16h May 2010.

vallenet@genoscope.cns.fr

GhentU SystemsBiology

Postdoc position in Systems Biology

The Division of Bioinformatics and Systems Biology at the VIB Department of Plant Systems Biology, Ghent University invites applications for an Expert Scientist position in the field of Computational Systems Biology.

We seek highly-motivated individuals with an interest in developing novel algorithms and software tools for the integration of high-throughput genomic data and the inference and modeling of regulatory networks. The ideal candidate should hold a doctoral degree in a relevant field (physics, computer science, applied mathematics, engineering or life sciences), with several years of postdoctoral experience, and have a proven record of its application for the life sciences.

Major duties include:

- Responsible for the functioning of a small group of researchers (PhD students and postdocs). - Develop new and innovative (breakthrough) projects in line with the strategic plan of the Department and VIB. - Provide scientists in the Department and VIB with transfer of in-depth knowledge. - Transfer science into publications in high impact journals. - Detect potential technology transfer possibilities.

The position will initially be available for 2 years (starting September 1st 2010), with the possibility of a 3 year extension depending on positive evaluation. For further information please consult our homepage (http://bioinformatics.psb.ugent.be/) or contact the Scientific Director Prof. Dr. Yves Van de Peer (yves.vandepeer@psb.vib-ugent.be).

Applications including a motivation letter, CV, list of publications, names and contact information of three references and a research proposal (2-3 pages) should be sent to Prof. Dr. Yves Van de Peer before July 1st 2010.

– Yves Van de Peer, PhD.

Professor in Bioinformatics and Genome Biology Associate Department Director, VIB Department of Plant Systems Biology Group Leader Bioinformatics and Systems Biology Ghent University Technologiepark 927 B-9052 Ghent Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 Fax: +32 (0)9 331 3809 email: yves.vandepeer@psb.vib-ugent.be

http://bioinformatics.psb.ugent.be/ Yves Van de Peer <yves.vandepeer@psb.vib-ugent.be>

HatfieldMarineCenter GenomicDiversityWhales

Postdoctoral Position in 'Genomic Diversity of Endangered Whales', Marine Mammal Institute and Department of Fisheries, Wildlife and Conservation Biology, Oregon State University

The Marine Mammal Institute offers a full-time (1.0 FTE), 12-month, fixed-term position as a Postdoctoral Scholar in the Cetacean Conservation and Genetic Laboratory, under the direction of Prof. Scott Baker. The successful candidate will work collaboratively with the senior scientist and graduate students in developing methods for 'reduced representation', genomic sequencing of individual right whales using Illumina (short-read, pair-end reads) or similar next-generation technologies. The project requires laboratory skills for preparing genomic DNA for the reduced-representation sequencing and bioinformatics skills for de novo assembling and alignment of orthologous contigs. The resulting high-resolution, 'genomic profiles' will be used to estimate the effective size of this critically endangered population and to identify individuals harboring unique genetic diversity or that might represent currently unknown subpopulations. To avoid depletion of valuable tissue samples, the project will evaluate the use of Whole Genome Amplification (WGA) in preparation for the genomic sequencing. In addition to the primary research responsibilities, duties will include mentoring of graduate students, preparation of manuscripts for publication and the organization and curation of large datasets. The applicant is required to have a Ph.D. in biological sciences with expertise in population genetics, molecular ecology or bioinformatics. Experience with the Linux operating system and computer programming is desirable.

Salary will be commensurate with experience and there is potential for annual renewal depending on funding.

To apply for this position: please send (by email, with subject header "Genomic diversity postdoc application") a cover letter describing previous training and research interests, a CV, copies of publications and the names and contact information for 3 professional references to:

Sheri Woods OSU Marine Mammal Institute Hatfield Marine Science Center 2030 SE Marine Science Drive Newport, OR 97365

Email: sheri.woods@oregonstate.edu Web site: http://mmi.oregonstate.edu/ Closing date: June 15, 2010 or until the position is filled Position available July 1, 2010

agajoh@oregonstate.edu

HatfieldMarineCenter WhaleGenomicDiversity

Postdoctoral Position in 'Genomic Diversity of Endangered Whales', Marine Mammal Institute and Department of Fisheries, Wildlife and Conservation Biology, Oregon State University

The Marine Mammal Institute offers a full-time (1.0 FTE), 12-month, fixed-term position as a Postdoctoral Scholar in the Cetacean Conservation and Genetic Laboratory, under the direction of Prof. Scott Baker. The successful candidate will work collaboratively with the senior scientist and graduate students in developing methods for 'reduced representation', genomic sequencing of individual right whales using Illumina (short-read, pair-end reads) or similar next-generation technologies. The project requires laboratory skills for preparing genomic DNA for the reduced-representation sequencing and bioinformatics skills for de novo assembling and alignment of orthologous contigs. The resulting high-resolution, 'genomic profiles' will be used to estimate the effective size of this critically endangered population and to identify individuals harboring unique genetic diversity or that might represent currently unknown subpopulations. To avoid depletion of valuable tissue samples, the project will evaluate the use of Whole Genome Amplification (WGA) in preparation for the genomic sequencing. In addition to the primary research responsibilities, duties will include mentoring of graduate students, preparation of manuscripts for publication and the organization and curation of large datasets. The applicant is required to have a Ph.D. in biological sciences with expertise in population genetics, molecular ecology or bioinformatics. Experience with the Linux operating system and computer programming is desirable.

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Sheri Woods OSU Marine Mammal Institute Hatfield Marine Science Center 2030 SE Marine Science Drive Newport, OR 97365

Email: sheri.woods@oregonstate.edu Web site: http://mmi.oregonstate.edu/ Closing date: June 15, 2010 or until the position is filled Position available July 1, 2010

agajoh@oregonstate.edu

IowaStateU EvolBiology

ISU is soliciting applications for a post-doctoral position for a scientist interested both in research and in pedagogy. This is a split position, about half "scientific pedagogy", and the remainder more traditional scientific research in a host laboratory. The latter can be with any faculty member at ISU willing to host the post-doc. The formal ad follows:

Science Teaching Fellow

The Howard Hughes Program for Innovation in Undergraduate Science Education at Iowa State University invites applications for two Post-doctoral Science Teaching Fellow positions in the fields of Biology and Chemistry. Specific responsibilities of these grant-funded positions will include working in coordination with science faculty to identify specific learning goals for core undergraduate courses, decide on assessments of student progress toward these goals, and develop and prototype innovative in-class and out-of-class course activities and laboratory materials to promote student learning. Fellows will have the opportunity to join a research group, providing additional opportunities for scholarship, publication, and professional development in the sciences. ISU is located in a vibrant college town and is committed to excellence and world-class diversity.

Qualified candidates must have a Ph.D. in the biological sciences, chemistry, or science education; excellent organizational and interpersonal communication skills; teaching experience; and have the potential for contributing to science education scholarship and research. To apply, send the following to cesmeestaff@iastate.edu: a cover letter briefly summarizing qualifications, curriculum vitae, a statement of scholarly interests and expertise, and contact information for three references. For questions regarding this position, please contact Prof. Ogilvie at cogilvie@iastate.edu. Review of applications will begin on June 28, 2010 and will continue until the position is filled.

Applications from women and members of under represented groups are strongly encouraged. Iowa State

University is an EO/AA employer.

Jonathan F. Wendel, Professor and Chair Department of Ecology, Evolution, & Organismal Biology, Iowa State University Ames, IA 50011 Voice (515) 294-7172; FAX 515-294-1337; jfw@iastate.edu<mailto:jfw@iastate.edu> http://www.eeob.iastate.edu/faculty/WendelJ/ (Personal home page) http://www.eeob.iastate.edu/ (Department home page)

"Wendel, Jonathan F [EEOBS]" <jfw@iastate.edu>

MaxPlanckTubingen Bioinformatics

PhD and postdoc positions in bioinformatics

New sequencing technologies are revolutionizing both bottom-up and top- down approaches in biology. The Weigel lab has been a leading early adopter of these technologies and was one of the first in Europe to extensively exploit the Illumina sequencing platform (since 2007). We have developed a variety of analysis tools based on our SHORE pipeline, and are using these for diverse applications, from genome sequencing and epigenetic profiling to transcriptome and transcription factor binding studies, in bacteria, animals and plants. Two positions are available both for developing new algorithms and strategies for primary analysis of second- and soon third-generation sequencing technologies, and for using these data to study a wide array of biological questions. The flagship project in this area is the 1001 Genomes project for Arabidopsis thaliana (http://1001genomes.org), which we have initiated and for which we have already delivered over 80 genomes.

We are also taking a leading role in having the genomes of several members of the Brassicaceae, to which the model plant Arabidopsis thaliana belongs, sequenced. Our first efforts in this area resulted in reference genome sequences for Arabidopsis lyrata and Capsella rubella. One position is available for comparative genomics studies that will take advantage of these data sets.

Finally, automated image analyses are beginning to play an important role in high-throughput phenotyping projects aimed at linking genotypic to phenotypic diversity. One position is available in this area.

Candidates will have knowledge and interest in sequence and genome analyses, and experience in programming (PERL/PYTHON, Java, SQL, C/C++) and in the use of Linux OS.

We are working closely with other groups in Tübingen that are primarily informatically oriented. These include Daniel Huson at the University Tübingen, Gunnar Rätsch at the Friedrich Miescher Laboratory and Bernhard Schölkopf at the Max Planck Institute for Biological Cybernetics on the same campus, as well as Karsten Borgwardt, who heads a departmental research group jointly sponsored with Bernhard Schölkopf. Our work in this and other areas routinely results in high-profile publications (e.g., Maizel et al., Science 2005; Wigge et al., Science 2005; Clark et al., Science 2007; Sureshkumar et al., Science 2009; Wang et al., Cell 2009; Ossowski et al., Science 2010; Todesco et al., Nature in press), and presents extraordinary opportunities for talented and ambitious students and postdocs. Additional information on the group, the institute, and Tübingen can be found on our website (http://weigelworld.org).

Please send applications, with a statement of purpose, names of references, and the subject line <bioinformatics posting> to

Detlef Weigel

Director, MPI for Developmental Biology

weigel@tue.mpg.de

Detlef Weigel <detlef.weigel@tuebingen.mpg.de>

MiamiU InsectEvodevo

Postdoctoral position in insect evolutionary developmental biology at Miami University

A full-time NSF-funded postdoctoral position is available in the Tomoyasu lab, Miami University of Ohio. Our research focus is to understand how changes in patterning mechanisms have contributed to the evolution of morphological diversity by using insect wings as a model system. The researcher will study wing development (with a focus on a Hox gene Ultrabithorax) in the red flour beetle (Tribolium castaneum), by using a combination of transgenic and gene knockdown techniques. Visit our website for more information (http://web.me.com/tomoyasu/lab/home.html)

The successful candidate must have strong technical skills in molecular biology. Experience in Drosophila genetics is preferred. Review of applications will begin June 14, 2010 and continue until position is filled. One-year appointment with potential for renewal for up to four years. Start date is September 1, 2010.

Send an application package via e-mail or mail (a cover letter detailing experience, CV, and contact information for three references) to Dr. Yoshinori Tomoyasu, Department of Zoology, Miami University, Oxford OH 45056 Email: tomoyay@muohio.edu

Miami University is an Equal Opportunity/ Affirmative Action Employer.

Yoshinori Tomoyasu Ph.D Assistant Professor Department of Zoology Miami University 252 Pearson Hall Oxford OH 45056 Tel: 513-529-3126 http://web.me.com/tomoyasu/lab/home.html Yoshi Tomoyasu <tomoyay@muohio.edu>

Netherlands EvolutionaryPopulationDynamics

POST-DOC POSITION

IN POPULATION ECOLOGY / EVOLUTIONARY ECOLOGY (m/f)

Job description: The post-doc position is part of the NWO-VICI project Adapting to a warmer world: phenology, physiology and fitness. In this project, we study selection on phenotypic plasticity in timing of reproduction in great tits in relation to global climate change. There are five integrated subprojects ranging from quantitative genetics, population dynamics and reproductive physiology to genomics. Four of these subprojects are underway and we are now looking for a post-doctoral candidate for the fifth subproject on population dynamics. This project will be carried out in collaboration with Prof Bernt-Erik Saether (NTNU, Trondheim, Norway) and Dr Stephanie Jenouvrier (CNRS, France & WHOI, USA).

Project description: The aim of the project is to develop an eco-evolutionary population dynamic model for the great tit to predict the effects of climate change on population viability. We will use climate projections from selected Atmosphere-Ocean General Circulation Models (AOGCMs) for a range of Intergovernmental Panel on Climate Change (IPCC) scenarios to predict the phenology of the birds (taking evolutionarily processes into account) and of their prey (taking ecological processes into account). The resulting phenological (mis)match will affect demographic rates and thereby population viability. Ultimately, we will calculate the critical rate of climate change that populations can cope with.

Requirements: We are looking for an enthusiastic candidate with a PhD in Population Ecology, Evolutionary Ecology or Animal Ecology and with mathematical modelling and statistical skills. A limited amount of fieldwork may be part of the project.

Appointment: The appointment will be on a temporary basis for a maximum of 2 years. The gross salary starts at EUR 2.861,- per month, scale 10.4, 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: Additional information about this position is available upon request from Prof. Marcel E. Visser (m.visser@nioo.knaw.nl or +31-26-4791253), head of department Animal Ecology. More information about the NIOO can be found on our website (www.nioo.knaw.nl).

Applications: Please send your application including complete curriculum vitae and names of three referees to Prof. Marcel E. Visser at NIOO-KNAW, P.O. Box 40, 6666 ZG Heteren, The Netherlands or g.giesen@nioo.knaw.nl. The closing date for application is 9 June 2010, and the interviews will take place at the end of June.

Prof. Dr Marcel E. Visser Head of Department Animal Ecology Netherlands Institute of Ecology (NIOO-KNAW) P.O. Box 40 6666 ZG Heteren The Netherlands

Phone: +31-26-4791253 Fax: +31-26-4723227 E-mail: m.visser@nioo.knaw.nl

Website: www.nioo.knaw.nl Personal page: www.nioo.knaw.nl/users/mvisser "Visser, Marcel" <M.Visser@nioo.knaw.nl>

Netherlands GeneSpread

PostDoc position - Spatial Modelling

Modelling the ecological implications of the spread of genes from transgenic crop into wild relatives

Project information: In order to assess the ecological implications associated with the introduction of transgenic crops the Dutch Science Foundation (NWO) has launched the focal programme Ecology Regarding Genetically Modified Organisms (ERGO). The project "Introgression of crop (trans-)genes into wild relatives: hybrid fitness, background selection and hitchhiking" (for more info see vacancies at www.rug.nl/biol/theobio) is a joint effort of the Universities of Groningen (Centre for Ecological and Evolutionary Studies,), Amsterdam (Institute for Biodiversity and Ecosystem Dynamics) and Wageningen (Laboratory for Plant Breeding,). The project comprises both various experimental studies (in which the wild lettuce species Lactuca serriola is used as a model) and a theoretical approach. This job offer concerns the subproject "The potential spread of crop genes in a crop/wild system: analysis and modelling of an invasive process." It is the continuation of a previous project (for more info see vacancies at www.rug.nl/biol/theobio) and the models developed in this earlier project should serve as a point of departure.

Project description: Computer models will be developed for the spatial dispersal of transgenes (through pollen, seed, or vegetatively) in wild populations. The main objective is to predict the dispersal pattern and invasion prospects of a transgene on basis of the genetics and life history of the plant species involved. The potential effect of transgenes on dispersal characteristics will receive special attention. Model development will strongly reflect the developments in the related projects. The models developed in various subprojects will be integrated and validated with existing data, including those generated on L. serriola.

Profile: PhD with knowledge of population biology, population genetics and modelling. Extensive experience with programming and computer simulations. Good communication skills for interaction within a multidisciplinary programme.

Renumeration: Depending on age and experience, the gross salary per month will range between ? 2861 and ? 3088. Duration of the contract: 2.5 years (with an evaluation after the first year).

Location: Theoretical Biology Group at the Centre for Ecological and Evolutionary Studies (CEES) of the University of Groningen (The Netherlands). The group develops theory in two major research areas: evolutionary ecology and self-organization. Current research projects focus on evolutionary game theory, life history theory, evolutionary immunology, kin selection, sex determination, sex allocation, sexual selection, sexual conflict, metapopulation genetics, sympatric speciation, allometric scaling laws, resource and interference competition, host-parasite co-evolution, and the emergence of social structure. It offers a stimulating and exiting environment for doing research

Further information: Prof. Dr. Franjo Weissing (f.j.weissing@rug.nl; Tel: +31 50 363 2131) and Prof. Dr. Kuke Bijlsma (r.bijlsma@rug.nl; Tel: +31 50 363 2117).

Application: To apply for this position, send your application (including letter of motivation, detailed CV, PDFs of three most relevant publications, and the names and email addresses of three potential referees) in electronic form before 1 July to the office manager of the Theoretical Biology Group, Hinke Tjoelker (theobio@rug.nl). Please include the text 'ERGO PostDoc' in the subject line of your email.

joke.bakker@rug.nl

NewYorkU EvolutionarySystemsBiology

Postdoctoral Researcher, Siegal Lab, New York University

A postdoc position is available in Mark Siegal's lab at NYU's Center for Genomics and Systems Biology. The Siegal lab uses a variety of experimental and computational approaches to understand the causes and consequences of phenotypic robustness. The successful candidate will work on an NIH-funded project to dissect genetic and environmental sources of variation in yeast cell morphology, using high-throughput fluorescence microscopy and automated image analysis. The postdoc will also have the opportunity to pursue independent research related to this work.

The Center for Genomics and Systems Biology is a dynamic and interactive research environment, with a unique concentration of labs investigating questions at the intersection of functional genomics and evolution. NYU is located in the wonderful Greenwich Village neighborhood of New York City.

Applicants should be motivated, creative and collegial. Prior experience with relevant experimental methods (yeast molecular genetics, microscopy, image analysis) is advantageous. Review of applications will begin immediately and continue until the position is filled. To apply please email Mark Siegal <mark.siegal AT nyu.edu> with CV, a list of references and a brief statement of research experience and interests. New York University is an equal opportunity employer.

Mark L. Siegal Assistant Professor Center for Genomics and Systems Biology Department of Biology New York University 100 Washington Square East New York, NY 10003 http://homepages.nyu.edu/˜ms4131 mark.siegal@nyu.edu

NorthCarolinaStateU StatisticalGenetics Bioinformatics

A full-time statistician position and multiple postdoc positions are available in Bioinformatics Research Center at North Carolina State University.

The Statistician position is supported by a large scale multiple year pharmacometabolomics network sponsored by NIH. The statistician is expected to perform statistical and bioinformatics data analysis on the research projects in the network, and interact closely with network personnel in data analysis and interpretation. Candidates for the position need to have a Ph.D. or M.S. in statistics, biostatistics or bioinformatics, and have extensive experience in statistical data analysis and consulting. Good communication skills are essential. The position carries competitive salary and fringe benefits. Applicants should send a cover letter, CV and names of three referees to Prof. Zhao-Bang Zeng, Bioinformatics Research Center, North Carolina State University, Raleigh NC 27695-7566, zeng@statgen.ncsu.edu. Review of applications will begin immediately, and continue until the position is filled.

Multiple postdoc positions are available to perform research in statistical genetics and bioinformatics in Bioinformatics Research Center at North Carolina State University. The positions are supported by a five-year NIEHS training grant in bioinformatics. Postdoc can work with any faculty in the training grant with research interests and projects ranging from statistical genetics, molecular evolution, QTL mapping, association mapping, microarray data analysis, proteomics, metabolomics, and systems genetic study. Candidates for the positions need to have Ph.D. and be U.S. citizen or permanent resident. Applicants should send a cover letter, statement of research, CV and names of three referees to Prof. Zhao-Bang Zeng, Bioinformatics Research Center, North Carolina State University, Raleigh NC 27695-7566, zeng@statgen.ncsu.edu.

Consult http://bioinformatics.ncsu.edu/ for information about the Bioinformatics Research Center at North Carolina State University.

zhao.bang.zeng@gmail.com

QueenMaryULondon CulturalEvolution

Postdoctoral research opportunity

Cultural Evolution Lab, School of Biological and Chemical Sciences, Queen Mary University of London

Internationally competitive post-doctoral candidates interested in conducting research in the field of human cultural evolution are encouraged to contact Dr Alex Mesoudi (a.mesoudi@qmul.ac.uk <mailto:a.mesoudi@qmul.ac.uk>) to apply for appropriate fellowships (e.g. Marie Curie, Newton). Possible projects might involve any experimental or theoretical simulations of cultural evolution, including (but not limited to) (1) experimental simulations of social learning biases underlying cumulative technological evolution; (2) agent-based modelling of culturally transmitted health-related behaviours such as smoking, obesity and suicide; (3) experimental simulations of cultural group selection using economic games. See publications at http://sites.google.com/-site/amesoudi2/publications for further research areas.

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Alex Mesoudi, PhD Lecturer in Psychology Biological and Experimental Psychology Group School of Biological and Chemical Sciences Queen Mary, University of London Mile End Road, London E1 4NS United Kingdom Tel: (+044) 020 7882 7486 Email: a.mesoudi@qmul.ac.uk Website: http://sites.google.com/site/amesoudi2/

a.mesoudi@qmul.ac.uk

QueenMaryULondon Mimicry

Postdoctoral research opportunities

Queen Mary University of London, Research Centre for Psychology

Lars Chittka's laboratory

We are seeking candidates who are internationally competitive, taking into account the current stage of their career. The strongest candidates may be offered a short term departmental fellowship during which time they would be expected to seek external funding, especially for Marie-Curie postdoctoral fellowships. We will provide candidates with help in applying for appropriate fellowships that can be hosted at QMUL.

For more information, please contact Prof Lars Chittka: l.chittka@qmul.ac.uk

Possible projects: *

1. Cognitive* *responses of birds to warning colours in insects* < http://www.sbcs.qmul.ac.uk/staff/larschittka.html >

This is a collaborative project with Prof Daniel Osorio at the University of Sussex. Many palatable animals, for example hoverflies, deter predators by mimicking well-defended insects such as wasps. However, for human observers, these flies often seem to be little better than caricatures of waspstheir visual appearance and behaviour are easily distinguishable from those which they are attempting to mimic. This imperfect mimicry baffles evolutionary biologists, because one might expect natural selection to do a more thorough job. The goal of this project is to test domestic chicks for two types of cognitive processes that might explain why distinguishable mimics could enjoy increased protection from predation. Speed-accuracy tradeoffs in predator decision making might give imperfect mimics sufficient time to escape, and predators under time constraint might avoid time-consuming discriminations between well-defended models and inaccurate edible mimics and instead adopt a “safety first” policy of avoiding insects with similar appearance. Categorisation of prey types by predators could mean that wholly dissimilar mimics may be protected, provided they share some common property with noxious prey. If predators use experience with multiple prey types to learn rules rather than just memorising the appearance of individual prey types, it follows that different individual predators should form different categories, each including separate types of novel prey. Experimental studies to test these hypotheses should be straightforward, because we can use the relatively simple signals (e.g., striped patterns) with which prey manipulate predator behaviour as tools for investigating cognitive processes that underlie decision making and object recognition in animals’ daily lives*. *

* ** 2. Social* *learning across species boundaries* - Lars Chittka

The study of social learning - how animals obtain information not by individual exploration of the environment, but instead by extracting information from other animals - has almost entirely focussed on information transmission within species boundaries. This raises the question on whether animals do, or should, predominantly copy from conspecifics. While genetic information, by definition, might be transmitted only within species, social information might transcend species boundaries freely. Some animals might be relatively flexible in what other animals they copy, and subsequently evaluate the usefulness of the copied behaviour, or the usefulness of the particular model in general. In fact, where resources as shared (e.g. flowers between generalist pollinators) or where generalist predators lurk (e.g. crocodiles in a river), picking up information from heterospecifics may be just as valuable as from members of the same species. This raises the question of whether conspecifics are indeed a unique entity in social learning, or whether animals might simply learn to pick any environmental cue that facilitates identifying salient conditions in the environment. In this project, we will study these questions using bumblebee pollinators.

* 3. How* *fast should colour vision be? An electrophysiological study of the early visual system* < http://www.sbcs.qmul.ac.uk/staff/peterskorupski.html >

Metabolic costs are a major constraint on brain design. How much should be invested in brain specifications? Consider colour vision. Colour entails wavelength sensitivity, which in turn requires comparisons of signals from photoreceptors with differing spectral sensitivities. However, much of the basic business of vision (form and motion perception) is colour-blind, relying on the input from a single spectral class of photoreceptor (or pooled inputs from similar classes). To a considerable extent, chromatic and achromatic information are processed in parallel and the chromatic channel is slower. Since fast temporal processing is metabolically expensive, the question arises of how the

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RiceU HybridizationAndAdaptation

Post-doctoral Research Associate, Role of Hybridization in Adaptive Evolution in Plants

Applications are currently being solicited for a postdoctoral research associate in the area of plant hybridization and adaptive evolution at Rice University in Houston, TX. The lab examines the evolutionary ecology of plants and plant-animal interactions, including hybridization, invasion biology, effects of population genetic diversity, and plant genome size evolution. The associate will participate in NSF-funded research examining whether hybridization increases rates of adaptation, focusing on a set of control and hybrid field populations of wild sunflowers. The associate will use SNP genotyping and QTL mapping techniques to a) identify QTL loci controlling adaptive traits and b) test microevolutionary hypotheses by describing changes in QTL allele frequencies in the hybrid lineages across the past 7 years. In addition, the associate will maintain a field common garden, perform laboratory experiments, and other tasks as required by the research.

The ideal candidate would have a Ph.D. and substantial experience in statistical genetics and molecular biology. Experience in fieldwork is a bonus but not required (training will be provided). This is a full-time, one-year, benefits eligible position, with a second year continent upon performance and funding. Ideal start date: Sept 1st, 2010 (negotiable). To apply, send a single pdf containing a short statement of interest, CV, and contact information for three references to Diane Hatton (rdh@rice.edu) with "Whitney Lab postdoc" as the subject line. Applications will be reviewed starting on 10 May and will continue until the position is filled. Rice is an Equal Opportunity and Affirmative Action Employer. Rice University offers staff members a comprehensive benefit package.

kwhitney@rice.edu

SanDiegoStateU PlantEvolutionaryGenomics

Post-Doctoral Research Position in Plant Evolutionary Genomics:

A National Science Foundation funded Post-Doctoral Research Position is available in the lab of Dr. Elizabeth Waters (Biology Department San Diego State University). The research project is focused on uncovering the molecular and physiological traits responsible for differences in organismal thermotolerance among Boechera species. Research projects include transcriptomics using next-generation sequencing, analysis of photosynthetic rate, and evolutionary analysis of protein sequences. A PhD degree in evolutionary biology, genomics, plant biology or a related field is required. Experience with next generation sequence analysis is desirable. Funding for this project is available for two years. Applicants need to start by September 15, 2010

Applicants should apply via the SDSU Research Foundation Human Resources web site http://jobsfoundation.sdsu.edu/hr. This position is Job Number: 100076. For further information please contact ewaters@sciences.sdsu.edu.

Elizabeth Waters Associate Professor Dept. of Biology San Diego State University San Diego, CA 92182 619-594-7036 ewaters@sciences.sdsu.edu

Elizabeth Waters <ewaters@sciences.sdsu.edu>

Switzerland EvolutionaryGenomics

A Postdoc position in evolutionary genomics is available in a collaborative project of the research groups of Dieter Ebert (University of Basel, Switzerland) and Christoph Haag (University of Fribourg, Switzerland).

We are looking for a highly motivated candidate with interest in evolutionary genomics. A background in bio-informatics and genomics is helpful. The position is funded to work on the genetic architecture of local adaptation in Daphnia magna. The suggested methodology includes genome scans, population surveys, SNP genotyping using microarrays, and comparative genomics. Previous experience with Daphnia is not required, but excellent written, verbal, and interpersonal skills, good work ethics, and the ability to think creatively and critically are desired. Starting dates are flexible, from August 2010 onwards. Positions are funded for 3 years.

The position is part of the European Science Foundation (ESF) EUROCORES EuroEEFG project STRESSFLEA, which includes collaborators working on Daphnia genomics in several countries.

The post-docs will be mostly located in Dieter Ebert's group working at Basel University, but will frequently interact with the Haag group at Fribourg University. Details about the groups: http://evolution.unibas.ch/ http://www.unifr.ch/biol/ecology/haag/haag_lab_home.html Please send your application by E-mail to Dieter Ebert (dieter.ebert@unibas.ch). Applications should include a single pdf-file containing CV, a list of publications and a 1 page description of your research interests and motivation. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 7. June 2010 will be given full consideration. Interviews will be held in the first half of July 2010.

Contact information:

Prof. Dr. Dieter Ebert, University of Basel, Zoologisches Institut, Vesalgasse 1, CH-4051 Basel, Switzerland, Email: dieter.ebert@unibas.ch Phone: +41-(0)61-267 03 60 Fax +41-(0)61-267 03 62

Dr. Christoph Haag University of Fribourg Department of Biology Chemin du Musée 10 CH-1700 Fribourg, Switzerland Email: christoph.haag@unifr.ch Phone: +41-(0)26-300 88 71 Fax: +41-(0)26-300 96 98

dieter.ebert@unibas.ch

UArizona OriginMulticellularLife

POSTDOCTORAL POSITION

Origin of multicellularity

A POSTDOCTORAL POSITION is available immediately in the laboratory of Dr. Richard E. Michod (http://www.eebweb.arizona.edu/Michod/) in the Department of Ecology and Evolutionary Biology at the University of Arizona (Tucson, AZ; http://eebweb.arizona.edu/). We are looking for a motivated, enthusiastic and independent individual with a strong background in evolutionary biology and/or genomics and molecular biology to address questions concerned with the evolution of multicellularity, using the green algal group Volvocales (Chlamydomonas and its multicellular relatives) as a model-system. Current projects in the lab include studying the genetic basis for the evolution of germ-soma differentiation, measuring life history trade-offs as colony size changes and artificial selection experiments on body size in volvocalean green algae.

To apply, please e-mail (michod@u.arizona.edu) with the following information: a statement detailing your research interests and qualifications, a CV, and the names and contact information of three references. Please describe what interests you about this postdoctoral position and whether you have any particular ideas that you wish to pursue.

The initial appointment is for one year, with an additional two years' funding available conditional on satisfactory performance. The position is funded by an NSF grant, at 35K per year (plus benefits).

The University of Arizona is an EO/AA Employer.

Rick Michod <michod@u.arizona.edu>

UBern EvolutionaryPlantEpigenetics

Postdoc position - Ecological and evolutionary plant epigenetics*

A postdoc position is available in the Plant Ecology lab at the Institute of Plant Sciences, University of Bern, Switzerland, to work on ecological and evolutionary consequences of heritable epigenetic variation. The postdoc will conduct quantitative genetic screenings, selection experiments and molecular epigenetic analyses to test the idea that rapid evolution by natural selection is possible based on epigenetic variation only.

The project, led by Oliver Bossdorf and Markus Fischer, is part of a larger, pan-European project (funded by the European Science Foundation) on ecological and evolutionary plant epigenetics in which we collaborate with several excellent groups from other European countries.

We are seeking an enthusiastic researcher who has a background in genetics and a keen interest in ecology and evolutionary biology, or vice versa. Most of the pratical work will involve growth experiments, other will be molecular. Part of the molecular work will be done in a collaborating lab in Paris. There will be a possibility for an extended research stay in Paris. For more information about the project please contact Oliver Bossdorf (bossdorf@ips.unibe.ch).

We are offering a stimulating research environment in a young and rapidly growing lab (see www.botany.unibe.ch/planteco). Bern is a beautiful city with a high quality of life. The position is for 2.5 years, with a gross salary of 80'000 – 85'000 CHF per year.

Applicants should send an email with a statement of research experience and interests, CV, and contact details of three references to Dr. Oliver Bossdorf, Institute of Plant Sciences, University of Bern, Altenbergrain 21, CH-3013 Bern, Switzerland, bossdorf@ips.unibe.ch.

Applications will be reviewed starting 15 June 2010 and continue until the position is filled. An ideal starting date for the project would be 1 August 2010, or shortly thereafter.

– Dr. Oliver Bossdorf Institute of Plant Sciences University of Bern Altenbergrain 21 CH-3013 Bern, Switzerland Phone +41 31 631 4923 bossdorf@ips.unibe.ch http://sites.google.com/site/-obossdorf/ Oliver Bossdorf <bossdorf@ips.unibe.ch>

UBristol BehaviourEvolution

A 5-year European Research Council grant "The evolution of mechanisms that control behaviour" provides funding for 3 postdoctoral researchers. The project involves working with Prof Alasdair Houston (Biological Sciences, Bristol) and Prof John McNamara (Maths, Bristol) to develop mathematical models of the evolution of decision-making mechanisms. For further details see

http://www.bris.ac.uk/boris/jobs/feeds/ads?ID=-86628 Research Fellow (ref. 15406)

http://www.bris.ac.uk/boris/jobs/feeds/ads?ID=-86630 Research Assistants (two posts) (ref. 15405)

AI Houston Professor of Theoretical Biology School Biological Sciences University of Bristol Woodland Road Bristol BS8 1UG A.I.Houston@bristol.ac.uk

A.I.Houston@bristol.ac.uk

UBritishColumbia EvolGenomics

Postdoctoral Fellow positions are available in the lab of Dr. Keith Adams at the University of British Columbia in the area of evolutionary genomics. My lab's research combines evolutionary biology with molecular genetics to study how gene expression, alternative splicing patterns, functions, structures, and sequences evolve. We use a combination of bioinformatics analyses of large data sets and lab experiments to answer questions and test hypotheses. We focus on evolution and expression of duplicated genes in plants. See my web page at http://www.botany.ubc.ca/people/kadams.html for a description of current research. I am looking for two postdocs to study genomics of duplicate gene evolution, expression, and/or alternative splicing in plants. One position will be to study genomics of duplicate gene expression and alternative splicing in a polyploid plant using RNA-seq transcriptome profiling. My lab is housed in new research building with excellent computational infrastructure.

Candidates should have a strong background in evolutionary genomics, molecular evolution, bioinformatics, or genome analysis in any organism. Experience with computational analysis of sequence or gene expression data is required. Candidates with some computer programming expertise are preferred, and experience with next generation sequence analysis (Illumina, 454, or SOLiD) is desirable. The positions are available immediately and the preferred start date is by October 1, 2010. Funding is available for at least two years.

For more information contact Keith Adams at keitha@interchange.ubc.ca Informal inquiries about the research area and projects are welcome. To apply, send a CV, a description of your research interests and your Ph.D. research, and contact information for three references to the above email address.

Keith Adams Botany Department and Centre for Plant Research University of British Columbia Vancouver, Canada

keitha@interchange.ubc.ca

UCaliforniaMerced CoralReefGenomics

POSTDOCTORAL POSITION IN CORAL REEF GENOMICS - UC MERCED A full-time postdoctoral position is available as part of an ongoing NSF-funded project to look at coral health in the Caribbean species Montastraea faveolata and Acropora palmata using comparative genomic and cell biology approaches. Primary research questions will focus on, but are not limited to, genomics and cell biology of coral-algal symbiosis, the effect of ocean acidification on corals, coral response to disease, the role of the microbial community in the coral holobiont. There is opportunity to work with larval and adult stages. Field sites are located in Puerto Morelos, Mexico, south of Cancun (Mayan Riviera) and Bocas del Toro, Panama.

The position is available immediately. Initial appointment will be one year, with possible renewal on a year-to-year basis. Renewal of appointment is contingent on performance and availability of funds. The position includes postdoctoral scholar benefit package. The University of California Merced campus is located at the base of the Sierra Nevada foothills, near Yosemite and the San Francisco Bay Area.

The University of California at Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff, and students. Qualifications: Ph.D. in Coral Reef Science, Genome Biology, Cell Biology, Bioinformatics or related fields. Applicants with experience in bioinformatics and/or microarray analysis are especially encouraged to apply.

Salary: Negotiable, based on the University of California pay scale To Apply: Interested applicants are required to submit 1) a cover letter 2) curriculum vitae 3) a list of three references with contact information including mailing address, phone number and e-mail address. For more information: Please contact MÃ³nica Medina (mmedina@ucmerced.edu).

Monica Medina Associate Professor School of Natural Sciences University of California, Merced 5200 North Lake Road, Merced, CA 95343 tel: 209-228-7863 fax: 209-228-4053 mmedina@ucmerced.edu http://sequoia.ucmerced.edu/MedinaLab/ Monica Medina <mmedina@ucmerced.edu>

UCaliforniaSanDiego YeastEvolution

Postdoctoral Associate Rifkin Lab University of California, San Diego

A postdoctoral position is open in Scott Rifkin's lab at the University of California, San Diego. The position is part of a Human Frontiers Science Program funded project to study the evolution and variability of the dynamics of signaling networks in yeast. The Rifkin lab uses both yeasts and nematodes to study how the dynamics of genetic networks generate and shape phenotypic variation. The successful candidate will also be encouraged to develop independent projects in this general area.

Applicants should have a good publication record and strong quantitative skills. Experimental techniques will include yeast molecular genetics, fluorescence microscopy, dynamical systems modeling, and quantitative genetics, and experience in any of these is advantageous.

The start date would ideally be in September 2010. The initial appointment will be for 1 year and will be renewable for up to a total of 3 years. Salary will be commensurate with NIH standards.

The project is a collaboration between the labs of Scott Rifkin, Christian Landry (Univ. Laval, Quebec) and Madan Babu (Cambridge, UK) and there will be ample opportunities to interact with them and with the strong quantitative biology community in San Diego.

To apply please email Scott Rifkin <sarifkin _at_ ucsd.edu> with a CV, summary of previous research and current interests, and a list of references. Please put “HFSP POSTDOC” in the subject line. Review of applications will continue until the position is filled.

Scott Rifkin Assistant Professor Ecology, Behavior, and Evolution Division of Biology University of California, San Diego sarifkin _at_ ucsd.edu http://www.biology.ucsd.edu/labs/rifkin/ Scott Rifkin <sarifkin@ucsd.edu>

UCaliforniaSantaCruz PlantEvolutionaryGenetics

Postdoctoral Scholar Kay Lab University of California, Santa Cruz

A postdoc position is open in Kathleen Kay's lab in the Department of Ecology and Evolutionary Biology at UCSC to participate in research on the evolutionary and ecological genetics of speciation in the neotropical spiral gingers. The postdoc will be involved in the design and analysis of (1) a genetic linkage mapping experiment and QTL study of floral and vegetative traits involved in reproductive isolation and reinforcement in a wild plant system, and (2) a microsatellite-based population genetic study of divergence with gene flow. SNPs have been identified for the mapping project with Illumina sequencing, and SNP genotyping will be outsourced. The postdoc will work collaboratively with the PI and help oversee student assistants. The selected candidate will have considerable intellectual input into the development of the projects, and there are good opportunities to develop lines of inquiry after the candidate's own interests.

Minimum qualifications: Ph.D. or equivalent in Biology, Genetics, or related field. Expertise in one or more of the following areas: evolutionary quantitative genetics, QTL mapping, molecular evolution, population genetics or statistical genetics.

Preferred qualifications: Preference will be given to candidates with a track record of successful grant funding and publishing in leading journals. A strong interest in the evolutionary biology of natural systems and experience working with plants is preferred. Some familiarity with next-generation sequencing platforms and bioinformatic tools are definite assets. The selected candidate will be highly motivated, have strong written and oral communication skills, and be able to work well both independently and as part of a small team.

Initial appointment is for one year, with reappointment contingent upon availability of funding and a favorable performance review. The position is available immediately, with a preferred start date no later than September 2010.

Salary is commensurate with qualifications and experience, according to UC pay scales. Benefits are provided.

To apply, please send a cover letter describing your research background and interests, a curriculum vitae, and contact information for three references by email (in pdf format) to <kay at biology.ucsc.edu>.

Informal inquiries are welcome!

Kathleen Kay Assistant Professor Ecology and Evolutionary Biology UC Santa Cruz Santa Cruz, CA 95064 http://bio.research.ucsc.edu/people/kay kay@biology.ucsc.edu

UCLondon ExcellenceFellowships

University College London - Excellence Fellowship programme

UCL's School of Life and Medical Sciences is launching an Excellence Fellowship programme. The aim is to attract the best early career researchers and allow them to develop their research with the help of a generous award. Fellowships include three years of salary cost, funds for a PhD studentship and £50K to support research costs. Applicants can come from across the life and medical sciences, but the proposed research should have some biomedical dimension.

The Department of Genetics, Evolution and Environment is seeking to actively promote candidates for the Excellence Fellowship scheme. The research of applicants could fall within or complement the research themes covered by the Department. We in particular wish to strengthen our activities in evolution and population biology. Candidates with strong research interests in computation biology, systems biology or infection and immunity are particularly encouraged to apply.

Expressions of interest should be directed to Dr Max Reuter (m.reuter@ucl.ac.uk) before 2 June (the scheme deadline is 16 June). Please include a cover letter, CV, the names of two referees, and an outline of your research proposal (2 pages maximum). The Department will select a shortlist of candidates to provide support in developing your project, writing the application and preparing for interview.

The call for fellowship applications can be found at https://atsv7.wcn.co.uk/search_engine/-jobs.cgi?owner=3D5041178&ownertype=-3Dfair&jcode=1138992 The closing date for the full application is 16 June 2010.

For more information about UCL, please visit

- Department of Genetics, Evolution and Environment http://www.ucl.ac.uk/gee - CoMPLEX (maths and physics in the life sciences) http:/-/www.ucl.ac.uk/complex - UCL Systems Biology http://www.ucl.ac.uk/systems-biology Max Reuter

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

Phone: +44-20-76795095 (internal 25095)

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

UCollegeLondon FlatwormEvolution

Dear colleagues,

I would be very grateful if you would bring this opportunity to the notice of anyone suitable.

A Postdoctoral Research Associate is required to work in the laboratory of Max Telford, carrying out research into the molecular patterning of the nervous system and photoreceptors of the larva of the polyclad flatworm Maritigrella crozieri.

The project will make comparisons with other ciliated marine larvae with the aim of establishing whether they are homologous or have evolved convergently.

The work is supported by a Leverhulme grant and is funded for 36 months in the first instance.

The starting date will be Sept 1st 2010.

Key Requirements

The successful applicant will have a PhD (or be working towards a PhD) in a relevant area. The ideal candidate will have experience in molecular developmental biology and evolutionary biology. The successful candidate should also be familiar with common molecular biological techniques.

Knowledge of flatworm developmental biology and phylogenetics would be welcome.

Further Details

Please go to... http://www.ucl.ac.uk/hr/jobs/ Click Here for UCL Current Vacancies

put in job code 1138745

Many thanks

Max

Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/-telford/telford.html Telford & Littlewood: Animal Evolution. OUP http://ukcatalogue.oup.com/-product/9780199570300.do Files and software for downloading:

Mrimpatient: If you cant wait to see latest result of MrBayes analysis.

TranslatorX: Align nt sequence according to the aa translation.

Xstem and Ystem: Software for 2y structure data in rRNA phylogenetic analyses.

MtZoa and MtHydro : new amino acid substitution matrices

Hacked version of MrBayes using these matrices

http://web.mac.com/maxtelford/iWeb/Work/-Downloads.html Xenoturbella You Tube video http://uk.youtube.com/watch?v=yJXNcoxL2Xs The Linnean Society of London http://www.linnean.org/ Max Telford <m.telford@ucl.ac.uk>

UExeter BehaviourEvolution

School of Biosciences - Evolutionary Genetics of Behaviour

School of Biosciences

Evolutionary Genetics of Behaviour

Postdoctoral Research position (Ref: N2664)

Salary will be in the range £26,523 to £27,319 per annum

Fixed Term appointment for 3 years

The School of Biosciences, Cornwall wishes to recruit a Postdoctoral Researcher to work in the laboratory of Professor Allen Moore on a grant funded by the Natural Environment Research Council (NERC) from 1st July 2010 (or as soon as possible thereafter). The successful applicant will join a research group studying the genetics and evolution of social behaviour. This three-year project is concerned with investigating the role of genetic differences between males and females in the expression of parental care in the burying beetle, Nicrophorus vespilloides (Walling et al. 2008 Proc Natl Acad Sci USA 105: 18430-18435).

Applicants will possess a PhD in quantitative genetics, evolutionary biology, animal behaviour, or behavioural ecology. The applicant should also be a confident, independent scientist with knowledge in the discipline and of contemporary research and statistical methods and techniques to work within established research programmes. Applicants must be able to design their own experiments, prepare data for publication and assist in training of graduate students.

For further information please contact Professor Allen Moore, e-mail: a.j.moore@ex.ac.uk<mailto:a.j.moore@ex.ac.uk> or telephone (01392) 725151.

To apply, please send your CV and covering letter with the contact details of three referees to Professor Allen Moore, Professor of Evolutionary Genetics, School of Biosciences, Geoffrey Pope Building, University of Exeter, Stocker Road, Exeter, EX4 4QD (e-mail: a.j.moore@ex.ac.uk<mailto:a.j.moore@ex.ac.uk>) quoting the job reference N2664.

The closing date for completed applications is Friday 11th June 2010.

The University of Exeter is an equal opportunity employer and promotes diversity in its workforce and, whilst all applicants will be judged on merit alone, is particularly keen to consider applications from groups currently underrepresented in the workforce.

a.j.moore@exeter.ac.uk<mailto:a.j.moore@exeter.ac.uk>

Allen J. Moore Professor of Evolutionary Genetics Head of School School of Biosciences University of Exeter Geoffrey Pope Building Stocker Road Exeter EX4 4QD United Kingdom

In Exeter: Tel: +44 (0)1392 725151 (PA - Amanda Trick) Fax: +44 (0)1392 723434

In Cornwall: Tel: +44 (0)1326 255986 (PA - Sally Bennett)

"Moore, Allen" <A.J.Moore@exeter.ac.uk>

UGeorgia CoralGeneticDiversity

Postdoc: Microbial Genetics and Ecology of Infectious Disease in Caribbean Corals

A postdoctoral position is available at the University of Georgia, working with Dr. Erin Lipp (Environmental Health Sciences) and Dr. John Wares (Genetics), along with other collaborators at the University of Georgia. The project involves exploration of genetic diversity in the Acropora palmata holobiome (coral, symbionts, and microbial community) to better understand patterns of infection and mortality in the endangered staghorn coral. Salary starts at $42,000.

Applicants must have a strong background in microbiology and/or genetics, in particular skills in DNA sequencing, data curation, and analysis. Experience with next-generation sequence data is preferred, and we will be looking for researchers who can work well with the entire collaborative team.

Applications should be sent by July 17, 2010, by email (jpwares@uga.edu) as a single PDF file that includes cover letter, CV, and 1-2 representative publications. We also ask that you have three letters of recommendation sent by email to the same address. Additionally, Wares and collaborator Andrew Park will be at the Evolution meeting in Portland, Oregon and welcome the opportunity to interview applicants in person from June 25-29. Start date may be as early as September 1, 2010. For further information on the position, please contact John Wares (jpwares@uga.edu) or Erin Lipp (elipp@uga.edu)

The University of Georgia is an Equal Opportunity/Affirmative Action Employer. Employer.

UJohannesburg PlantDNABarcoding

Postdoctoral position: DNA barcoding of medicinal plants in southern Africa. by Michelle van der Bank, on April 28th, 2010

Outstanding applicants are sought for a two-year postdoctoral position at the University of Johannesburg (South Africa), focusing on the development of molecular identification methodology (DNA barcoding) for southern African medicinal plants. This will include original research, participation in the assembly and coordination of large-scale international collaborations, participating in the groups research and supervision and mentoring of postgraduate students. The candidate will be based in the department of Botany & Plant Biotechnology at the University of Johannesburg, will have access to a molecular lab and is expected to do fieldwork in southern Africa.

Candidates must meet the following requirements:

1. Applicants must have a PhD by start date of work (no exceptions). 2. Experienced in PCR, DNA sequencing, and related analytical approaches. 3. A strong background in Plant Systematics. 4. Applicants must possess excellent written and oral communication skills in English. 5. Expertise in digital photography will be an asset.

The position is available immediately.

Applicants should send a CV including a brief overview of experience and research interests and two recent reference letters to mvdbank@uj.ac.za not later than May 20th, 2010. Review of applications will commence May 21st, 2010.

Prof. Michelle van der Bank Department of Botany and Plant Biotechnology University of Johannesburg PO BOX 524, Auckland Park, 2006 SOUTH AFRICA TEL: +27 11 559 2495 FAX: +27 11 559 2411

mvdbank@uj.ac.za

"Van der Bank, Michelle" <mvdbank@uj.ac.za>

ULausanne FrogSexChromosomes

A post doc position is available at the Department of Ecology and Evolution, University of Lausanne (switzerland), to join a team working on the evolution of sex-chromosomes and sex-linked genes in European tree frogs. We presently aim at obtaining (from BAC- and/or lambda phage libraries) X and Y sequences of sex-linked genes in Hyla arborea and related species, and localize these sequences on the sex chromosome.

We are looking for a candidate with a strong experience in molecular- biology techniques and interest in theoretical aspects of sex- chromosome evolution. The starting date is flexible, from August 2010 onwards. The position is funded for 3 years.

Please send your application by E-mail to nicolas.perrin@unil.ch, including in a single pdf-file your CV and list of publications as well as a one page description of research interests and motivation. Please also provide names and email addresses of two referees who are willing to write a letter of recommendation. We will consider applications received before June 10th 2010 and plan to organize interviews in July 2010.

References

Perrin N, 2009. Sex reversal: a fountain of youth for sex chromosomes? Evolution 63(12), 3043-3049

Niculita-Hirzel H., Stöck M., Perrin N., 2008. A key transcription cofactor on the nascent sex chromosomes of European tree frogs (Hyla arborea). Genetics 179(3), 1721-1723.

Stöck M., Dubey S., Klütsch C., Litvinchuk S.N., Scheidt U., Perrin N., 2008. Mitochondrial and nuclear phylogeny of circum-Mediterranean tree frogs from the Hyla arborea group. Mol Phyl Evol 49(3), 1019-1024.

Berset-Brändli L., Jaquiéry J., Broquet T., Ulrich Y., Perrin N., 2008a. Extreme heterochiasmy and nascent sex chromosomes in European tree frogs. Proc.R.Soc.B 275(1642), 1577-1585.

Berset-Brändli L., Jaquiéry J., Perrin N., 2007. Recombination is suppressed and variability reduced in a nascent Y chromosome. J Evol Biol 20(3), 1182-8.

Nicolas.Perrin@unil.ch

UMaryland Computational Comparative Phylogenetics

COMPUTATIONAL COMPARATIVE PHYLOGENETICS

A postdoctoral position is available for a project that brings computational comparative phylogenetic approaches to bear on questions in population ecology, including the prediction of unobserved life history traits based on phylogenetic context.

Candidates should have a background in computational evolutionary biology, computational ecology, statistics, or a related discipline. Requirements include 1) experience with statistical and/or mechanistic (stochastic) modeling of continuous and/or discrete characters in evolutionary models, 2) understanding of how comparative phylogenetic methods work mathematically, and 3) strong writing skills. The project draws upon compiled databases of life history traits for mammals and birds, so previous ecoinformatic research or other experience with object-oriented databases is a plus.

This position, which features both theoretical and applied components, is funded via a collaborative Department of Defense (SERDP) research grant that seeks to develop quantitative approaches to the establishment of conservation targets for poorly known species that are not amenable to population viability analyses. The position will be housed in Dr. Bill Fagan's lab at the University of Maryland, College Park (http://www.clfs.umd.edu/biology/faganlab/) with an additional opportunity to collaborate with Dr. Maile Neel (alyxia.umiacs.umd.edu).

This postdoc position features a competitive salary and a 24-30 month duration (depending on start date and subject to satisfactory progress). The position is available immediately, with a preferred start no later than 1 September 2010.

To apply, please email a CV, brief statement of interest in this position, and the names and email addresses of three references to:

Dr. Bill Fagan bfagan@umd.edu Department of Biology 3235 Biology-Psychology Building University of Maryland College Park, MD 20742

bfagan@umd.edu

UNebraska Lincoln AphidBioinformatics

Postdoc in aphid bioinformatics

A postdoctoral position is available in the lab of Dr. Jenn Brisson in the School of Biological Sciences at the University of Nebraska, Lincoln (UNL). Our lab uses evolutionary, genetic, developmental, and genomic approaches to study how pea aphids produce winged and wingless morphs. See http://biosci.unl.edu/labs/-brisson/ for more information. The successful candidate will work on an NIH funded project combining transcriptional (RNA-Seq) and metabolomic data to examine the mechanistic basis of wing morph induction.

Candidates should have a PhD in biology or bioinformatics or a related field. Programming skills and experience with next-generation sequence data are necessary. Funding for this position is available for two years, subject to review after the first year. Applications will be accepted until June 25th. The start date is flexible, but would ideally be near the end of summer in 2010.

For additional information, including informal inquiries, please contact Jenn Brisson at jbrisson2@unl.edu. To apply, please send a CV, short letter of research interests and accomplishments, and contact information for three references to jbrisson2@unl.edu.

Further information about the School of Biological Sciences at UNL can be found at: http://-www.biosci.unl.edu/. The Brisson lab is a member of the Integrative Evolutionary Biology (IEB) program. IEB consists of an interactive group of faculty (Zoya Avramova, Alexandra Basolo, Larry Harshman, Eileen Hebets, Etsuko Moriyama, Hideaki Moriyama, Jay Storz, Bill Wagner, Tony Zera, Stacey Smith) tackling interesting questions in evolutionary biology using multidisciplinary approaches. As noted on its web page, members of IEB have “diverse research interests that include the following: physiological, biochemical and molecular studies of life history evolution; genomic-to-physiological investigations of complex adaptations such as dispersal polymorphism; molecular-population-genetic and functional studies of hemoglobin adaptations in mammals; molecular evolutionary and bioinformatic analyses of protein functions and multi-gene families, neurophysiological, ecological, and genetic investigations of invertebrate behavior, with a special focus on sexual selection; and ecological, biochemical, and phylogenetic investigations of metabolic pathway evolution in plants and animals.” See biosci.unl.edu for more details.

The School of Biological Sciences is located on UNL’s City Campus in downtown Lincoln, NE. The city boasts a budding live music and arts scene, an extensive park system, a friendly citizenry, excellent restaurants, enthusiastic football fans, and a low cost of living. Lincoln has a population of ~260,000 and is the capital of Nebraska. It is an hour from Omaha and three hours from Kansas City.

jbrisson2@unl.edu

UNebraska Lincoln AphidEvolution

Postdoc in aphid evolution/development

A postdoctoral position is available in the lab of Dr. Jenn Brisson in the School of Biological Sciences at the University of Nebraska, Lincoln (UNL). Our lab uses evolutionary, genetic, developmental, and genomic approaches to study how pea aphids produce winged and wingless morphs. See http://biosci.unl.edu/labs/-brisson/ for more information. The postdoctoral project can be tailored to the specific interests of the successful candidate, but will focus on one or more of the following areas: 1. transcriptomics and metabolomics of wing induction 2. investigating the differences in wing development between winged and wingless morphs, 3. the role of epigenetics in the pea aphid wing polyphenism.

Candidates should have a PhD in molecular evolution, evolutionary genetics, evo-devo, or a related field. Funding is available for up to three years, subject to review after each year. Applications will be accepted until June 25th and the start date is flexible.

For additional information, including informal inquiries, please contact Jenn Brisson at jbrisson2@unl.edu. To apply, please send a CV, short letter of research interests and accomplishments, and contact information for three references to jbrisson2@unl.edu.

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(Zoya Avramova, Alexandra Basolo, Larry Harshman, Eileen Hebets, Etsuko Moriyama, Hideaki Moriyama, Jay Storz, Bill Wagner, Tony Zera, Stacey Smith) tackling interesting questions in evolutionary biology using multidisciplinary approaches. As noted on its web page, members of IEB have “diverse research interests that include the following: physiological, biochemical and molecular studies of life history evolution; genomic-to-physiological investigations of complex adaptations such as dispersal polymorphism; molecular-population-genetic and functional studies of hemoglobin adaptations in mammals; molecular evolutionary and bioinformatic analyses of protein functions and multi-gene families, neurophysiological, ecological, and genetic investigations of invertebrate behavior, with a special focus on sexual selection; and ecological, biochemical, and phylogenetic investigations of metabolic pathway evolution in plants and animals.” See biosci.unl.edu for more details.

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jbrisson2@unl.edu

UNotreDame InvasiveSpeciesEvolution

Post-Doctorate (quantitative analysis and modeling)

Position Description: At least one postdoctoral research position is available to pursue collaborative projects involving the spread and ecological and economic impacts of aquatic invasive species in the Laurentian Great Lakes and neighboring inland waterways. Supported by funding from a new 5-year NOAA-funded project and other on-going and pending projects, the postdoc housed in the Department of Biological Sciences, University of Notre Dame will report to project leader David Lodge, and will collaborate with risk analyst Roger Cooke (Resources for the Future), economists Richard Jensen (UND) and David Finnoff (U Wyoming), and ecologists including Lodge and Lindsay Chadderton (The Nature Conservancy) to apply new tools in research at the interface of science with management and policy.

Qualifications: We are seeking postdoc(s) with some combination of the following skills and experience: population modeling, food web modeling, structured expert judgment, and spatial and multivariate statistics. Screening of applicants will begin in early May. Salary and benefits will be competitive.

Contact: Applicants should consult the project abstract (Research - Ecological Risk Analysis and Bioeconomics), and then email (in one pdf document) a letter describing their prior research experience and current interests, a curriculum vitae, and the names and contact information of three references to:Joanna McNulty, Center for Aquatic Conservation, Galvin LifeScience Center, University of Notre Dame, Notre Dame, IN 46556 (fax: 574-631-7413; email: McNulty.9@nd.edu (with a cc to dlodge@nd.edu).

Michelle Budny <Michelle.L.Budny.4@nd.edu>

UOklahoma BiologicalStation EvolBiology

POSTDOCTORAL FELLOW - THE UNIVERSITY OF OKLAHOMA BIOLOGICAL STATION (UOBS). The University of Oklahoma (OU), Norman, Oklahoma, invites applications for a Postdoctoral Fellowship in Ecology and Evolutionary Biology to be a resident research scientist based at the universitys Biological Station (UOBS) on Lake Texoma (Texas-Oklahoma border; 2-hr drive from campus). This is a 12-month (0.80 FTE; equivalent to 9-10 mo) appointment with benefits (i.e. medical, dental), renewable on an annual basis for up to three years. The fellow will be responsible for developing a research program in conjunction with UOBS faculty and assisting with the educational outreach program at the station via occasional presentations to visiting groups. In addition, the fellow will be given the opportunity to teach a two-week long (3 cr. hr.) course at the Station during summer for extra compensation. The targeted starting date is 1 September 2010, but is flexible. More information on UOBS and UOBS faculty research interests can be found at http://www.ou.edu/-uobs .Applicants should include a curriculum vitae, reprints of representative publications, a detailed 3-5 page outline of the research to be conducted at UOBS and arrange to have three letters of recommendation sent on the applicants behalf. Applicants are encouraged to contact one or more UOBS faculty prior to submitting the application. All materials should be sent electronically to Lawrence J. Weider, Director, UOBS (ljweider@ou.edu<mailto:ljweider@ou.edu>). Applicant review will begin 15 June 2010 and continue until the position is filled. The University of Oklahoma encourages diversity in the workplace. The University of Oklahoma is an Affirmative Action/Equal Opportunity employer.

"Weider, Lawrence J." <ljweider@ou.edu>

UOxford SocialEvolution

DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OXFORD

Postdoctoral Research Assistant - Evolutionary Social Ecology Grade 7: Salary in the range £28,983-35,646 per annum.

A postdoctoral position is available, for three years, from 1 October 2010, to study social structure and dispersal in birds from an ecological and evolutionary perspective. The post is funded as part of an ERC Advanced Investigator grant of euro 2.5M over five years to Prof Ben Sheldon. The post will be based in the Edward Grey Institute, Department of Zoology, University of Oxford. The post- holder will study the causes and consequences of variation in social structure. Particular emphasis will be placed on the role of dispersal, and how this affects and is affected by the social structure of the population.

A key part of the project will be to design and carry out experiments to test how the social environment affects dispersal in both adults and young, involving cross-fostering experiments as well as manipulations at feeding sites during the winter. This is an exceptional opportunity to participate in the development of a major research project, for which extensive pilot data are already available, and funding is guaranteed at a very high level.

The successful candidate will have, or be about to obtain, a PhD in behavioural ecology, ecology, evolutionary biology or a related subject and fieldwork experience, preferably with birds. Candidates should have proven skills in the use of multivariate statistics (skills in spatial analysis, mark-recapture or network analysis an advantage) and in writing and publishing papers in leading journals in the field. In addition, experience of working as part of a multi-disciplinary team is desirable. The post is based in a dynamic and expanding research-active institute, of c. 45 people, fully integrated within the Department of Zoology. Further details about the institute available at: http://-www.zoo.ox.ac.uk/egi/ Informal inquiries (with CV) to Prof Ben Sheldon (ben.sheldon@zoo.ox.ac.uk); start date 1 October 2010.

Further particulars and application forms can be downloaded from http://www.zoo.ox.ac.uk/jobs or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS (tel: 01865 271190); email: recruit@zoo.ox.ac.uk . Applications, together with CV and contact details of three referees, an electronic copy of three publications and a cover letter explaining how the candidate meets the selection criteria, as outlined in the further particulars, should be sent to the above address quoting reference number AT10016. The closing date for applications is 14th June 2010. Interviews will take place in early July.

ben.sheldon@zoo.ox.ac.uk

USydney MathematicalBiology

POSTDOCTORAL RESEARCH ASSOCIATE IN MATHEMATICAL BIOLOGY REFERENCE NO. 753/0310

THE SCHOOL OF INFORMATION TECHNOLOGIES

The University of Sydney is Australia's first University with an outstanding global reputation for academic and research excellence, and employs over 6,800 permanent staff supporting over 46,000 students.

Funded by the Australian Research Council (ARC), within a cross disciplinary project with the School of Information Technologies, we are delighted to announce an opportunity for an outstanding researcher to work in an exciting area of mathematical biology at the University of Sydney.

Nothing evolves in isolation. In 150 years since the publication of Darwin's Origin of Species our understanding of evolution has come a huge distance, yet our understanding of coevolution is less developed. While there has been a vast development in the last few decades in phylogenetic methods, which uncover evolutionary history at the species level and above, this development has not been paralleled in the study of how such histories relate to each other for ecologically linked groups of species, such as parasites or pathogens and their hosts. Understanding coevolution at the macroscopic level is the key to understanding the "big picture" of how parasites and pathogens coevolve with, and switch between, their hosts.

The central aim of this project is to develop and extend the statistical framework of coevolution at the species level and above, to fill this gap in our knowledge.

You should have a solid PhD in bioinformatics or computational/theoretical biology. Your thorough understanding of modern statistical methods is crucial, as are proven computational skills and biological knowledge. Programming expertise in an object-oriented language such as C++/Java will be highly regarded, as will previous research experience related to some or all of the following: health, conservation/biodiversity, evolution and/or coevolution, phylogenetics, and cophylogenetics.

This is a fantastic opportunity to work in a dynamic environment and to conduct unique research in a wide diversity of areas as well as engaging with outstanding local research and undergraduate students. You will closely work with Associate Professor Michael Charleston and will assist in a challenging topic that will have major contributions to health, conservation and biodiversity, as well to fundamental knowledge of coevolution.

The position is full-time fixed-term for up to three years subject to the completion of a satisfactory probation period for new appointees. Membership of a University approved superannuation scheme is a condition of employment for new appointees.

Remuneration package: up to $90,055 p.a. (which includes a base salary Level A, leave loading and up to 17% employer's contribution to superannuation)

Some assistance towards relocation cost and visa sponsorship may be available for the successful appointee if required and level of appointment will be commensurate with experience and qualifications.

All applications must be submitted via The University of Sydney careers website. Visit sydney.edu.au/positions and search the reference number for more information and to apply.

CLOSING DATE: 16 May 2010 (11:30pm Sydney time)

The University is an Equal Opportunity employer committed to equity, diversity and social inclusion. Applications from equity target groups and women are encouraged. The University reserves the right not to proceed with any appointment.

Michael Charleston <mike.charleston@gmail.com>

UTexasArlington TransposonGenomeEvolution

Postdoctoral Position: Transposon and Genome Evolution

A postdoctoral position is available in the lab of Cedric Feschotte at the University of Texas at Arlington. I am seeking an individual with a strong interest in transposable elements and genome evolution/ function to work on an ongoing NIH-funded project investigating mammalian DNA transposons. This research combines experimental and computational approaches and encompasses a broad range of topics, including but not limited to:

(i) Mechanisms and consequences of horizontal transfer (e.g. Pace et al. PNAS 105:17023-17028; Gilbert et al. 2010 Nature 464: 1347-1350)

(ii) Lineage-specific amplification and structural variation (e.g. Pace & Feschotte, Genome Res 17:422-432; Pritham & Feschotte 2007 PNAS 104:1895-1900; Ray et al. Genome Res 18:717-728)

(iii) Evolution and function of human transposase-derived proteins (e.g. Cordaux et al. 2006 PNAS 103:8101-6).

For more details, visit the lab website: http://www3.uta.edu/faculty/cedric/ A Ph.D. is required and strong written and oral communication skills are essential. A strong background in evolutionary/comparative genomics and/or functional genomics (in any organisms) is desirable. The initial appointment is for one year but may be extended for at least 2 years upon mutual agreement. The position is available immediately, fully funded and open to citizens from any country.

UT Arlington is a fast-growing, comprehensive university in the University of Texas System and has recently established an exciting and interactive group of genome biologists. See: http://biology.uta.edu/genome_group/ The university is located in the Dallas-Fort Worth metroplex, which features all the amenities of a large metropolitan area with the added advantage of a low cost of living.

To apply send a cover letter detailing previous experience and your specific interest in the position, curriculum vitae and the names and contact information of three references. Direct all inquiries and applications to cedric@uta.edu

Cedric Feschotte, Ph.D Associate Professor Department of Biology University of Texas, Arlington

cedric@uta.edu

UWashington InvertebrateTaxonomy

University of Washington and Alaska Fisheries Science Center, Seattle, Washington: Postdoctoral Position in Invertebrate Taxonomy

The University of Washington and Resource Assessment and Conservation Engineering (RACE) Division of NOAAs Alaska Fisheries Science Center, both based in Seattle, Washington, are looking for a broad-based marine invertebrate taxonomist to identify and conduct research on the subtidal marine macroinvertebrates of Alaska.

The RACE Division conducts bottom-trawl surveys of the subtidal continental shelf and upper slope of Alaskan waters. The Bering Sea shelf south of the Bering Strait is surveyed annually and the upper slope is surveyed biennially. The Gulf of Alaska and Aleutian Islands are also surveyed biennially, alternating regions every year. Benthic invertebrates comprise a large proportion of the catch, especially on the Bering Sea shelf and in the Aleutian Islands, presenting significant challenges for field identification. The postdoctoral appointee will serve an important role in increasing our understanding of the diversity of invertebrate species obtained in the surveys, enhancing the identification skills of field fisheries biologists, and providing significant specimens to the scientific community through the collection and identification of specimens serving as vouchers for catch records.

As a primary requirement, the postdoctoral appointee will serve as lead author of an annotated checklist of the marine macroinvertebrates of Alaska. The appointee will also provide an annual training session for field biologists deploying to sea, and will be expected to participate in at least one, annual, three-week leg of a bottom-trawl survey, with the primary responsibility of identifying invertebrates and collecting significant voucher specimens. The appointee will be the lead taxonomist in processing benthic marine macroinvertebrates collected as vouchers for catch records of survey operations.

The position is funded for one year, but may be renewed for two additional years based on satisfactory performance and available funds.

The qualified applicant will have completed an earned doctorate in biology or a related discipline by 1 July 2010. The successful candidate will have significant experience in the taxonomy of marine invertebrates, and will be familiar with one or more components of the eastern North Pacific marine invertebrate fauna. Experience at sea, curatorial experience, and taxonomic publications are preferred.

For additional information on the position, contact James W. Orr (James.Orr@noaa.gov) or Ted Pietsch (twp@uw.edu). To apply, send a letter of application with CV, by hard copy or email to either contact, and arrange to have three letters of recommendation sent to the following address:

Dr. Theodore W. Pietsch School of Aquatic and Fishery Sciences University of Washington Campus Box 355020 Seattle, Washington 98195

James Orr <James.Orr@noaa.gov>

UWesternSydney InsectAdaptations

The Centre for Plants and the Environment is seeking to appoint two energetic Postdoctoral Research Fellows with strong track records to initiate and conduct research projects that complement research currently being undertaken within one or more of the Centre for Plants and the Environment research themes (Climate Change, Ecological Systems and Biodiversity, and Sustainable Plant Production).

Applicants will be expected to submit a research proposal for a three year project that has been planned in conjunction with one or more core members of the Centre for Plants and the Environment www.uws.edu.au/cpe

Australia's natural, agricultural and forest ecosystems are under increasing pressure from accelerating climate change and a growing population. The Centre for Plants and the Environment at the University of Western Sydney is providing pivotal information for the sustainable management of these ecosystems by advancing basic and applied research in a diverse range of disciplines including soil microbiology, entomology, plant biology, and ecology from cells to ecosystems.

Remuneration Package: Academic Level A $78,903 to $84,467 p.a. (comprising Salary $66,674 to $71,376 p.a., 17% Superannuation and Leave Loading)

Position Information: https://uws.nga.net.au/cp/ (position ref 440/10; Closing Date: 15 June 2010)

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

Interested researchers with a research focus on Insect Adaptations to Plants/Insect Symbiosis/Applied Insect Symbiosis please contact Dr Markus Riegler (m.riegler@uws.edu.au) in order to discuss applications. My research interests are insect symbioses, their contribution to insect adaptations to plants in changing environments, as well as their application in biological and biotechnological control. Ongoing research projects on symbiotic interactions of insects expand from molecular, species and community interactions, and their evolution. More information is available on www.uws.edu.au/cpemarkusriegler

Dr Markus Riegler Centre for Plants and the Environment School of Natural Sciences University of Western Sydney Locked Bag 1797 Penrith South DC NSW 1797 Australia email: m.riegler@uws.edu.au office: +61-(0)2-4570 1229 fax: +61-(0)2-4570 1314

www.uws.edu.au/cpemarkusriegler "be part of symbiosis research"

M.Riegler@uws.edu.au

UWisconsinMilwaukee EcologicalGenetics

Postdoctoral Position: Ecological Genetics of Invasive Species.

A postdoctoral position in ecological genetics is available at the University of Wisconsin-Milwaukee. The successful candidate will work on a collaborative project examining genetic structure of an invasive plant in its native and introduced ranges in the lab of Drs. Sara Hoot, Gretchen Meyer and Mai Phillips. Using existing plant collections, the postdoctoral associate will assist in the following projects: 1) develop molecular markers to investigate genetic variation of /Solidago gigantea/ in its native range (US) and introduced range (Europe), 2) explore relationships among the genetic data and previously-collected datasets on secondary chemistry, susceptibility to herbivory, and growth and reproductive characters of the same plants, and 3) develop a molecular phylogeny of the /Solidago canadensis/ complex (including the species most closely related to /S. gigantea/).

A Ph.D. and a strong background in ecological genetics, systematics, or evolution is required. Experience extracting and amplifying DNA from plant tissue is preferred, and interest or experience with genetics of invasive plants is desirable. The University of Wisconsin-Milwaukee has a strong research group in ecology and evolution (http://www4.uwm.edu/letsci/biologicalsciences/grad/eeb/index.cfm) and Milwaukee is a vibrant city offering many cultural and recreational opportunities (http://www4.uwm.edu/visitors/amazing_milwaukee.cfm).

We offer a competitive salary and full benefits. The position is for one year with an opportunity to contribute to grant-writing for further funding. Start date will be between July - Aug 2010. Review of applications will begin June 10 and continue until position is filled. To apply, send letter of interest highlighting your relevant experience and interests, a complete CV, and contact information for 3 referees to Gretchen Meyer (gmeyer@uwm.edu or by mail to UWM Field Station, 3095 Blue Goose Rd, Saukville WI 53080).

gmeyer@uwm.edu

Xishuangbanna TropicalGarden Biodiversity

The Ecological Evolution group based in the Xishuangbanna Tropical Botanical Garden (XTBG - part of the Chinese Academy Of Sciences) invites applications for a bioinformatics postdoctoral fellow. The Ecological Evolution Group promotes basic and conservation related research in Asian tropical forests. Our group members work on a wide range of topics including, comparative genomics, phylogeography, remote sensing and community ecology. We are now starting a new initiative on the genomics of tropical biodiversity.

The candidate should have a Ph.D. and experience in evolutionary genomics, computational biology, bioinformatics, biophysics, biochemistry, computer science, or related disciplines. Programming skills and experience with Illumina short-read genomic data are desirable.

Candidates with excellent programming skills but no prior biological research experience are also encouraged to apply. The candidate would be responsible for the analysis of genomic data from numerous species of tropical forest trees. We are actively developing novel analytical approaches for comparative genomics and phylogenomics. The candidate would participate in international multidisciplinary collaborative projects. Over the next few years, we will be organizing a series of international workshops and working groups on tropical genomics, starting in April 2011 with a working group focused on fig (Ficus) genomics.

The 2-year fellowship includes a research package of 200,000 RMB (ca. 30,000 USD). The annual salary is 60,000 RMB, equivalent to a salary of 32,000 USD based on cost of living. Additional benefits include free housing, utilities, and week-day lunches. All travel/visa costs are covered. Additional salary and research bonuses can be obtained by publishing in ISI indexed journals. The candidate will live in a tropical botanical garden in a rural area close to the Chinese-Laotian border, thus a taste for adventure, natural beauty, and unique cultural experiences is helpful. Despite the remote location, XTBG is an established and well-supported international research institute with strong, reliable connectivity to necessary computing and internet resources. For more information about XTBG and our research group visit www.ecologicalevolution.org and en.xtbg.ac.cn.

Interested candidates should submit a CV and contact information for at least two references to Professor Chuck Cannon chuck <at> xtbg.ac.cn.

www.ecologicalevolution.org Charles Cannon, Ph.D. $B[I?NBn(B Professor of Ecological Evolution Chinese Academy of Sciences Xishuangbanna Tropical Botanic Garden 666303 Yunnan P.R. China

tel +86.691.8717187 (Banna office) tel: +86.871.5160155 (Kunming office) fax +86.691.8715070

chuck.cannon@gmail.com

Zurich AngiospermRadiations

Switzerland, Zurich: Ph.D. and Post-Doctoral Positions in Angiosperm Radiations

The goal of the interdisciplinary project “Cenozoic Radiations” is to test the hypothesis that the modern Angiosperm diversity has been assembled through a series of adaptive radiations during the Cenozoic, resulting from the interaction between evolving plant functional traits and environmental change. The project will link recent advances in building and analysing huge phylogenetic trees, with an increased understanding of plant functional traits, and substantial progress in documenting Cenozoic Angiosperm fossils. The project is based at the Institute of Systematic Botany of the University of Zurich, with close collaborations with researchers in Switzerland (Nicolas Salamin, Colin Hughes), Germany (Volker Mosbrugger, Dieter Uhl), the US (Peter Wilf, Kevin Nixon, Maria Gandolfo), Mexico (Susana Magallon), Australia (Greg Jordan) and South Africa (William Bond). Funding comes from the Swiss National Fund for Science (SNF).

There are three positions, each with funding for three years:

PhD / Postdoc in building and analysing the Angiosperm phylogenetic tree. This position will focus on identifying significant shifts in the Angiosperm diversification rate during the Cenozoic by mapping species richness over a large, dated Angiosperm phylogeny. This involves building the tree, rate correcting and age-calibrating it, and calculating the diversification rate shifts on the tree.

PhD / Postdoc in plant functional traits (PFT’s). This researcher will identify potential important plant functional traits, and interpret the evolution of these traits in the context of the Angiosperm phylogeny. Correlations between global and local environmental changes and shifts in the diversification rates can be used to evaluate the importance of the PFT’s in the diversification of particular clades.

PhD / Postdoc in Cenozoic Angiosperm palaeobotany. This will link shifts in the diversification rates and in the PFT’s to fossil sites, by placing the nearest living relatives of the fossils on the Angiosperm phylogenetic tree. This places the radiations in a spatial context, as well as corroborating the temporal context.

For further information, contact Peter Linder (Peter.linder@systbot.uzh.ch).

Applications MUST be received no later than Wednesday, 30 June 2010. Interviews to be held either middle July or middle August, with a start date in November or December 2010.

To apply, send the following materials, as separate PDF files, to Peter Linder (Peter.linder@systbot.uzh.ch):

1. PDF of cover letter, indicating –position applied for –your career goals –your research interests in context

of the Cenozoic Radiations project –a detail of how the previous experience and skills shown in your CV prepare you specifically for the position for which you are applying

2. PDF of CV, complete, showing contact information, title of thesis and dissertation, date, universities, research experience, notable skills, advanced courses, publication list, posters and talks presented, awards, service, etc. If your Masters / PhD is not yet completed, please indicate by when you expect to graduate.

3. PDF of the abstract of your Masters thesis or Ph.D. dissertation research. If your Masters / PhD is not yet completed, please provide a summary.

4. PDF of university report of coursework, showing grades and degrees earned (must be in English)

5. PDF's of published papers and papers in-press.

Peter Linder Institute for Systematic Botany Zollikerstrasse 107 CH 8008 Zürich Switzerland Ph: +41 (0)44 634 8410 Fax: +41 (0)44 634 8403

Peter Linder <peter.linder@systbot.uzh.ch>

WorkshopsCourses

Austria IST EvolutionaryGenetics Sep28-Oct1

Introduction to Evolutionary Genetics 28 September - 1 October 2010

Evolutionary genetics is central to a wide range of biological questions, and is expanding dramatically with the flood of DNA sequence data. This intensive four-day course will give a thorough introduction to the subject, showing its broad scope, and teaching a variety of techniques that can be used to model the evolutionary process, and that can be applied to diverse problems.

The course is aimed at graduate students with diverse backgrounds - both in evolutionary biology, and coming in from different fields. Teaching will be a combination of lectures, discussion groups, and worked examples; simulation software will be provided.

For details, see www.ist.ac.at/evogen-workshop Faculty

Nick Barton, Jon Bollback, Sylvia Cremer (IST Austria) Reinhard Bürger, Joachim Hermisson, Ines Hellman (U Vienna) Magnus Nordborg (Gregor Mendel Institute, Vienna) Christian Schlötterer (Vetmeduni Vienna) Daniel Kronauer (Harvard U) Daven Presgraves (U Rochester) Michael Turelli (U California, Davis)

This workshop is a joint initiative between IST Austria and the Vienna Graduate School of Population Genetics. For more information, see www.popgen-vienna.at/ and www.univie.ac.at/evolvienna/

Dates

28 September - 1 October 2010. The course runs for four full days, with students arriving for a welcome reception on the evening of Monday 27 September.

Costs The course fee is euro 330,-. This includes lodging on the IST campus, meals, course material, and social events.

Location The course will be held at the campus of IST Austria, which is just outside Vienna. Accommodation will be in the Guesthouse on campus.

Registration Application deadline is May 16, 2010. Successful applicants will be notified by end of May 2010

n.barton@ed.ac.uk

Bologna HumanEvolution May17-19

Dear all,

You can still register for the Course in Genomic and Cultural Evolution of Humans< http://-192.168.253.20/course/course-genomic-and-cultural-evolution-humans > (link). As of today no more accommodation facilities are available. You can attend the course (only coffee breaks and lunch provided) by paying a fee of 300 euros + Vat 20 % (if you have to pay VAT - see note below).

The course will take place in Bologna (Italy) at the EuroMediterranean University Centre of Ronzano on May 17-19, 2010. The course will provide detailed information on the tools useful for the study of human genomic evolution. High-throughput and large scale genotyping, using both microarrays and massive sequencing to survey both SNP and CNV, will bring increasing power to studies of genomic diversity in the near future. Bioinformatics is an essential tool in studies of human genomic evolution. Mornig lectures and afternoon workshops will show how bioinformatic tools can be used to analyze SNP and CNV diversity within an evolutionary framework. The course will be of interest to researchers, graduate students and post-docs interested in genome biology and human evolution. It will also offer an exposure to the "state of the art" to investigators contemplating studies or the utilization of tools in this field.

Course Directors: D. Luiselli (Bologna, Italy), D. Pettener (Bologna, Italy), M. Rocchi (Bari, Italy), R. Stanyon (Florence, Italy)

Faculty Members: G. Barbujani (Ferrara, Italy), F. Calafell (Barcelona, Spain), L.L. Cavalli Sforza (Milan, Italy), C. Guardiano (Reggio Emilia, Italy), J. Krause (Leipzig, Germany), P. Longobardi (Trieste, Italy), D. Pettener (Bologna, Italy), A. Qasim (Cambridge, UK), M. Rocchi (Bari, Italy), R. Stanyon (Florence, Italy), M. Stoneking (Leipzig, Germany),C. Tyler-Smith (Cambridge, UK), S. Wells (Cornell, USA).

For further information regarding VAT and other questions please write to: serena.paterlini@eurogene.org * If YOU ARE ITALIAN AND WORK FOR A PUBLIC INSTITUTION (PhD, students, Researchrs, Post Doc, ...) you are exempted from the payment of VAT. * If YOU WORK IN A FOREIGN COUNTRY WITHIN EC and the bill is addressed to your Institution/Company completing the field VAT Number during the registration to the Course, you are exempted from the payment of VAT . * If YOU WORK IN A FOREIGN COUNTRY OUTSIDE EC and the bill is addressed to your Institution/Company you are exempted from the payment of VAT

If the bill is addressed to yourself you are not exempted from Vat payment.

For further info visit EGF website (www.eurogene.org) or write to serena.paterlini@eurogene.org

Thank you in advance, Serena Paterlini

Useful links: Course Program< http://-192.168.253.20/course/course-genomic-and-cultural-evolution-humans > EGF Website< http://-www.eurogene.org/course/course-mitochondrial-metabolism-and-cancer >

Serena Paterlini Training and EU Projects European Genetics Foundation Via di Gaibola, 16 40138 Bologna tel:0039051-2088414 fax:0039-0515870611

"European Genetics Foundation [serena.paterlini@eurogene.org]" <serena.paterlini@eurogene.org>

Edinburgh PopulationSequencing Aug31

2nd UK RAD Sequencing Meeting 31st August 2010, 9:00 am - 5:00 pm Edinburgh University http://-www.nesc.ac.uk/esi/events/1090/ Dear all,

The 2nd UK meeting on RAD (Restriction-site Associated DNA) Sequencing, a new method for SNP discovery and genetic mapping by sequencing thousands of markers in multiple individuals using next generation DNA sequencing, will be held in Edinburgh on August 31st.

The meeting is intended to bring together UK and European researchers who are implementing or are interested in RAD sequencing. There is no charge for attendance.

Dr Paul Hohenlohe from the University of Oregon, coauthor on a recent major paper on RAD Sequencing (http://dx.doi.org/10.1371/journal.pgen.1000862), will be attending the meeting to talk about his work, using RAD Sequencing to study population genomics of threespine stickleback.

The meeting will cover the use of RAD Sequencing for genotyping, linkage mapping, genome scaffolding and population genomics. A range of ongoing projects will be presented and there will be opportunity to discuss the wet lab and bioinformatics aspects of the method.

If you would like to attend, please register online at http://www.nesc.ac.uk/esi/events/1090/. If you have any queries, please contact me at john.davey@ed.ac.uk. Please feel free to forward this message on to anyone you think may be interested.

Best wishes, John Davey

Background to RAD Sequencing method:

By cutting genomic DNA with a restriction enzyme, it is possible to sequence thousands of markers with high coverage in a single individual using next generation sequencing. By adding a short DNA identifying sequence to the fragments for one individual, it is possible to pool multiple individuals together, sequence them all on one lane of an Illumina Genome Analyzer run, and separate out the sequences for each individual bioinformatically by examining the identifiers.

Because each fragment can be sequenced with high coverage, and the fragments from a particular restriction enzyme site can be easily aligned, it is easy to call SNPs in these sequences. If a reference genome is present, it is also easy to identify recombination regions and so produce genetic maps for the sequenced individuals.

Dr. John Davey Bioinformatics Researcher and Support Provider Institute of Evolutionary Biology University of Edinburgh

Post : Room 354 Ashworth Laboratories King's Buildings West Mains Road Edinburgh EH9 3JT UK Email : john.davey@ed.ac.uk Phone : +44 (0) 131 650 7403 Web : genepool.bio.ed.ac.uk www.nematodes.org John Davey <john.davey@ed.ac.uk>

Perth SexualSelection Oct2

2 October 2010, directly after the ISBE-meeting in Perth, Western Australia, a Post-Congress Symposium will be arranged on the theme "How Can Sexual Selection be Measured?"

Measuring sexual selection is not straightforward and since this is still an unresolved question, with no general consensus, we think this will be a highly stimulating subject for a post-ISBE symposium.

Our aim is to create an open minded discussion on this subject. We hope to achieve this by talks and participants that represent a mix of theoretical and empirical approaches. Eight short talks will be given by Particia Gowaty, Stephen Hubbel, John Hunt, Hope Klug, Aline Magdalena Lee, Patrick Lorch, Michael Wade and Michael Webster. In addition, we will devote a fair amount of time to discussion, both in smaller groups and in a joint discussion.

Registration: All participants of the symposium have to register for the main meeting (http://isbeperth2010.com/index.html). As part of the registration, you'll be asked to tick a box for a Post Congress Symposium: Please tick ours! :-) N.B. The deadline for Early Bird registration is 28 May 2010.

We look forward to see you in Perth!

Lotta Kvarnemo (lotta.kvarnemo@zool.gu.se), Adam Jones (agjones@tamu.edu) & Kai Lindström (kai.lindstrom@abo.fi)

lotta.kvarnemo@zool.gu.se

Poznan Poland BioinformaticsSummerSchool Jul5-10

Dear colleagues,

We are happy to announce the 8th edition of Poznan Summer School of Bioinformatics. The course will take place on 5th â 10th July 2010 in Poznan (Poland). The workshop covers the most interesting and up-to-date subjects of bioinformatics. It is a great opportunity to improve your skills and knowledge in this dynamically developing field.

Details can be found at the workshop website: http://lemur.amu.edu.pl/bioinfo Please forward this announcement to anyone who might be interested.

Best regards,

Organizing Committee

Contact: genomics@amu.edu.pl

Wojciech MakaÅowski <wojmak@uni-muenster.de>

Sevilla PopulationGeneticsClimateChange Sep20-Oct1

The Estacion Biologica de Donana (Sevilla, Spain) invites applications for an international course entitled -Ecological Consequences of Climate Changes: Integrating Research Approaches' that will take place from 20 September to 1 October 2010 in the heart of the Doñana National Park. The course is dedicated to students at the PhD and Master/advanced Diploma levels who are involved in research related with global change. Its aim is to provide a synthetic overview upon different research perspectives ranging from palaeoecology to population genetics, ecophysiology and bioclimatic modelling. The course will include lectures provided by an international panel of high-profile researchers, exercises using data of the Doñana environmental monitoring programme (http://icts.ebd.csic.es), as well as field trips within the National Park.

Invited teachers:

Miguel Araujo, Museo Nacional de Ciencias Naturales, Madrid, Spain Gary Bortolotti, University of Saskatchewan, Canada Jose S. Carrion, Universidad de Murcia, Spain Miguel Ferrer, Estacion Biologica de Donana, Sevilla, Spain Clive Finlayson, Gibraltar Museum, Gibraltar, UK Arndt Hampe, Estacion Biologica de Donana, Sevilla, Spain Josep Peñuelas, Centre de Recerca Ecologica i Aplicacions Forestals, Barcelona, Spain Fernando Valladares, Centro de Ciencias Medioambientales, Madrid, Spain Katherine Willis, University of Oxford, UK

Local organizers: Juan Jose Negro and Arndt Hampe

The course language will be English. Support from the Gas Natural Chair -Biodiversity Conservation under Climate Change' enables us to waive registration fees and to cover all costs for the transport between Sevilla and Donana National Park, accommodation and meals during the course. Applicants should provide a brief CV (max. two pages) as well as a statement (max. 500 words) about their research interests/current projects and why they would like to attend to the course. Application deadline is 15 June. Please send applications in a single pdf file to Begona Arrizabalaga (bego@ebd.csic.es) and any related questions to Juan Jose Negro (negro@ebd.csic.es).

Arndt Hampe Ramón y Cajal postdoctoral fellow Integrative Ecology Department Estación Biológica de Doñana (CSIC) Av. Américo Vespucio s/n E-41092 Sevilla Spain email: arndt@ebd.csic.es http://ieg.ebd.csic.es/arndthampe/ Tlf: ++34 954 466700 ext. 1451 Fax: ++34 954 621125

arndt@ebd.csic.es

UCopenhagen EvolutionaryGenetic SocialEvolution Jul5-10

Residential Ph.D. course: Evolutionary Genetic Approaches to Study Social Evolution

University of Copenhagen, Denmark, 5-10 July, 2010

Final Announcement

Location: The course will be held at Sømine Station nearby Copenhagen, Denmark.

Aims: To introduce evolutionary genetic theory and empirical approaches to study social evolution. The course will emphasize both traditional and post-genomic evolutionary genetic approaches.

Target group: The course is aimed at PhD students but interested postdocs or MSc students will also be considered as space permits. Class size will be approximately 20 students.

Topics

The course will consist of lectures, readings, and discussion on the following subjects:

*Relation of evolutionary genetic approaches to phenotypic optimality approaches to study social evolution

*Basic concepts in population genetics

*Basic concepts in quantitative genetics

*Maternal effects and parent-offspring coadaptation

*Indirect genetic effects arising from social interactions

*Empirical approaches to estimate indirect genetic effects

*Evolutionary response to selection with indirect genetic effects

*Predicted patterns of sequence variation for genes with social effects; mutation-kin selection balance

*Levels of selection and kin selection theory

*Evolution of societies

*Evolution of interspecific interactions

*Participants will also briefly describe their own research

Teachers

Timothy Linksvayer, Centre for Social Evolution, Department of Biology, U. Copenhagen, Denmark

Michael Wade, Department of Biology, Indiana U., USA

Guest teachers

Piter Bijma, Animal Breeding and Genomics Centre, Wageningen U., The Netherlands

David Queller, Department of Ecology & Evolutionary Biology, Rice U., USA

Joan Strassmann, Department of Ecology & Evolutionary Biology, Rice U., USA

Jacobus Boomsma, Centre for Social Evolution, Dep. Biology, U. Copenhagen, Denmark

Cost: 2600 DKK per participant

ECTS credits: 5

Application and contact: To apply please send a CV by June 10 to Tim Linksvayer (talinksvayer@bio.ku.dk) along with a brief description of:

1. The relevance of the course to your research

2. Your background and relevant experience.

Please contact Tim Linksvayer (talinksvayer@bio.ku.dk) with any questions.

tlinksvayer@gmail.com

UManchester Morphometrics Nov8-Dec17

Dear colleagues

I am pleased to announce this year's morphometrics course from the University of Manchester. This year's course will run in the six weeks from 8 November to 17 December 2010.

The course information can be found on the following we site: http://www.flywings.org.uk/MorphoCourse Course content: * Data acquisition: the kinds of data and the equipment used to collect them. * Definitions of size and shape * Geometric methods to characterise shape from a configuration of landmark points (Procrustes superimposition) * Statistics of variation, scatter plots, basic multivariate statistics * Principal component analysis * Measurement error and outliers * Shape transformations and 'warping' – the thin plate spline * Analysis of outline shapes * Distinguishing between groups (taxonomy, clinical diagnosis, etc.) * Allometry and size correction * Influence of external factors on shape (ecomorphology, dose- response studies) * Symmetric forms and measurement of asymmetry. * Morphometric inferences on developmental processes, morphological integration, modularity * Genetics of shape: analyses of resemblance between relatives, QTL analyses. * Phylogeny: reconstructing the evolution of shape

Practice examples: As far as possible, practical exercises are provided to accompany the course content. These practice exercises consist of data sets and explanations on how to run the respective analyses using the MorphoJ software (http://www.flywings.org.uk/-MorphoJ_page.htm). Participants who already have their own data are encouraged to use those and to discuss them as part of the course. I hope there will be a bit of a 'workshop' feel to the course unit.

Group work: Participants will work in small groups to prepare web presentations of possible morphometric studies (wikis prepared by the groups). This activity stimulates discussion and provides a broad overview of the broad range of questions that can be addressed with morphometric methods.

The fee for the course is GBP 250.00 (I'm afraid it's gone up again from last year – this is out of my control).

All prospective participants need to pre-register for the course. The deadline for this is the *10 September 2010*.

For further details, see the course web page: http:/-/www.flywings.org.uk/MorphoCourse Best wishes, Chris

–

Christian Peter Klingenberg Faculty of Life Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT United Kingdom

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cpk@manchester.ac.uk

UMichigan EvolutionaryEpidemiology Jul12-16

A One week Graduate Summer Seminar on Evolutionary Epidemiology

EPID 788 (1 credit hour) July 12-16 1:30-5 PM at the University of Michigan School of Public Health Course website: http://sites.google.com/site/evepid/ Professor: Randolph Nesse

Overview: New applications of evolutionary theory to medicine are growing and helping to explain apparent paradoxes, such as rapidly increasing rates of breast cancer, increased asthma vulnerability in certain populations and the metabolic syndrome (For details see The Evolution and Medicine Review at http://evmedreview.com). Epidemiologists have begun to apply these principles and ask new questions, such as do genes that vary by latitude explain hypertension, and how might public health interventions for infectious disease be 'evolution-proofed' (see discussion of the American College of Epidemiology 2008 meeting: Dawn of Evolutionary Epidemiology (http://acepidemiology.org/meetings/2008Tuscon/08AMSpeakerHandouts.asp). This course will explore how epidemiologists and other public health workers can make use of these advances in their own work. Applying evolutionary theory can sharpen research questions, raise new possible explanations for observed phenomena and identify new types of exposure and outcome measures. Pre-requisite: No prior training in evolutionary biology is assumed.

Information: http://www.sph.umich.edu/epid/GSS/courses/1week.html Registration: https://www.sph.umich.edu/scr/includes/gss/login.cfm For more information contact Randolph Nesse, M.D. The University of Michigan nesse@umich.edu http://nesse.us nesse@umich.edu

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.